

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 28, 2005, 00:52:17 ; Search time 12680 Seconds
(without alignment)
11662.880 Million cell updates/sec

Title: US-10-790-562-33

Perfect score: 3052

Sequence: 1 cgtgtagtattatcacc.....cgatgaagatacagattgag 3052

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*

1: gb_da:*

2: gb_hhg:*

3: gb_in:*

4: gb_cm:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sg:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3052	100.0	11570	14 AD5001	X02996 Adenovirus
2	3052	100.0	32802	6 CQ854906	CQ854906 Sequence
3	3052	100.0	33699	6 AX084506	AX084506 Sequence
4	3052	100.0	34448	6 AX084507	AX084507 Sequence
5	3052	100.0	35934	14 AY339865	AY339865 Human ade
6	3052	100.0	35935	6 AR091533	AR091533 Sequence
7	3052	100.0	35935	6 AR102226	AR102226 Sequence
8	3052	100.0	35935	6 AR116313	AR116313 Sequence
9	3052	100.0	35935	6 CQ854907	CQ854907 Sequence
10	3052	100.0	35935	6 AR230724	AR230724 Sequence
11	3052	100.0	35935	6 AX451988	AX451988 Sequence
12	3052	100.0	35935	6 AX683770	AX683770 Sequence
13	3052	100.0	35935	14 ADRCOMGEN	M73360 Mastadenovir
14	3052	100.0	35978	6 AR403723	AR403723 Sequence
15	3006.8	98.5	7090	6 AR310582	AR310582 Sequence
16	3006.8	98.5	7090	6 AX150263	AX150263 Sequence
17	2994	98.1	3408	6 AX770195	AX770195 Sequence
18	2959.4	97.0	11152	6 BD268208	BD268208 Adenoviru
19	2959.4	97.0	11152	6 AX356041	AX356041 Sequence

20	2959.4	97.0	11152	6 BD021940	BD021940 Packaging
21	2959.4	97.0	14455	6 BD268211	BD268211 Adenoviru
22	2959.4	97.0	14455	6 AX356044	AX356044 Sequence
23	2959.4	97.0	14455	6 BD021943	BD021943 Packaging
24	2959	97.0	7607	6 BD268237	BD268237 Adenoviru
25	2948	96.6	35937	6 AX770200	AX770200 Sequence
26	2948	96.6	35937	14 ADRCG	J01917 Adenovirus
27	2903.6	95.1	36001	14 AF534906	AF534906 Human ade
28	2822	92.5	33592	6 AX084504	AX084504 Sequence
29	2822	92.5	33598	6 AX084517	AX084517 Sequence
30	2822	92.5	34341	6 AX084505	AX084505 Sequence
31	2822	92.5	34737	6 AX084518	AX084518 Sequence
32	2822	92.5	35724	6 AX084516	AX084516 Sequence
33	2822	92.5	35871	6 AR403724	AR403724 Sequence
34	2822	92.5	36114	6 AX084519	AX084519 Sequence
35	2161	70.8	34303	6 AR091536	AR091536 Sequence
36	2161	70.8	34303	6 AR102229	AR102229 Sequence
37	2161	70.8	34303	6 AR230727	AR230727 Sequence
38	2043	66.9	31976	6 CQ854905	CQ854905 Sequence
39	2041.4	66.9	31976	6 CQ854904	CQ854904 Sequence
40	1432.4	46.9	6575	6 AX449148	AX449148 Sequence
41	1229	40.3	1802	6 AX817767	AX817767 Sequence
42	1229	40.3	1802	6 AX838364	AX838364 Sequence
43	1066.8	35.0	1356	6 I32051	I32051 Sequence 1
44	1066.8	35.0	1356	6 I38383	I38383 Sequence 1
45	1066.8	35.0	1356	6 I43358	I43358 Sequence 1

ALIGNMENTS

RESULT 1	AD5001	11570 bp	DNA	linear	VRL 09-SEP-2004
LOCUS	AD5001	Adenovirus type 5 left 32% of the genome (coordinates 0% to 32.39% as measured by <ad2>).			
DEFINITION	AD5001	Adenovirus type 5 left 32% of the genome (coordinates 0% to 32.39% as measured by <ad2>).			
ACCESSION	X02996	J01967	J01968	J01970	J01971
VERSION	J01978	J01979	K00515	V00025	V00026
KEYWORDS	X02996.1	GI:58484			
		alternate splicing; DNA polymerase; overlapping genes; polymerase; RNA polymerase III; terminal protein; terminal repeat; transfer RNA.			
SOURCE	Human adenovirus type 5				
ORGANISM	Human adenovirus type 5				
REFERENCE	1 (bases 1 to 194)				
AUTHORS	Steenbergh, P.H., Maat, J., van Ormondt, H. and Suseenbach, J.S.				
TITLE	The nucleotide sequence at the termini of adenovirus type 5 DNA				
JOURNAL	Nucleic Acids Res. 4 (12), 4371-4389 (1977)				
MEDLINE	78093872				
PUBMED	600799				
REFERENCE	2 (bases 1 to 1574)				
AUTHORS	Van Ormondt, H., Maat, J., De Waard, A. and Van der Eb, A.J.				
TITLE	The nucleotide sequence of the transforming HpaI-E fragment of adenovirus type 5 DNA				
JOURNAL	Gene 4 (4), 309-328 (1978)				
MEDLINE	79128735				
PUBMED	744489				
REFERENCE	3 (bases 1575 to 2809)				
AUTHORS	Maat, J. and Van Ormondt, H.				
TITLE	The nucleotide sequence of the transforming HindIII-G fragment of adenovirus type 5 DNA. The region between map positions 4.5 (HpaI site) and 8.0 (HindIII site)				
JOURNAL	Gene 6 (1), 75-90 (1979)				
MEDLINE	80004833				
PUBMED	478299				
REFERENCE	4				
AUTHORS	Petricaudet, M., Akusjärvi, G., Vartanen, A. and Pettersson, U.				
TITLE	Structure of two spliced mRNAs from the transforming region of human subgroup C adenoviruses				
JOURNAL	Nature 281 (5733), 694-696 (1979)				
MEDLINE	81012104				
PUBMED	551290				

REFERENCE 5 (bases 10524 to 10696)
AUTHORS Thimmappa,B., Jones,N. and Shenk,T.
TITLE A mutation which alters initiation of transcription by RNA
JOURNAL polymerase III on the Ad5 chromosome
MEDLINE Cell 18 (4), 947-954 (1979)
PUBMED 80090080
REFERENCE 519773
AUTHORS 6 (bases 1 to 6246)
TITLE Broker,T.R.
JOURNAL Appendix d: nucleotide sequences, transcription and translation
MEDLINE analyses, and restriction endonuclease cleavage maps of group-c
PUBMED human adenoviruses
(1n) Toozee,J. (Ed.) ;
JOURNAL DNA TUMOR VIRUSES: 937-1002;
AUTHORS 7 (bases 2804 to 4125)
TITLE Cold Spring Harbor Laboratory (1980)
JOURNAL Mat,J., van Beveren,C.P. and van Ormondt,H.
MEDLINE The nucleotide sequence of adenovirus type 5 early region E1: the
PUBMED region between map positions 8.0 (HindIII site) and 11.8 (SmaI
Gene 10 (1), 27-38 (1980)
JOURNAL 81005097
MEDLINE 6250944
REFERENCE 8
AUTHORS Pericaudet,M., le Moulec,J.M. and Pettersson,U.
TITLE Predicted structure of two adenovirus tumor antigens
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 77 (7), 3778-3782 (1980)
MEDLINE 81054654
PUBMED 6253988
REFERENCE 9 (bases 1 to 4125)
AUTHORS van Ormondt,H., Maat,J. and van Beveren,C.P.
TITLE The nucleotide sequence of the transforming early region E1 of
JOURNAL adenovirus type 5 DNA
MEDLINE Gene 11 (3-4), 299-309 (1980)
PUBMED 6260576
REFERENCE 10 (bases 10555 to 10733)
AUTHORS Fowlkes,D.M. and Shenk,T.
TITLE Transcriptional control regions of the adenovirus VAI RNA gene
JOURNAL Cell 22 (2 Pt 2), 405-413 (1980)
MEDLINE 81088343
PUBMED 7448868
REFERENCE 11 (bases 1653 to 4043)
AUTHORS Bos,J.L., Polder,L.J., Bernards,R., Schrier,P.I., van den
TITLE Elben,P.J., van der Eb,A.J. and van Ormondt,H.
JOURNAL The 2.2 kb E1b mRNA of human Ad12 and Ad5 codes for two tumor
MEDLINE antigens starting at different AUG triplets
PUBMED Cell 27 (1 Pt 2), 121-131 (1981)
REFERENCE 12 (bases 4001 to 6246)
AUTHORS van Beveren,C.P., Maat,J., Dekker,B.M. and van Ormondt,H.
TITLE The nucleotide sequence of the gene for protein IVa2 and of the 5'
JOURNAL leader segment of the major late mRNAs for adenovirus type 5
MEDLINE Gene 16 (1-3), 179-189 (1981)
PUBMED 82211779
REFERENCE 13 (bases 325 to 604)
AUTHORS Heering,P. and Shenk,T.
TITLE Functional analysis of the nucleotide sequence surrounding the cap
JOURNAL site for adenovirus type 5 region E1a messenger RNAs
MEDLINE J. Mol. Biol. 167 (4), 809-822 (1983)
PUBMED 83268691
REFERENCE 6876165
AUTHORS deletion mutants
TITLE 14 (bases 1 to 66)
JOURNAL Negata,K., Guggenheimer,R.A. and Hurwitz,J.
MEDLINE Specific binding of a cellular DNA replication protein to the
PUBMED origin of replication of adenovirus DNA
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 80 (20), 6177-6181 (1983)
MEDLINE 84016017
PUBMED 6336326
REFERENCE 15 (bases 6242 to 11570)

AUTHORS Dekker,B.M. and van Ormondt,H.
TITLE The nucleotide sequence of fragment HindIII-C of human adenovirus
JOURNAL type 5 DNA (map positions 17.1-31.7)
MEDLINE Gene 27 (1), 115-120 (1984)
PUBMED 84183604
REFERENCE 6325298
AUTHORS 16
TITLE Downey,J.F., Ewlesgh,C.M., Branton,P.E. and Bayley,S.T.
JOURNAL Peptide maps and N-terminal sequences of polypeptides from early
MEDLINE region 1A of human adenovirus 5
PUBMED J. Virol. 50 (1), 30-37 (1984)
REMARK 84138826
COMMENT 6699947
sites; cds start for E1a proteins
sites; splice sites in E1a 13S mRNA
sites; splice sites and termini for E1b mRNAs
Notes on the presentation of ADENO in the EMBL data library: The
genetic map of Adeno is customarily presented from left to right,
the 0% position being left and the 100% position being right. The
two strands of Adeno are normally represented like this: r-strand:
3'-----5'
1-strand: 5'-----3'
0% 100%
This often causes confusion because the generally accepted way to
represent DNA molecules is:
5'-----3'
3'-----5'
Here Adeno virus sequences are always given in 5' to 3' direction
and the sequence of the 1-strand is displayed irrespective of the
direction the viral transcription takes.
This sequence corresponds to bases 1 to 11560 of <ad2>, which serve
as some basis for the annotation of sites. The differences between
<ad2> and <ad5> are too many to report herein, however a printout
of those is available upon request from genbank. The map
coordinates in the sites presume 360 bases per map unit. Although
there are approximately 115 sequence differences between the two
strains over this region, no site difference exceeds 0.02% by this
calculation.
the sequence represents the early mra transcripts e1a and e1b and
the intermediate mra transcript ix, all of which are transcribed
rightwardly off the r-strand; the Iva2 and e2b mrae which are
transcribed leftwardly off the 1-strand (indicated by '(c)' and
'comp strand' below); and the 5' end of the 28 kb major late mra.
the cap sites and possible promoter sequences for these are
summarized in the following table:
mra cap site possible promoter region -----
----- e1a 499
tattataa at bases 468-475 [6] e1b 3582
tattataa at bases 1672-1678[6] ix 5838 +/- 2 (c)
tattataa at bases 3551-3557 [6] Iva2
tattataa at bases 5979-5974 on the comp strand (10)
major 6049 tattataa at bases 6018-6024 [10] as
with ad2, not all the transcripts from this region have been
characterized at the sequence level. the nine proteins given in
features table below are not the only possible gene products (see
the main adenovirus 2 entry).
large amounts of small mras are produced from the vai and vaii
genes late in development for unknown reasons. [5] and [6]
demonstrate that vai gene activity influences vaii expression; that
the 5' flank affects the start site of the rna but that an
intragenic promoter (bases 10626 to 10690 below) determines whether
the rna is actually produced; and that there is striking similarity
between this rna and trna.
Location/Qualifiers
1. 11570
/organism="Human adenovirus type 5"
/mol_type="genomic DNA"
/db_xref="taxon:28285"
499. 1632
/note="primary transcript of E1a region"
join(499, 1112,1229, 1632)
/note="mRNA 1 (part 1)"

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mRNA
CD8
      join(499..974,1229..1632)
      /note="mRNA 2 (part 1)"
      /join(560..1112,1229..1545)
      /note="unnamed protein product; B1a protein from 13s mrna
      (32k,regulation and transformation)"
      /codon_start=1
      /protein_id="CABA0663.1"
      /db_xref="GI:4584382"
      /db_xref="GOA:P03255"
      /translation="MRHICGHVITEEMASLIDQIEVIADNLPPSPHPEPTLH
      ELVDLDTABDEBAVSQIPDSVMLAVOEGDILTFPAPSGSPHLSRQEDP
      EQALGVSMPNLYPVIYDILNCHGASPPDDBEBEERVDVYEHGRCRCHN
      RRTNGDDIMCSLCYMRTCGMFVTSVSEPEPEPEPEPARPRKMAPIILRPT

Query Match      100.0%; Score 3052; DB 14; Length 11570;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGTGTAGTATTTTATACCCGGTAGTTCTCAAGAGCCACTCTTGATGCCAGACT 60
Db      459 CGGTATGATTTATATACCCGGTAGTTCTCAAGAGCCACTCTTGATGCCAGACT 518
QY      61 AGAGTTTCTCCCGACCGGCTCCGACACCGGGACTGAATAAGACATATTATCTGCC 120
Db      519 AGAGTTTCTCTCCGACCGGCTCCGACACCGGGACTGAATAAGACATATTATCTGCC 578
QY      121 ACCGAGGTGTTATTAACGAAAGAAATGGCCGCACTTTTGGACCACTGATCGAAGG 180
Db      579 ACCGAGGTGTTATTAACGAAAGAAATGGCCGCACTTTTGGACCACTGATCGAAGG 638
QY      181 TACTGGCTGATATCTTCCACTCTCTTACCCATTGTAACCACTTACCTTACGAACTGT 240
Db      639 TACTGGCTGATATCTTCCACTCTCTTACCCATTGTAACCACTTACCTTACGAACTGT 698
QY      241 ATGATTTAGACGTACGGGCGCCGGAAGATCCCAAGAGGAGGGTTTCGAGATTTTTC 300
Db      699 ATGATTTAGACGTACGGGCGCCGGAAGATCCCAAGAGGAGGGTTTCGAGATTTTTC 758
QY      301 CCGACTCTGATATGTTGGCGGTGACGAAAGGATTTGACTTACTCTTCCGCGGGGC 360
Db      759 CCGACTCTGATATGTTGGCGGTGACGAAAGGATTTGACTTACTCTTCCGCGGGGC 818
QY      361 CCGGTTCTCCGAGACCGGCTTACCTTTCGCGGACCCCGAGACCCGAGACGAGCTT 420
Db      819 CCGGTTCTCCGAGACCGGCTTACCTTTCGCGGACCCCGAGACCCGAGACGAGCTT 878
QY      421 TGGGTCGGGTTTCTATGCAAACTTGTACCGGAGGTGATGATCTTACCTGCCAGAG 480
Db      879 TGGGTCGGGTTTCTATGCAAACTTGTACCGGAGGTGATGATCTTACCTGCCAGAG 938
QY      481 CTGGCTTTCCACCCAGTACGACGAGATGAAGAGGTGAGAGATTGTGTAGATTATG 540
Db      939 CTGGCTTTCCACCCAGTACGACGAGATGAAGAGGTGAGAGATTGTGTAGATTATG 998
QY      541 TGGAGCACCCCGGCGACGTTGCAAGTCTTGTCAATTACCCGAGGAATACGGGGAGCC 600
Db      999 TGGAGCACCCCGGCGACGTTGCAAGTCTTGTCAATTACCCGAGGAATACGGGGAGCC 1058
QY      601 CAGATATTATGTGTGCTTGTGATATGAGGACCTGGGCACTGTTGTCTACAGTAAGT 660
Db      1059 CAGATATTATGTGTGCTTGTGATATGAGGACCTGGGCACTGTTGTCTACAGTAAGT 1118
QY      661 GAAATATTATGGCAGTGGGTGATAGAGTGTGGTGTGTGTAATTTTTTTTTTAAT 720
Db      1119 GAAATATTATGGCAGTGGGTGATAGAGTGTGGTGTGTGTAATTTTTTTTTTAAT 1178
QY      721 TTTTACAGTTTGTGCTTTAAAGATTTTGTATTGTGATTTTTTAAAGGTCTGTGTC 780
Db      1179 TTTTACAGTTTGTGCTTTAAAGATTTTGTATTGTGATTTTTTAAAGGTCTGTGTC 1238
QY      781 TGAACCTGAGCTTAGCCCGACGAAACGGAGCTTGCAAGACTCCGCGGTCTTAA 840
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Db      1239 TGAACCTGAGCTTAGCCCGACGAAACGGAGCTTGCAAGACTTACCGCGGTCTTAA 1298
QY      841 AATGGCCCTGTATTCCTGAGACGCCGACATCACTGTGTCTTAGAGAAATGCAATAGTAG 900
Db      1299 AATGGCCCTGTATTCCTGAGACGCCGACATCACTGTGTCTTAGAGAAATGCAATAGTAG 1358
QY      901 TACGGAATGCTGATCTCCGCTCTTTTACACACCTTCCAGATTAACCCGGTGTGCC 960
Db      1359 TACGGAATGCTGATCTCCGCTCTTTTACACACCTTCCAGATTAACCCGGTGTGCC 1418
QY      961 GCTGTGCCCCATTAAACAGTTCGCTGAGAGTTGTGTGGCGTGCAGAGCTGTGGAATG 1020
Db      1419 GCTGTGCCCCATTAAACAGTTCGCTGAGAGTTGTGTGGCGTGCAGAGCTGTGGAATG 1478
QY      1021 TATCGAGACTTGTCTTAACGAGCTTGGGCAACCTTTGAGCTTGAGCTGTAACGCCCCAG 1080
Db      1479 TATCGAGACTTGTCTTAACGAGCTTGGGCAACCTTTGAGCTTGAGCTGTAACGCCCCAG 1538
QY      1081 GCCATAAGTGTAAACCTGTGATTTGCTGTGTGTGTAACGCCCTTGTGTGTGTAATAGT 1140
Db      1539 GCCATAAGTGTAAACCTGTGATTTGCTGTGTGTGTAACGCCCTTGTGTGTGTAATAGT 1598
QY      1141 TGATGTAGTTTAAATTAAGGTGAGATTAATGTTTAACTTGCAATGCGGTGTTAAATGGGCG 1200
Db      1599 TGATGTAGTTTAAATTAAGGTGAGATTAATGTTTAACTTGCAATGCGGTGTTAAATGGGCG 1658
QY      1201 GGGGCTTAAAGGTATTAATGCGCGGTGGCTTAATCTTGTTACATCTGACTCATGGA 1260
Db      1659 GGGGCTTAAAGGTATTAATGCGCGGTGGCTTAATCTTGTTACATCTGACTCATGGA 1718
QY      1261 GGCCTGGAGAGTGTGGAAGATTTTCTGCTGTGCGTAACTTGTGGAACAGAGCTCTAA 1320
Db      1719 GGCCTGGAGAGTGTGGAAGATTTTCTGCTGTGCGTAACTTGTGGAACAGAGCTCTAA 1778
QY      1321 CAGTACCTCTTGTTTGAAGGTTTCTGTGGGCGTCAATCCAGGCAAAAGTTAGCTGACAG 1380
Db      1779 CAGTACCTCTTGTTTGAAGGTTTCTGTGGGCGTCAATCCAGGCAAAAGTTAGCTGACAG 1838
QY      1381 AATTAAAGAGATTAACAAGTGGGAATTTGAAGACTTTTGAATCTGTGTGAGCTGTT 1440
Db      1839 AATTAAAGAGATTAACAAGTGGGAATTTGAAGACTTTTGAATCTGTGTGAGCTGTT 1898
QY      1441 TGATTTCTTGAATCTGTGTGACACGAGGCTTTTCCAGAGAGGTCAATCAAGACTTTTGA 1500
Db      1899 TGATTTCTTGAATCTGTGTGACACGAGGCTTTTCCAGAGAGGTCAATCAAGACTTTTGA 1958
QY      1501 TTTTTCACACCGGGGCGGCTGTGCGCTGTGCTTTTGTGAGTTTAAAGATTA 1560
Db      1959 TTTTTCACACCGGGGCGGCTGTGCGCTGTGCTTTTGTGAGTTTAAAGATTA 2018
QY      1561 ATGAGCGGAAGAAACCATCTGAGCGGGGGTACCTGTGGAATTTCTGGCATGCACTT 1620
Db      2019 ATGAGCGGAAGAAACCATCTGAGCGGGGGTACCTGTGGAATTTCTGGCATGCACTT 2078
QY      1621 GTGAGAGCGGTTGTGAGACACAAGAAATGCGCTGTCTACTGTGTCTTCCGTCGCCCGGCG 1680
Db      2079 GTGAGAGCGGTTGTGAGACACAAGAAATGCGCTGTCTACTGTGTCTTCCGTCGCCCGGCG 2138
QY      1681 GATTAATACGACGAGAGAGACGACGACGACGAGAGGAAGCCAGGCGCGCGGACGAG 1740
Db      2139 GATTAATACGACGAGAGAGACGACGACGACGAGAGGAAGCCAGGCGCGCGGACGAG 2198
QY      1741 GCAGAGCCCATGAAACCCGAGAGCCGAGCTTGGACCTCTGGGAAATGAATGTTGTACAGGTG 1800
Db      2199 GCAGAGCCCATGAAACCCGAGAGCCGAGCTTGGACCTCTGGGAAATGAATGTTGTACAGGTG 2258
QY      1801 GCTGAACCTGTATCCAGAACTGAGACGCAATTTTGAATTAACAAGGATGCGCAGAGGCTTA 1860
Db      2259 GCTGAACCTGTATCCAGAACTGAGACGCAATTTTGAATTAACAAGGATGCGCAGAGGCTTA 2318
QY      1861 AAGGGGTTAAAGAGAGAGCGGGGCTTGTGAGGCTACAGAGAGCTAGGAATCTAGCT 1920
Db      2319 AAGGGGTTAAAGAGAGAGCGGGGCTTGTGAGGCTACAGAGAGCTAGGAATCTAGCT 2378
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QY 1921 TTTAGCTTAATGACACGACACGTCCTGAGTATTAATCTTTTCAACAGATGAGATAT 1980
DB 2379 TTTAGCTTAATGACACGACACGTCCTGAGTATTAATCTTTTCAACAGATGAGATAT 2438
QY 1981 TGCCTAATGAGCTTGATCTGTGCGCAGAGATATTCATAGAGACAGCTGACCTTAC 2040
DB 2439 TGCCTAATGAGCTTGATCTGTGCGCAGAGATATTCATAGAGACAGCTGACCTTAC 2498
QY 2041 TGCCTGACGACGAGGATGATTTTGAAGAGCTATTAGGGTATATGCAAGGTGACCTT 2100
DB 2499 TGCCTGACGACGAGGATGATTTTGAAGAGCTATTAGGGTATATGCAAGGTGACCTT 2558
QY 2101 AGGCAGATTGCAATGACATGACCAACTTGTAAATATCAGAAATGTTGCTACATT 2160
DB 2559 AGGCAGATTGCAATGACATGACCAACTTGTAAATATCAGAAATGTTGCTACATT 2618
QY 2161 TCTGGGAAACGGGGCCGAGGTGAGATAGATACGAGATAGAGGTGCTTTAGATGTAGC 2220
DB 2619 TCTGGGAAACGGGGCCGAGGTGAGATAGATACGAGATAGAGGTGCTTTAGATGTAGC 2678
QY 2221 ATGATTAATATGTGCGCCGGGGGTGCTTGGCATGACGCGGGTGTATTATGATGTAAGG 2280
DB 2679 ATGATTAATATGTGCGCCGGGGGTGCTTGGCATGACGCGGGTGTATTATGATGTAAGG 2738
QY 2281 TTTACTGGCCCCAATTTTAGCGGTACGGTTCCTGCGCCAAATCAACCTTATCCTACAC 2340
DB 2739 TTTACTGGCCCCAATTTTAGCGGTACGGTTCCTGCGCCAAATCAACCTTATCCTACAC 2798
QY 2341 GGTGTAAAGCTTCTATGCGTTTAAACATACCTGTGTGAAGCCTGGAACGATGTAAAGGTT 2400
DB 2799 GGTGTAAAGCTTCTATGCGTTTAAACATACCTGTGTGAAGCCTGGAACGATGTAAAGGTT 2858
QY 2401 CGGGGCTGTGCTTTTACTGTCTGTGAAAGGGGGTGTGTCCGCCAAAAGAGAGGCT 2460
DB 2859 CGGGGCTGTGCTTTTACTGTCTGTGAAAGGGGGTGTGTCCGCCAAAAGAGAGGCT 2918
QY 2461 TCAATTTAAGAAATGCTCTTTGAAAGGTACTCTTGGGTATCTGTGTGAAGGATACCTC 2520
DB 2919 TCAATTTAAGAAATGCTCTTTGAAAGGTACTCTTGGGTATCTGTGTGAAGGATACCTC 2978
QY 2521 AGGGTGGCCCAATGTGTGCTCCGACTGTGGTTCCTTCAATGATGAAAAAGGTGCT 2580
DB 2979 AGGGTGGCCCAATGTGTGCTCCGACTGTGGTTCCTTCAATGATGAAAAAGGTGCT 3038
QY 2581 GTGATTAAGCAATACTGTATGTGTGCAACCTGCGAGACAGGGCTCTCAATGTCTGACC 2640
DB 3039 GTGATTAAGCAATACTGTATGTGTGCAACCTGCGAGACAGGGCTCTCAATGTCTGACC 3098
QY 2641 TGTCTCGACGCGCACTGTCACTGTGAGACCAATTCAGTACGACGACCTCTCGCAAG 2700
DB 3099 TGTCTCGACGCGCACTGTCACTGTGAGACCAATTCAGTACGACGACCTCTCGCAAG 3158
QY 2701 GCCTGGCCAGTGTTTAGCATTAACATACCTGCGCTGCTCTTGACATTTGGGTAAACAG 2760
DB 3159 GCCTGGCCAGTGTTTAGCATTAACATACCTGCGCTGCTCTTGACATTTGGGTAAACAG 3218
QY 2761 AGGGGGGGTTCCTCAATCTTACCAATGCAATTTGAGTCACTAAGATATTTGAGAGCC 2820
DB 3219 AGGGGGGGTTCCTCAATCTTACCAATGCAATTTGAGTCACTAAGATATTTGAGAGCC 3278
QY 2821 GAGAGCATGTCCAAGGTGAACCTGAAACGGGGTGTTTGACATGACCAATGAATCTGAAAG 2880
DB 3279 GAGAGCATGTCCAAGGTGAACCTGAAACGGGGTGTTTGACATGACCAATGAATCTGAAAG 3338
QY 2881 GTGTGAGATGACATGAGACCCGACACAGGTGTGACAGACCTTGCAGGTGTGGCGGTAAACAT 2940
DB 3339 GTGTGAGATGACATGAGACCCGACACAGGTGTGACAGACCTTGCAGGTGTGGCGGTAAACAT 3398
QY 2941 ATTGAGAACCGAGCTGTGATCTGTGATGTGACCGAGAGCTGAAGCCCGGATCTACTGTG 3000
DB 3399 ATTGAGAACCGAGCTGTGATCTGTGATGTGACCGAGAGCTGAAGCCCGGATCTACTGTG 3458

QY 3001 CTGGCTTCGACCCGCGCTGAGTTTGCTCTAGCGATGAGATACAGATTGAG 3052
DB 3459 CTGGCTTCGACCCGCGCTGAGTTTGCTCTAGCGATGAGATACAGATTGAG 3510

RESULT 2
LOCUS COB54906 32802 bp DNA linear PAT 23-AUG-2004
DEFINITION Sequence 3 from Patent WO2004066947.
VERSION COB54906
KEYWORDS GI:51510466
SOURCE unidentified adenovirus
ORGANISM unidentified adenovirus
REFERENCE 1. dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
AUTHORS Hu, F. and Wu, B.
TITLE Therapy for primary and metastatic cancers
JOURNAL Patent: WO 2004066947-A 3 12-AUG-2004;
Shanghai Sunway Biotech Co Ltd (CN)
FEATURES
source Location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 3052; DB 6; Length 32802;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 519 AGAGTTTTCCTTCGAGCCGCTCCGACACCGGAGCTGAAATGAGACATATTAATCTGCC 578
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QY 181 TACTGCTGATTAATCTTCAACCTCTGACATTTTGAACCACTTACCTTACGAACTGT 240
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QY 361 CCGGTTCTCGGAGCCGCTCACTTCCCGGAGCCCGAGCAACCGGAGAGAGGCT 420
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RESULT 4
AX084507
LOCUS AX084507 34448 bp DNA linear PAT 28-FEB-2001
DEFINITION Sequence 4 from Patent WO0104282.
ACCESSION AX084507
VERSION AX084507.1 GI:13185915
KEYWORDS
SOURCE
ORGANISM Human adenovirus C
Human adenovirus C
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
REFERENCE
1 Mould, W.S., Toth, K., Doronin, K. and Tollefson, A.E.
AUTHORS Replication-competent anti-cancer vectors
TITLE Patent: WO 0104282-A 4 18-JAN-2001;
JOURNAL Saint Louis University (US)
location/Qualifiers
FEATURES
source
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ORIGIN
Query Match 100.0%; Score 3052; DB 6; Length 34448;
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Qy 1 CGTGTAGTATTTTAAACCGGTGAGTTCTCAAGAGCCACTTTGAGTCCAGCGAGT 60
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ACCESSION AR116313
VERSION AR116313.1 GI:14096635
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 35935)
AUTHORS Imber,J.-L., Menthall,M. and Paviran,I.A.
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JOURNAL Patent: US 6133028-A 43 17-OCT-2000;
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VERSION CQ854907.1 GI:51510467
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
Hu, F. and Wu, B.
TITLE Therapy for primary and metastatic cancers
JOURNAL Patent: WO 2004066947-A 4 12-AUG-2004;
Shanghai Sunway Biotech Co Ltd (CN)
FEATURES
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Db	2739	TTTATCGGGCCCAATTTTAAAGGGTACGGGTTTTCCCTGGCCAAATPACAACCTTATCCTACAC	2798
QY	2341	GGTGTAACTTCTATGGGTTTAAACAATACCTGTGTGAAAGCTTGACCGATGTAAAGGTT	2400
Db	2799	GGTGTAACTTCTATGGGTTTAAACAATACCTGTGTGAAAGCTTGACCGATGTAAAGGTT	2858
QY	2401	CGGGGCTGTGCTTTTATCTGCTGCTGGAAGGGGGTGTGTGTCCGCCAAGAGGCT	2460
Db	2859	CGGGGCTGTGCTTTTATCTGCTGCTGGAAGGGGGTGTGTGTCCGCCAAGAGGCT	2918
QY	2461	TCAATTAAGAAATGTGCTCTTGAAGAGTGTAACCTTGGGTATCCTGTCTGAAGGTAACTCC	2520
Db	2919	TCAATTAAGAAATGTGCTCTTGAAGAGTGTAACCTTGGGTATCCTGTCTGAAGGTAACTCC	2978
QY	2521	AGGGTGGCCACAATGTGGCCCTCCGACTGTGGTTGCTTATGCTGTAGTAAAGCGTGCT	2580
Db	2979	AGGGTGGCCACAATGTGGCCCTCCGACTGTGGTTGCTTATGCTGTAGTAAAGCGTGCT	3038
QY	2581	GTGATTAAGCATATCATGTATGTGGCAATCTGCGAGAAGGGCTCTCAATGTGTCAC	2640
Db	3039	GTGATTAAGCATATCATGTATGTGGCAATCTGCGAGAAGGGCTCTCAATGTGTCAC	3098
QY	2641	TGCTCGAGCGGCACTGTCACTGCTGTGAAGACATTCAGTACGAGGCACTCTCGCAG	2700
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QY	2701	GCTTGCCAGTGTGTTGAGCATTAACATTAACCTGACCCCGCTGTCTTGTCATTTGGGTAAACGG	2760
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QY	2761	AGGGGGGTGTTCTTACCTTACCAATGCAATTTGAGTCACTAAGATATGCTTGAGGCC	2820
Db	3219	AGGGGGGTGTTCTTACCTTACCAATGCAATTTGAGTCACTAAGATATGCTTGAGGCC	3278
QY	2821	GAGACATATGCCAAGGTAACTGAAACGGGGTGTGATGACCATTAAGATCTGAGAG	2880
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QY	2881	GTGCTGAAGTACGATGAGACCCGACCAAGGTGACAGCCCTGCGAGTGTGGCGTAAACAT	2940
Db	3339	GTGCTGAAGTACGATGAGACCCGACCAAGGTGACAGCCCTGCGAGTGTGGCGTAAACAT	3398
QY	2941	ATTAGAAACCAAGCTGTGATGTGATGTGACCGAGAGCTGAGGCCGATCACTTGCTG	3000
Db	3399	ATTAGAAACCAAGCTGTGATGTGATGTGACCGAGAGCTGAGGCCGATCACTTGCTG	3458
QY	3001	CTGGCTGCACCCGGCGTGAAGTTGGCTTACGCAATGAAGTATACAGATTGAG	3052
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DEFINITION	Sequence 1 from patent US 6451596.	linear	PAT 20-DEC-2002
ACCESSION	AR230724		
VERSION	AR230724.1	GI:27271505	
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 35935)		
	Chamberlain,J.S., Amalfitano,A., Hauser,M.A., Kumar-Singh,R. and		
	Hartigan,O'Connor,D.J.		
	Heiper adenovirus vectors		
	Patent: US 6451596-A 1 17-SEP-2002;		
	Location/Qualifiers		
TITLE			
JOURNAL			
FEATURES			

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Best Local Similarity	100.0%;	Pid. No. 0;	
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DB	519	AGAGTTTCTCTCCGAGCCGCTCCGACCCGGACTGAAAATGACATTTATCTGCC	578
QY	121	ACGGAGGTATTTATACCGAAGAAATGCGCGCACTTTTGACACAGTGTATCGAAGAG	180
DB	579	ACGGAGGTATTTATACCGAAGAAATGCGCGCACTTTTGACACAGTGTATCGAAGAG	638
QY	181	TACTGCGTATATCTTCCACTCTCTAGCATTATTGAAACCACTACCTTACGAACTGT	240
DB	639	TACTGCGTATATCTTCCACTCTCTAGCATTATTGAAACCACTACCTTACGAACTGT	698
QY	241	ATGATTTAGACTGACGGCCCTCCGAAGTCCCAAGAGAGGCGGTTCCGAGATTTTC	300
DB	699	ATGATTTAGAGTACGGCCCTCCGAAGTCCCAAGAGAGGCGGTTCCGAGATTTTC	758
QY	301	CCGACTCTGTATGTGGCGGTGAGAGGAAGGATTTGACTTACCTACTTTTCCGCGCGGC	360
DB	759	CCGACTCTGTATGTGGCGGTGAGAGGAAGGATTTGACTTACCTACTTTTCCGCGCGGC	818
QY	361	CCGGTCTCCGGAGCCGCTTCACTTTTCCGGAGCCCGAGCAGCCGAGCAGAGAGCTT	420
DB	819	CCGGTCTCCGGAGCCGCTTCACTTTTCCGGAGCCCGAGCAGCCGAGCAGAGAGCTT	878
QY	421	TGGGTCCGGTTCTATATGCCAACTTTGTACCGAGGTGATGATCTTAACCTGCCACGAG	480
DB	879	TGGGTCCGGTTCTATATGCCAACTTTGTACCGAGGTGATGATCTTAACCTGCCACGAG	938
QY	481	CTGCTTTTCCACCCAGTGAAGACAGAGATGAAAGGATGAGAGATTTGTGTAGATTATG	540
DB	939	CTGCTTTTCCACCCAGTGAAGACAGAGATGAAAGGATGAGAGATTTGTGTAGATTATG	998
QY	541	TGAGACACCCCGGACAGGTTGCAGGTCTTGTCTTATTCACCGAGGAAATCGGAGAC	600
DB	999	TGAGACACCCCGGACAGGTTGCAGGTCTTGTCTTATTCACCGAGGAAATCGGAGAC	1058
QY	601	CAGATATTATGTGTGCTTTGCTATATAGAGACCTGTGGCATGTTGTCTACAGTATG	660
DB	1059	CAGATATTATGTGTGCTTTGCTATATAGAGACCTGTGGCATGTTGTCTACAGTATG	1118
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DB	1119	GAAATATTAGGCGAGTGGGATGATGAGTGTGGGTTTGATGGTAAATTTTTTTTTTAA	1178
QY	721	TTTTTACGTTTGTGGTTTAAAGATTTTGTATTGTGATTTTTTTTAAAGGCTCTGTGC	780
DB	1179	TTTTTACGTTTGTGGTTTAAAGATTTTGTATTGTGATTTTTTTTAAAGGCTCTGTGC	1238
QY	781	TGAACCTGAGCCTBAGCCCGAGCCAGAAACCGAGACCTGCAAGACTTACCGCGCTCTTA	840
DB	1239	TGAACCTGAGCCTBAGCCCGAGCCAGAAACCGAGACCTGCAAGACTTACCGCGCTCTTA	1298
QY	841	AATGGCGCTGCTATCTTGAAGCCCGACATCACTGTGTCTTGAAGATGCAATAGTAG	900
DB	1299	AATGGCGCTGCTATCTTGAAGCCCGACATCACTGTGTCTTGAAGATGCAATAGTAG	1358
QY	901	TACGGATAGCTGTACCTCCGCTCTTTTAAACAACCTCTCTGAATATACCCGGGTGTGCC	960
DB	1359	TACGGATAGCTGTACCTCCGCTCTTTTAAACAACCTCTCTGAATATACCCGGGTGTGCC	1418

QY	961	GCTGTCGCCCAATTAAACCAAGTTGCCGTGAGAGAGTTGCTGAGCGCTGCGCCAGGCTGTGAAATG	1020
Db	1419	GCTGTGCCCCCAATTAAACCAAGTTGCGGTAGAGTTGGTGTGGGCGTGGCCAGGCTGTGAAATG	1478
QY	1021	TATCGAGAGACTTGCTTTAAAGAGCCCTGGGCAACCTTTGACCTTGAAGCTGTAAAGCCCCAG	1080
Db	1479	TATCGAGAGACTTGCTTTAAAGAGCCCTGGGCAACCTTTGACCTTGAAGCTGTAAAGCCCCAG	1538
QY	1081	GCCATAAGGTGTAAACCTGTGATTTGCGTGTGTGTTAAAGCCCTTGTGTGCTGAATGAT	1140
Db	1539	GCCATAAGGTGTAAACCTGTGATTTGCGTGTGTGTTAAAGCCCTTGTGTGCTGAATGAT	1598
QY	1141	TGATGTAAAGTTTAAATAAAAGGTGAGATATATGTTTAACTTGCAATGGCGTGTAAATGGGCG	1200
Db	1599	TGATGTAAAGTTTAAATAAAAGGTGAGATATATGTTTAACTTGCAATGGCGTGTAAATGGGCG	1658
QY	1201	GGGGCTTAAAGGTTATATATATGCGCGGGGCTATCTTGGTTTACATGTGACCTATAGA	1260
Db	1659	GGGGCTTAAAGGTTATATATATGCGCGGGGCTATCTTGGTTTACATGTGACCTATAGA	1718
QY	1261	GGCTTGGGAGTGTGTGSAAGATTTTTCTGCTGTGCGTAACCTTGCTGAAACAGACTCTTAA	1320
Db	1719	GGCTTGGGAGTGTGTGSAAGATTTTTCTGCTGTGCGTAACCTTGCTGAAACAGACTCTTAA	1778
QY	1321	CAGTACCTCTTGTGTTTGGAGGTTTCTGTGGGCGTCAATCCAGCGAAATTAATGTCTGAG	1380
Db	1779	CAGTACCTCTTGTGTTTGGAGGTTTCTGTGGGCGTCAATCCAGCGAAATTAATGTCTGAG	1838
QY	1381	AAATTAAAGGAGATTACAGTGGGAAATTTGAAAGCCTTTGAAATTCGTGTGTGAGCTGTT	1440
Db	1839	AAATTAAAGGAGATTACAGTGGGAAATTTGAAAGCCTTTGAAATTCGTGTGTGAGCTGTT	1898
QY	1441	TGAATCTTGTGATCTGGGTCAACAGCGCTTTTCCAGAGAAAGGTCAATCAAGCTTTGGA	1500
Db	1899	TGAATCTTGTGATCTGGGTCAACAGCGCTTTTCCAGAGAAAGGTCAATCAAGCTTTGGA	1958
QY	1501	TTTTTCCAACCGGGGCGCGCTGCGGCTGTGTTCTTTTGAATTTTAAAGATTA	1560
Db	1959	TTTTTCCAACCGGGGCGCGCTGCGGCTGTGTTCTTTTGAATTTTAAAGATTA	2018
QY	1561	ATGAGAGGAABAAACCAATCTGACCGGGGGTTACTGCTGAAATTTTCTGGCATGCAACT	1620
Db	2019	ATGAGAGGAABAAACCAATCTGACCGGGGGTTACTGCTGAAATTTTCTGGCATGCAACT	2078
QY	1621	GTGAGAGAGCGGTTGTGAGACACAAGAAATCGCTGCTACTGTGTTCTTCCGTCGCGCGG	1680
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QY	1681	GATATAACCGAGCGAGAGACAGACAGACAGAGAGAAACCGAGCGCGCGCGGACAG	1740
Db	2139	GATATAACCGAGCGAGAGACAGACAGACAGAGAGAAACCGAGCGCGCGCGGACAG	2198
QY	1741	GCAAGAGCCCATGGAACCCGAGAGGCCCGGCTGTGACCTCTGGGAATGAAATGTTGTCAGGTG	1800
Db	2199	GCAAGAGCCCATGGAACCCGAGAGGCCCGGCTGTGACCTCTGGGAATGAAATGTTGTCAGGTG	2258
QY	1801	GCTGAACCTGTATCCAGAACTGAGACGCAATTTTGAATTAACAGAGGAATGGGACGGGCTA	1860
Db	2259	GCTGAACCTGTATCCAGAACTGAGACGCAATTTTGAATTAACAGAGGAATGGGACGGGCTA	2318
QY	1861	AAAGGGGTAAAGAGAGAGCGGGGGCTTGTGAGCTACAGAGAGGCTAGGAATCTAGCT	1920
Db	2319	AAAGGGGTAAAGAGAGAGCGGGGGCTTGTGAGCTACAGAGAGGCTAGGAATCTAGCT	2378
QY	1921	TTTATGCTTAATGACACACACCCGTCTGATGTATTAATTTTCAACAGATCAAGGATTAAT	1980
Db	2379	TTTATGCTTAATGACACACACCCGTCTGATGTATTAATTTTCAACAGATCAAGGATTAAT	2438
QY	1981	TGCGCTATATGAGCTTGATCTGCTGAGCGCAAGATTCATATAGAGAGCTGACACACTTAC	2040
Db	2439	TGCGCTATATGAGCTTGATCTGCTGAGCGCAAGATTCATATAGAGAGCTGACACACTTAC	2498
QY	2041	TGCGCTGACCCAGGGAGTGAATTTTGAAGAGGCTTAATAGGTTATATGCAAAAGTGTCACTT	2100

[illegible]

VERSION	AX451988.1	GI:21711988
KEYWORDS	Human adenovirus type 5	
SOURCE	Human adenovirus type 5	
ORGANISM	Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.	
REFERENCE	1	
AUTHORS	Arrendasiz Borunda,J. and Aguilar Cordova,E.	
TITLE	Recombinant viral and non-viral vectors containing the human urokinase plasminogen activator gene and its utilization in the treatment of various types of hepatic, renal, pulmonary, pancreatic and cardiac fibrosis and hypertrophic scars	
JOURNAL	Patient: WO 024393-A 1 06-JUN-2002;	
FEATURES	TGT LAB S A DE C V (MX)	
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Best Local Similarity	100.0%;	Pred. No. 0;
Matches 3052;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
QY	1 CGTGTAGTATTTATACCCGGTGAATTCCTCAAGAGCCACTCTTGAGTCCAGCGAGT 60	
DB	459 CGTGTAGTATTTATACCCGGTGAATTCCTCAAGAGCCACTCTTGAGTCCAGCGAGT 518	
QY	61 AGAGTTTCTCTCTCCGAGCCGCTCCGACACCGGGAAGTGAACATTTATCTGCC 120	
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QY	121 ACGGAGGTGTATTAACGGAATAATGGCCGACGCTTTTGACACAGCTGATCGAAGAG 180	
DB	579 ACGGAGGTGTATTAACGGAATAATGGCCGACGCTTTTGACACAGCTGATCGAAGAG 638	
QY	181 TACTGCTGATTAATCTTCCACTCTTACCAATTTGAAACCACTAACCTTACAGAACTGT 240	
DB	639 TACTGCTGATTAATCTTCCACTCTTACCAATTTGAAACCACTAACCTTACAGAACTGT 698	
QY	241 ATGATTTAGAGTGAACGGCCCCCGAAGATCCCAACGAGAGGCGGTTTGCAGATTTTTC 300	
DB	699 ATGATTTAGAGTGAACGGCCCCCGAAGATCCCAACGAGAGGCGGTTTGCAGATTTTTC 758	
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QY	361 CCGGTTCTCCGAGACCGCTCACCTTTCCTCCGACAGCCCGAGCAGCCGAGAGAGCTT 420	
DB	819 CCGGTTCTCCGAGACCGCTCACCTTTCCTCCGAGACCGCGAGCAGCCGAGAGAGCTT 878	
QY	421 TGGGTCGGTTTCTATGCAAACTTTGACCGGAGGTGATGATCTTAACCTGCAAGAG 480	
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QY	481 CTGGCTTTCCACCGAGTGAACGAGATGAAGAGGGTGAAGAGTTGTGTTAATATG 540	
DB	939 CTGGCTTTCCACCGAGTGAACGAGATGAAGAGGGTGAAGAGTTGTGTTAATATG 998	
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DB	999 TGGAGCACCCCGGACCGGTTGACAGTCTTGTCAATTACACCGAGAGATACGGGGAGC 1058	
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DB	1059 CAGATATTATGTGCTTGTGCTATATGAGGACTGTGGCAATGTTTGTCTACAGTAAGT 1118	
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DB	1119 GAAATATTAGGCAATGGGATGATGAGTGGGTTTGGTGGTAATTTTTTTTTTAAT 1178	
QY	721 TTTTACAGTTTGTGTTAAAGATTTTGTATTGTATTTTTTTAAAGGCTCCTGTCTC 780	

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QY	901	TACGATAGCTGTGACTCCGGTCTTCTTAACACACTCTGATAGATACCCGGTGTCTCC 960
DB	1359	TACGATAGCTGTGACTCCGGTCTTCTTAACACACTCTGATAGATACCCGGTGTCTCC 1418
QY	961	GCTGTGCCCATTTAAACCAATGTGCGTGAAGATTGGGGGTGCGCAGCTGTGAATG 1478
DB	1419	GCTGTGCCCATTTAAACCAATGTGCGTGAAGATTGGGGGTGCGCAGCTGTGAATG 1478
QY	1021	TATGAGGACTGTGCTTAACGAGCCTGGGCAACCTTTGAGCTGAGCTGTAAACGCCCCAG 1080
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QY	1141	TGATGTAACTTTAATAAGGTGAGATTAATGTTTAACTTGATGATGCGGTGTTAAATGGGGC 1200
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QY	1201	GGGCTTAAAGGGATTAATAATGCGCGTGGGCTTAATCTTGATTAATGATGATGAGT 1260
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QY	1261	GGCTTGGAGGTGTTGGAGATTTTCTGCTGTGCTGTAACCTGTGAAACAGACTCTTA 1320
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QY	1321	CAGTACTCTTGTGTTTGGAGCTTCTGTGGGCTCATCCAGGCAAAATTAAGTCTGAG 1380
DB	1779	CAGTACTCTTGTGTTTGGAGCTTCTGTGGGCTCATCCAGGCAAAATTAAGTCTGAG 1838
QY	1381	AATTAAGAGGATTAACAAGTGGGAAATTTGAAGACTTTTGAATCTGTGTGAGCTGT 1440
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QY	1741	GCAAGGCCATGGAACCGGAGAGCGGCGCTGAGACCTCTGGGAATGATGTTGTACAGGTG 1800
DB	2199	GCAAGGCCATGGAACCGGAGAGCGGCGCTGAGACCTCTGGGAATGATGTTGTACAGGTG 2258
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AX683770
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DEFINITION Sequence 1 from Patent WO03006662.
VERSION AX683770
KEYWORDS AX683770.1 GI:29370798
SOURCE Human adenovirus type 5
ORGANISM Human adenovirus type 5
VIRUSES; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
REFERENCE 1
AUTHORS 1990,R.D., Fuierer,C. and Homicko,K.G.
TITLE Anti-neoplastic viral agents
JOURNALS Patent: WO 03006662-A 1 23-JAN-2003;
BTG International Limited (GB)
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Query Match 100.0%; Score 3052; DB 6; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
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Db 459 CGTGTAGTGTATTTATATACCGGTGAGTTCTTCAAGAGGCCCTTGAATGCCAGCGT 518
Qy 61 AGAGTTTCTCTCCGAGCGGCTCCGACACCGGAGCTGAATAATGACATTTATCTGCC 120
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AUTHORS Chroboczek, J., Bieber, F., and Jacrot, B.
TITLE The sequence of the genome of adenovirus type 5 and its comparison
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RESULT 14
LOCUS AR403723 35978 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1 from patent US 6627190.
VERSION AR403723
KEYWORDS AR403723.1 GI:40151372
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 35978)
AUTHORS Wold, W.S.M., Toch, K., Doronin, K., Tollefson, A.B. and Kuppenswamy, M.
TITLE Recombinant adenovirus vectors that are replication-competent in
tert-expressing cells
JOURNAL Patent: US 6627190-A 1 30-SEP-2003;
FEATURES Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 3052; DB 6; Length 35978;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1119 GAAATTTATGGGCAGTGGGTGATAGAGTGTGGTGTGTGTGTATTTTTTTTAT 1178
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RESULT 15
AR310582
LOCUS AR310582 7090 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 18 from patent US 6558948.
ACCESSION AR310582
VERSION AR310582.1 GI:31703596
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.

1 (baves 1 to 7090)

Kochanek, S. and Schiedner, G.

Permanent amniocytic cell line, its production and use for the

production of gene transfer vectors

Patent: US 6558948-A 18 06-MAY-2003;

Location/Qualifiers

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Best local similarity	99.9%	Prod No. 0;		

Best Local Similarity 99.9%; Pred. No. 0;
Matches 3008; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Matches 3008; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY	463	ATCTTACTGCGACGAGGCTGGCTTTCACCCAGTACGACGAGGATGAAGAGGTGAG	522
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QY	523	AGTTTGTTAGATTATATGTGAGACACCCGGGACAGTGTGACAGCTTGTCATATCAC	582
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QY	763	TTTTAAAGGTCTGTGTCTGAACTGTAGCCTGTAGCCGAGCCGAGCCAGAACCGAGCTGTCAAG	822
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Db	3529	ACCTAACCGCGGCTCTTAAATATGGCGGCTGTATCTCTGAGAGGCCGACATACACTGTGTCTC	3588
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Search completed: October 28, 2005, 06:30:19
Job time : 12695 secs

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Db	5029	ACCAACCTTATCTACACGCGTGAAGCTTCTATGGGTTTAACAATACCTGTGTGAAGCC	5088
QY	2383	TGGAACCGATGTAAGGGGTGCGGGGCTGTGCTTTTACTGTGCTGGAAGGGGGTGTGT	2442
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XX Example 1, SEQ ID NO 3, 129bp, English.

CC The present invention relates to the compositions and methods for
CC ablating tumour cells in a subject having one or more tumour sites. The
CC method includes introduction of a lytic agent into a tumour (which forms
CC a treated tumour) and application of stimulus to the treated tumour. The
CC stimulus (physical, chemical or biological) induces the level of
CC chaperone proteins (heat shock proteins) in the tumour cells. The
CC combination of the lytic agent and tumour cell stimulus leads to tumour
CC shrinkage. The invention relates to the synchronisation between oncolysis
CC and elevated expression of a heat shock protein (HSP), which results in
CC sufficient release of HSP-CRA (cancer reactive antigen). The sufficient
CC levels of HSP-CRA exhibit a signal immunogenic enough to the immune
CC system in order to elicit an immune response against the cancer. The
CC method of the invention is useful in ablating tumour cells for treating
CC nasopharyngeal carcinoma, chondrosarcoma, colon cancer, breast cancer,
CC prostate cancer, ovarian cancer, stomach carcinoma, rectum cancer,
CC malignant hepatoma, melanoma, ascites etc. Mutations of the p53 gene
CC exist in more than half of cancer cases. The treated or non-treated
CC cancers which consist of a defective p53 tumour suppressor gene or an
CC activated oncogene are good candidates for this method of therapy. The
CC oncolytic viruses of this invention comprise genetically modified Ad5
CC variants. This oncolytic adenovirus selectively replicates in cancer
CC cells with a p53 mutation and lyses cancer cells with high specificity.
CC The genome of a wild type Ad5 is composed of 35,935 bps. Genetically
CC modified variant Ad5 (598-001) has an extra stop codon at position 2025
CC (E1b region) and possesses deletions in E1b region (in between 2,501 and
CC 3,328) and in E3 (in between 27865 and position 30,995) region. In normal
CC cells E1b-55KD binds and inactivates the protein encoded by the p53 gene
CC and initiates normal replication. The 598-001 variant is not able to
CC replicate in normal cells, but replicates rapidly in cancer cells in
CC which the p53 protein is dysfunctional. The function of E3 is related to
CC the ability of an adenovirus to escape from the surveillance of the
CC immune system. The complete deletion of the E3 region in 598-001 enables
CC the immune system easier recognition and elimination of this virus. 598
CC -002 is another genetically modified variant Ad5. It has deletions in the
CC region encoding E1b-55KD (in between 2,501 and 3,328) and of the entire
CC E3 region (in between 27865 and position 30,995). The variant sequences
CC of Ad5 are unable to integrate into the human genome, but selectively
CC replicate in cancer cells. So, 598-001 and 598-002 are safe for use in
CC humans and animals. The presented sequence is the 598-100 (32802bp)
CC adenovirus DNA which is used as positive control. Note: This sequence is
CC shown as SEQ ID No 3 in the sequence listing but not clearly mentioned in
CC example 1 of the specification.

XX Sequence 32802 BP; 7543 A; 9233 C; 9139 G; 6887 T; 0 U; 0 Other;

Query Match 100.0%; Score 3052; DB 13; Length 32802;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGTAGTGTATTTATACCGCGTGAATTCCTCAAGAGCCACTCTTGAGTCCAGCGAGT 60
DB 459 CGGTAGTGTATTTATACCGCGTGAATTCCTCAAGAGCCACTCTTGAGTCCAGCGAGT 518
QY 61 AGAGTTTCTCCTCGAGCGGCTCGACACGGGACGTGAATAATGACATATTATCTGCC 120
DB 519 AGAGTTTCTCCTCGAGCGGCTCGACACGGGACGTGAATAATGACATATTATCTGCC 578
QY 121 ACGGAGTGTATTATACCGAAGAAATGCGCGCAGTCTTTTGACAGAGCTGATCGAAGAG 180
DB 579 ACGGAGTGTATTATACCGAAGAAATGCGCGCAGTCTTTTGACAGAGCTGATCGAAGAG 638
QY 181 TACTGGCTGATTAATCTTCACTCTTACCACTTTTGAACCACTTACCTTACAGAACTGT 240
DB 639 TACTGGCTGATTAATCTTCACTCTTACCACTTTTGAACCACTTACCTTACAGAACTGT 698
QY 241 ATGATTTAGAGTGACGGGCCCCCGAAGATCCCAACGAGGAGCGGTTTCCGAGATTTTTC 300
DB 699 ATGATTTAGAGTGACGGGCCCCCGAAGATCCCAACGAGGAGCGGTTTCCGAGATTTTTC 758
QY 301 CCGACTCTGTATGTGGCGGTGACGAAAGGATTAATCACTTTCGCGCGGCGC 360

DB 759 CCGACTCTGTATGTGGCGGTGACGAAAGGATTAATCACTTTCGCGCGGCGC 818
QY 361 CCGGTTCTCCGAGACCGGCTTCACTTTTCCGGACGCCCGAGACCCGAGACAGAGAGCTT 420
DB 819 CCGGTTCTCCGAGACCGGCTTCACTTTTCCGGACGCCCGAGACCCGAGACAGAGAGCTT 878
QY 421 TGGGTCCGGTTTCTATGACCAAACTTGTACCGGAGTGATGATCTTAACCTGACAGAG 480
DB 879 TGGGTCCGGTTTCTATGACCAAACTTGTACCGGAGTGATGATCTTAACCTGACAGAG 938
QY 481 CTGGCTTTCCACCCAGTGAACGACGAGGATGAAGAGGTGAGAGATTGTGTAATATG 540
DB 939 CTGGCTTTCCACCCAGTGAACGACGAGGATGAAGAGGTGAGAGATTGTGTAATATG 998
QY 541 TGGAGCACCCCGGACAGGTTGACAGTCTTGTCATTATACCGAGAGATACGGGGAGCC 600
DB 999 TGGAGCACCCCGGACAGGTTGACAGTCTTGTCATTATACCGAGAGATACGGGGAGCC 1058
QY 601 CAGATATTATGTGTGCTTGTGATATGAGGACCTGCGGATGTTGTCTACAGTAACT 660
DB 1059 CAGATATTATGTGTGCTTGTGATATGAGGACCTGCGGATGTTGTCTACAGTAACT 1118
QY 661 GAAATTTATGGGACAGTGGATATAGAGTGTGGTGTGTTGTTTATAT 720
DB 1119 GAAATTTATGGGACAGTGGATATAGAGTGTGGTGTGTTGTTTATAT 1178
QY 721 TTTTACGTTTGTGTTTAAAGAAATTTGTATGTGATTTTTTAAAGATCCTGTGTC 780
DB 1179 TTTTACGTTTGTGTTTAAAGAAATTTGTATGTGATTTTTTAAAGATCCTGTGTC 1238
QY 781 TGAACCTGAGGCTGAGGCGGACGAGAACCGGAGCTGCAAGACCTTACCGCGCTCTTA 840
DB 1239 TGAACCTGAGGCTGAGGCGGACGAGAACCGGAGCTGCAAGACCTTACCGCGCTCTTA 1298
QY 841 AATGCGCCTGCTATCTCTGAGACGCCCGACATCACTGTGTCTAGAGAAATGCAATAGTAG 900
DB 1299 AATGCGCCTGCTATCTCTGAGACGCCCGACATCACTGTGTCTAGAGAAATGCAATAGTAG 1358
QY 901 TACGGAATAGCTGTACCTCGGCTCTTTTAAACACCTCTGAGATACACCGGCTGTGCC 960
DB 1359 TACGGAATAGCTGTACCTCGGCTCTTTTAAACACCTCTGAGATACACCGGCTGTGCC 1418
QY 961 GCTGTGCCCATTTAAACAGATGCGGAGAGTGTGGGGGTGCGCAGGCTGTGGAATG 1020
DB 1419 GCTGTGCCCATTTAAACAGATGCGGAGAGTGTGGGGGTGCGCAGGCTGTGTGAATG 1478
QY 1021 TATGAGAGACTTGTCTTAACGAGCCTGGGCAACCTTTGAACTTGAAGCTGTAAACGCCCCAG 1080
DB 1479 TATGAGAGACTTGTCTTAACGAGCCTGGGCAACCTTTGAACTTGAAGCTGTAAACGCCCCAG 1538
QY 1081 GCCATAAGCTGTAAACCTGTGATTTGCTGTGTGTGTAAACGCTTTGTTTCTGAAATGAT 1140
DB 1539 GCCATAAGCTGTAAACCTGTGATTTGCTGTGTGTGTAAACGCTTTGTTTCTGAAATGAT 1598
QY 1141 TGATGTAAAGTTTAAATAAGGAGTGAATATGTTTAACCTTGATGAGCGCTTGTGTAATGAT 1200
DB 1599 TGATGTAAAGTTTAAATAAGGAGTGAATATGTTTAACCTTGATGAGCGCTTGTGTAATGAT 1658
QY 1201 GGGGCTTAAAGGATATTAATGCGCGGTGAGCTTAATCTTGTTTACATCTGAATGA 1260
DB 1659 GGGGCTTAAAGGATATTAATGCGCGGTGAGCTTAATCTTGTTTACATCTGAATGA 1718
QY 1261 GGCCTGGAGAGTGTGGAAGATTTTCTGCTGTGCTTAATCTGCTGGAACAGAGCTCTTA 1320
DB 1719 GGCCTGGAGAGTGTGGAAGATTTTCTGCTGTGCTTAATCTGCTGGAACAGAGCTCTTA 1778
QY 1321 CAGTACTCTTGTGTTTGAAGGTTTCTGTGGGGGTCTATCCAGGCAAGTAAATGCTGAG 1380
DB 1779 CAGTACTCTTGTGTTTGAAGGTTTCTGTGGGGGTCTATCCAGGCAAGTAAATGCTGAG 1838
QY 1381 AATTAAGAGAGATTAACAAGTGGAAATTTGAAGACTTTTGAATCTGTGGTGAAGCTTT 1440

Db 1899 AATTAAAGGAGATTACAAAGTGGGAATTGGAAGCTTTGAAATCCTGTGAGACTGTT 1898
Qy 1441 TGAATTTCTTGAATCTGGGTCAACAGGCGCTTTTCCAGAGAAAGTCATCAAGACTTTTGA 1500
Db 1899 TGATTTCTTGAATCTGGGTCAACAGGCGCTTTTCCAGAGAAAGTCATCAAGACTTTTGA 1958
Qy 1501 TTTTTCACACCGGGGGCGGCTGGGCGTGTGCTTTTGTAGTTTATTAAGGAATA 1560
Db 1899 TTTTTCACACCGGGGGCGGCTGGGCGTGTGCTTTTGTAGTTTATTAAGGAATA 2018
Qy 1561 ATGAGCGAAGAAAACCATCTGAGCGGGGGTACTGCTGATTTTCTGGCATGCACTCT 1620
Db 2019 ATGAGCGAAGAAAACCATCTGAGCGGGGGTACTGCTGATTTTCTGGCATGCACTCT 2078
Qy 1621 GTGAGAGCGGTTGTGAGACACAGAAATCGCTGCTACTGTGTTCTTCCGTCGCCCGGC 1680
Db 2079 GTGAGAGCGGTTGTGAGACACAGAAATCGCTGCTACTGTGTTCTTCCGTCGCCCGGC 2138
Qy 1681 GATAAATCCGAGCGAGAGAGACAGACAGACAGAGAGAAACCGAGCGGCGGCGAGGA 1740
Db 2139 GATAAATCCGAGCGAGAGAGACAGACAGACAGAGAGAAACCGAGCGGCGGCGAGGA 2198
Qy 1741 GCAGAGCCCATGGAACCCGAGAGCGGCTGGAACCTCGGAAATGAATGTTGTACAGGTG 1800
Db 2199 GCAGAGCCCATGGAACCCGAGAGCGGCTGGAACCTCGGAAATGAATGTTGTACAGGTG 2258
Qy 1801 GCTGAATCTGATCCAGAACTGAGAGCAATTTTGAATTAAGAGATGGGCAAGGAGCTA 1860
Db 2259 GCTGAATCTGATCCAGAACTGAGAGCAATTTTGAATTAAGAGATGGGCAAGGAGCTA 2318
Qy 1861 AAGGGGGGTAAGAGAGAGAGCGGGGGCTTGTAGGCTAAGAGAGGCTAGGAATCTAGCT 1920
Db 2319 AAGGGGGGTAAGAGAGAGAGCGGGGGCTTGTAGGCTAAGAGAGGCTAGGAATCTAGCT 2378
Qy 1921 TTTAGCTTAATGACACAGACACCGTCTGTAGTGTATTAATTTTCAACAGATCAAGATAT 1980
Db 2379 TTTAGCTTAATGACACAGACACCGTCTGTAGTGTATTAATTTTCAACAGATCAAGATAT 2438
Qy 1981 TGGCCTAATGAGCTTGTCTGTGGCGAGAAAGTATTCATAGAGACAGCTGACCACTTAC 2040
Db 2439 TGGCCTAATGAGCTTGTGTCTGTGGCGAGAAAGTATTCATAGAGACAGCTGACCACTTAC 2498
Qy 2041 TTGGTGAAGCCAGGGGAGTATTTTGAAGAGGCTATTAAGGATATGCAAAAGTGGCATT 2100
Db 2499 TTGGTGAAGCCAGGGGAGTATTTTGAAGAGGCTATTAAGGATATGCAAAAGTGGCATT 2558
Qy 2101 AGGCGAGATTGCAAGTACAAAGTACGAAACTTGTAAATATCAGGAATTTGTGCTACATT 2160
Db 2559 AGGCGAGATTGCAAGTACAAAGTACGAAACTTGTAAATATCAGGAATTTGTGCTACATT 2618
Qy 2161 TCTGGGAAACGGGGCCGAGGTGAGATAGATAACGAGATAGGGTGGCTTTAGATGAGC 2220
Db 2619 TCTGGGAAACGGGGCCGAGGTGAGATAGATAACGAGATAGGGTGGCTTTAGATGAGC 2678
Qy 2221 ATGATTAATATGTGGCGGGGGGTGCTTGGCATGAGCGGGGTGTATTAATGAATGAAG 2280
Db 2679 ATGATTAATATGTGGCGGGGGGTGCTTGGCATGAGCGGGGTGTATTAATGAATGAAG 2738
Qy 2281 TTTTACTGGCCCAATTTTATAGCGGTATTTCTGTGSCAATAACCACTTATCTTACAC 2340
Db 2739 TTTTACTGGCCCAATTTTATAGCGGTATTTCTGTGSCAATAACCACTTATCTTACAC 2798
Qy 2341 GGTGTAAAGCTTCTATGGGTTTAAACATATCTGTGTGAAGCGTGGACCGATGAAGGTT 2400
Db 2799 GGTGTAAAGCTTCTATGGGTTTAAACATATCTGTGTGAAGCGTGGACCGATGAAGGTT 2858
Qy 2401 CGGGGCTGTGCTTTTATGCTGCTGGAAGGGGGGTGTGTCCGCCCAAAAGAGAGGCT 2460
Db 2859 CGGGGCTGTGCTTTTATGCTGCTGGAAGGGGGGTGTGTGTCCGCCCAAAAGAGAGGCT 2918
Qy 2461 TCAATTAAGAAATGCTCTTTGAAAGGTGTACTTGGGTATCTGTCTGAGAGGTTAACTCC 2520
Db 2919 TCAATTAAGAAATGCTCTTTGAAAGGTGTACTTGGGTATCTGTCTGAGAGGTTAACTCC 2978

Qy 2521 AGGTTGGCCCAATGTGGCTCCGACTGTGTTGCTTCACTGATGGAAGAGGTGGCT 2580
Db 2979 AGGGTGGCCCAATGTGGCTCCGACTGTGTTGCTTCACTGATGGAAGAGGTGGCT 3038
Qy 2581 GTGATTAAGCAATAATGTATGTGGCAATGCGAGAGACAGGGGCTCTCAGATGTGAGC 2640
Db 3039 GTGATTAAGCAATAATGTATGTGGCAATGCGAGAGACAGGGGCTCTCAGATGTGAGC 3098
Qy 2641 TGCTGGACCGCAACTGTCACTGCTGTAAGACCAATTCAGTAGCAGCACTTCGCAAG 2700
Db 3099 TGCTGGACCGCAACTGTCACTGCTGTAAGACCAATTCAGTAGCAGCACTTCGCAAG 3158
Qy 2701 GCTTGGCAAGTTTGTGACATTAATACTGACCCGCTGTTCTTGTGATTTGGGTAACAG 2760
Db 3159 GCTTGGCAAGTTTGTGACATTAATACTGACCCGCTGTTCTTGTGATTTGGGTAACAG 3218
Qy 2761 AGGGGGGGTTCCTACCTTACCAATGCAATTGAGTCACTAAGATATTGCTGAGCC 2820
Db 3219 AGGGGGGGTTCCTACCTTACCAATGCAATTGAGTCACTAAGATATTGCTGAGCC 3278
Qy 2821 GAGAGATGTCGAAAGTGAACCTGAAAGGGGTGTTGACATGACATGAAGATCTGAAG 2880
Db 3279 GAGAGATGTCGAAAGTGAACCTGAAAGGGGTGTTGACATGACATGAAGATCTGAAG 3338
Qy 2881 GTGCTGAGTACATGAGACCCGCAACAGGTGCAAGCCCTGAGTGTGGCGTAAATAT 2940
Db 3339 GTGCTGAGTACATGAGACCCGCAACAGGTGCAAGCCCTGAGTGTGGCGTAAATAT 3398
Qy 2941 ATTAGAAACCAAGCTGTGATGCTGATGTGAACGAGAGAGCTGAGGCCGATCACTGGTG 3000
Db 3399 ATTAGAAACCAAGCTGTGATGCTGATGTGAACGAGAGAGCTGAGGCCGATCACTGGTG 3458
Qy 3001 CTGGCTGCAACCGCGCTGAGTTTGGCTTACGATGAAGATACAGATTGAG 3052
Db 3459 CTGGCTGCAACCGCGCTGAGTTTGGCTTACGATGAAGATACAGATTGAG 3510

RESULT 2
AAC85020
ID AAC85020 standard; DNA; 33699 BP.
XX AC AAC85020;
XX DT 08-MAY-2001 (first entry)
XX DE Adenovirus anti-cancer vector GZ1 nucleotide sequence.
XX KW Adenovirus death protein; ADP; neoplastic; cell death; cancer therapy;
XX KW anti-cancer; gene therapy; cytosolic; GZ1; ds.
XX OS Mastadenovirus.
XX PN MO200104282-A2.
XX PD 18-JAN-2001.
XX PF 12-JUL-2000; 2000WO-US018971.
XX PR 12-JUL-1999; 99US-00351778.
XX PA (UTSL-) UNIV SAINT LOUIS.
XX PI Wold WSM, Toch K, Doronin K, Tollefson AE;
XX DR WPI; 2001-103079/11.
XX PT Recombinant vector which is replication-competent in a neoplastic cell
XX PT and overexpresses an adenovirus death protein, useful in cancer therapy
XX PT when used together with replication-defective adenovirus which expresses
XX PT an anti-cancer gene.
PS Claim 5; Page 138-147; 196pp; English.

XX	The invention relates to a recombinant vector (V1) which is replication-competent in a neoplastic cell and which overexpresses an adenovirus death protein (ADP). The vector can be used in a method for promoting death of a neoplastic cell that comprises contacting the neoplastic cell with at least one V1; and a composition comprising V1 and a second recombinant virus which is: (a) replication defective and which expresses an anti-cancer gene product, where V1 complements replication of the second recombinant virus; or (b) replication-competent in a neoplastic cell. V1, together with one or more replication-defective adenovirus which expresses an anti-cancer gene product, are useful in cancer therapy. Overexpression of ADP by V1 results in faster lysis of cells and spread of the virus throughout a cell monolayer than viruses expressing wild-type levels of ADP. The present sequence represents the complete nucleotide sequence of an adenovirus subgroup C anti-cancer vector G21 containing E3 deletion and overexpressing ADP									
XX	Sequence 33699 BP; 7771 A; 9497 C; 9310 G; 7121 T; 0 U; 0 Other;									
80	Query Match 100.0%; Score 3052; DB 4; Length 33699;									
	Best Local Similarity 100.0%; Pred. No. 0;									
	Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	CGGTACTGATTTATATACCCGGTAGTTCCTCAAGAGCCACTCTGTAGTGCACAGCT	60							
DB	459	CGGTAGTGTATATATATACCCGGTAGTTCCTCAAGAGCCACTCTGTAGTGCACAGCT	518							
QY	61	AGAGTTTCTCTCCGAGCCGCTCGACACCGGAGCTGAAATAGACATATATCTGCC	120							
DB	519	AGAGTTTCTCTCTCCGAGCCGCTCGACACCGGAGCTGAAATAGACATATATCTGCC	578							
QY	121	ACGAGGTGTTATTTACGAGAAATGCGCGCAGTCTTTGGACCACTGATCGAAGG	180							
DB	579	ACGAGGTGTTATTTACGAGAAATGCGCGCAGTCTTTGGACCACTGATCGAAGG	638							
QY	181	TACGAGCGTAAATCTTCCACCTCTACCAATTTTGAACCAACCTTACAGAACTGT	240							
DB	639	TACGAGCGTAAATCTTCCACCTCTACCAATTTTGAACCAACCTTACAGAACTGT	698							
QY	241	ATGATTTAGACGTACGGCCCCCGAAGATCCCAACGAGAGGCGGTTTCGAGATTTTC	300							
DB	699	ATGATTTAGACGTACGGCCCCCGAAGATCCCAACGAGAGGCGGTTTCGAGATTTTC	758							
QY	301	CCGACTCTGTAAATTTGGCGGTGACAGAAAGGATTAATTAATCTTTCGCGGAGC	360							
DB	759	CCGACTCTGTAAATTTGGCGGTGACAGAAAGGATTAATTAATCTTTCGCGGAGC	818							
QY	361	CCGATTTCCGGAGCCGCTCACTTTCGCCGAGCCGACGACGCGGAGAGAGAGCT	420							
DB	819	CCGATTTCCGGAGCCGCTCACTTTCGCCGAGCCGACGAGCGGAGAGAGAGCT	878							
QY	421	TGGGTCCGGTTCTATGCGAAACCTTGTACCGAGGTATGATTTTACCTGCCAGAG	480							
DB	879	TGGGTCCGGTTCTATGCGAAACCTTGTACCGAGGTATGATTTTACCTGCCAGAG	938							
QY	481	CTGGCTTTCCACCGAGTACGAGAGATGAAGAGGTGAGAGTTTGTTAGTATATG	540							
DB	939	CTGGCTTTCCACCGAGTACGAGAGATGAAGAGGTGAGAGTTTGTTAGTATATG	998							
QY	541	TGAGACACCCCGGACCGGTTGCAGGCTTGTCAATTAACCGAGGAATACGGGGACC	600							
DB	999	TGAGACACCCCGGACCGGTTGCAGGCTTGTCAATTAACCGAGGAATACGGGGACC	1058							
QY	601	CAGATTTAATGTGCTCGTTGCTATAGAGACCTGTGGCATGTTTGTCTACATAGT	660							
DB	1059	CAGATTTAATGTGCTCGTTGCTATAGAGACCTGTGGCATGTTTGTCTACATAGT	1118							
QY	661	GAAATTTATGAGGACGTGGGTATAGAGGTGTGGTTGTGTATTTTATTTTAT	720							
DB	1119	GAAATTTATGAGGACGTGGGTATAGAGGTGTGGTTGTGTATTTTATTTTAT	1178							
QY	721	TTTTCAGTTTGTGCTTTAAAGATTTTGTATTTTATTTTAAAGTCTGTGTC	780							


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OY 1861 AAGGGGTTAAAGAGGAGCGGGGGCTTGTAGGCTACAGAGAGGCTTAGGAATCTTACT 1920
DB 2319 AAGGGGGTAAAGAGGAGCGGGGGCTTGTAGGCTACAGAGAGGCTTAGGAATCTTACT 2378
OY 1921 TTTAGCTTAATGACAGACACCGTCTGTAGTGTATTTACTTTTCAACAGATCAAGGATAT 1980
DB 2379 TTTAGCTTAATGACAGACACCGTCTGTAGTGTATTTACTTTTCAACAGATCAAGGATAT 2438
OY 1981 TGGCTAAATGAGCTTGTCTGTGGCGGAGAAATTCATAGAGACGCTGACCACTTAC 2040
DB 2439 TGGCTAAATGAGCTTGTCTGTGGCGGAGAAATTCATAGAGACGCTGACCACTTAC 2498
OY 2041 TGGCTGACGACGAGGAGATTTTAAAGAGGCTATTAGGATATATGCAAGGTGCACATT 2100
DB 2499 TGGCTGACGACGAGGAGATTTTAAAGAGGCTATTAGGATATATGCAAGGTGCACATT 2558
OY 2101 AGGCCAGATTGCAAGTACAAAGATCAGCAAACTGTAAATATCAGGAATTTGTTGCTACATT 2160
DB 2559 AGGCCAGATTGCAAGTACAAAGATCAGCAAACTGTAAATATCAGGAATTTGTTGCTACATT 2618
OY 2161 TCTGGGAAACGGGGCGGAGGTGAGATAGATACGAGAGATAGGGTGGCTTTAGATGTAGC 2220
DB 2619 TCTGGGAAACGGGGCGGAGGTGAGATAGATACGAGAGATAGGGTGGCTTTAGATGTAGC 2678
OY 2221 ATGATAAATATGTGGCGGGGGTGTGGCATGACGGGGTGTATTATATGATGTAAAG 2280
DB 2679 ATGATAAATATGTGGCGGGGGTGTGGCATGACGGGGTGTATTATATGATGTAAAG 2738
OY 2281 TTTACTGGCCCCCAATTTTAGCGGTACGGTTTCTGGCGCAATACCAACTTATCCTTACAC 2340
DB 2739 TTTACTGGCCCCCAATTTTAGCGGTACGGTTTCTGGCGCAATACCAACTTATCCTTACAC 2798
OY 2341 GGTGTAAAGCTTCTATGGGTTTAAACATACCTGTGTGAAGCCTGACCGATGTAAAGGTT 2400
DB 2799 GGTGTAAAGCTTCTATGGGTTTAAACATACCTGTGTGAAGCCTGACCGATGTAAAGGTT 2858
OY 2401 CGGGGCTGTGCTTTTACTGCTGTGGAAGGGGGTGTGTGTCCGCCCAAAAGCGGCT 2460
DB 2859 CGGGGCTGTGCTTTTACTGCTGTGGAAGGGGGTGTGTGTCCGCCCAAAAGCGGCT 2918
OY 2461 TCAATTTAAGAAATGCTCTTTGAAAGGTGTACTTGGGTATCCTGTCTGAGGGTAACTCC 2520
DB 2919 TCAATTTAAGAAATGCTCTTTGAAAGGTGTACTTGGGTATCCTGTCTGAGGGTAACTCC 2978
OY 2521 AGGGTGCGCCCAATGTGTGCTCCGACTGTGTTGCTTCAATGCTAGTGAAGGCGTGCCT 2580
DB 2979 AGGGTGCGCCCAATGTGTGCTCCGACTGTGTTGCTTCAATGCTAGTGAAGGCGTGCCT 3038
OY 2581 GTGATTTAAGCATTAATGTGTGTGTGCAATGTCGAGAGACAGGGGCTCTCAGATGCTGACC 2640
DB 3039 GTGATTTAAGCATTAATGTGTGTGTGCAATGTCGAGAGACAGGGGCTCTCAGATGCTGACC 3098
OY 2641 TGCCTCGGACGGCAACTGTGCACTGCTGAAGCAATTCACGTAGCAGCACTCTCCGAAAG 2700
DB 3099 TGCCTCGGACGGCAACTGTGCACTGCTGAAGCAATTCACGTAGCAGCACTCTCCGAAAG 3158
OY 2701 GCCTGCGCAGTGTGTGACATATGACACCGGCTGTTCCTTGCATTTGGGTAAACAG 2760
DB 3159 GCCTGCGCAGTGTGTGACATATGACACCGGCTGTTCCTTGCATTTGGGTAAACAG 3218
OY 2761 AGGGGGGTGTTCTTACCTTACCAATGCAATTTGAGTCACTAAGATATTTCTTGAGCCC 2820
DB 3219 AGGGGGGTGTTCTTACCTTACCAATGCAATTTGAGTCACTAAGATATTTCTTGAGCCC 3278
OY 2821 GAGAGCATGTCCAGAGTGAACCTTGAACGGGGTGTGTCATGACCATGAAAGATCTGGAAG 2880
DB 3279 GAGAGCATGTCCAGAGTGAACCTTGAACGGGGTGTGTCATGACCATGAAAGATCTGGAAG 3338
OY 2881 GTGTGAGGTACGATGAGACCCGACACAGGTGACAGACCTTGCAGTGTGGCGGTAAACAT 2940
DB 3339 GTGTGAGGTACGATGAGACCCGACACAGGTGACAGACCTTGCAGTGTGGCGGTAAACAT 3398
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OY 2941 ATTAGGAACCAAGCCTGTGATGTCTGATGTGACCGAGAGACTGAGGCCCGATCATTTGCTG 3000
DB 3399 ATTAGGAACCAAGCCTGTGATGTCTGATGTGACCGAGAGACTGAGGCCCGATCATTTGCTG 3458
OY 3001 CTGGCCTTCGACCCCGCGCTGAGTTTGGCTCTGACCATGAAATACAGATTGAG 3052
DB 3459 CTGGCCTTCGACCCCGCGCTGAGTTTGGCTCTGACCATGAAATACAGATTGAG 3510

RESULT 3
AAC85021
ID AAC85021 standard; DNA; 34448 BP.
XX
AC AAC85021;
XX
DT 08-MAY-2001 (first entry)
XX
DE Adenovirus anti-cancer vector GZ3 nucleotide sequence.
XX
KW Adenovirus death protein; ADP; neoplastic; cell death; cancer therapy;
XX anti-cancer; gene therapy; cytosolic; GZ3; ds.
XX
OS Mastadenovirus.
XX
PN M0200104282-A2.
XX
PD 18-JAN-2001.
XX
PF 12-JUL-2000; 2000MO-US018971.
XX
PR 12-JUL-1999; 99US-00351778.
XX
PA (UWSL-) UNIV SAINT LOUIS.
XX
PI M01D WSM, Toch K, Doronin K, Tollefson AE;
XX WPI: 2001-103079/11.
XX
DR
XX
PT Recombinant vector which is replication-competent in a neoplastic cell
XX and overexpresses an adenovirus death protein, useful in cancer therapy
XX PT when used together with replication-defective adenovirus which expresses
XX an anti-cancer gene.
XX
PS Claim 5; Page 147-156; 196bp; English.
XX
CC The invention relates to a recombinant vector (VI) which is replication-
XX competent in a neoplastic cell and which overexpresses an adenovirus
XX death protein (ADP). The vector can be used in a method for promoting
XX death of a neoplastic cell that comprises contacting the neoplastic cell
XX with at least one VI; and a composition comprising VI and a second
XX recombinant virus which is: (a) replication defective and which
XX expresses an anti-cancer gene product, where VI complements replication
XX of the second recombinant virus; or (b) replication-competent in a
XX neoplastic cell, VI, together with one or more replication-defective
XX adenovirus which expresses an anti-cancer gene product, are useful in
XX cancer therapy. Overexpression of ADP by VI results in faster lysis of
XX cells and spread of the virus throughout a cell monolayer than viruses
XX expressing wild-type levels of ADP. The present sequence represents the
XX complete nucleotide sequence of an adenovirus subgroup C anti-cancer
XX vector GZ3 containing B3 deletion and overexpressing ADP
XX
SQ Sequence 34448 BP; 7978 A; 9698 C; 9489 G; 7283 T; 0 U; 0 Other;

Query Match 100.0%; Score 3052; DB 4; Length 34448;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGTGTAGTGTATTATTAACCCGGTGAAGTTCTCAAGAGCCCACTTTAGTGCCAGGAGT 60
DB 459 CGTGTAGTGTATTATTAACCCGGTGAAGTTCTCAAGAGCCCACTTTAGTGCCAGGAGT 518
OY 61 AGAGTTTCTCCCTCCGAGCGGCTCCGACACCGGACCTGAAGAAATGAACATATTCTGCC 120
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Db 519 AGAGTTTCTCCTCCGAGCCGCTCCGACACCGGGAGCTGMAAATGAGACATATTAATCTGCC 578
Oy 121 ACGGAGGTTATTAACGAGAAATGCGCGAGCTTTTGACACAGTGATTCGAAAGG 180
Db 579 ACGGAGGTTATTAACGAGAAATGCGCGAGCTTTTGACACAGTGATTCGAAAGG 638
Oy 181 TACTGGCTGATTAATCTTCACCTCCTAGCCATTTTGAACACACTACCTTCACGAACTGT 240
Db 639 TACTGGCTGATTAATCTTCACCTCCTAGCCATTTTGAACACACTACCTTCACGAACTGT 698
Oy 241 ATGATTTAGAGTGACGCGCCCCGAAAGATCCCAAGAGAGCGGTTTCGAGATTTTTC 300
Db 699 ATGATTTAGAGTGACGCGCCCCGAAAGATCCCAAGAGAGCGGTTTCGAGATTTTTC 758
Oy 301 CCGACTCTGATATGTGGCGGTGACGAAAGGATTAATCTTACTCATTTTCGCGCGCGC 360
Db 759 CCGACTCTGATATGTGGCGGTGACGAAAGGATTAATCTTACTCATTTTCGCGCGCGC 818
Oy 361 CCGGTTCTCCGAGCGGCTCACTTTCCGCGACGCCGAGCGCGAGGAGAGGCT 420
Db 819 CCGGTTCTCCGAGCGGCTCACTTTCCGCGACGCCGAGCGCGAGGAGAGGCT 878
Oy 421 TGGGTCGGGTTCTATGCGCAAACCTTGTAACGGAGTGATGATCTTAACCTGCCAGAG 480
Db 879 TGGGTCGGGTTCTATGCGCAAACCTTGTAACGGAGTGATGATCTTAACCTGCCAGAG 938
Oy 481 CTGGCTTCCACCGCGTAGACGACGAGATGAAGAGGTGAGAGGTTGTTAGATTATG 540
Db 939 CTGGCTTCCACCGCGTAGACGACGAGATGAAGAGGTGAGAGGTTGTTAGATTATG 998
Oy 541 TGGAGCACCCGCGGACGAGTTGACAGTCTGTCAATATCACCGAGAGAAACGCGGGAGC 600
Db 999 TGGAGCACCCGCGGACGAGTTGACAGTCTGTCAATATCACCGAGAGAAACGCGGGAGC 1058
Oy 601 CAGATATTATGTGTTCCGCTTGTCTATATGAGACCTGTGGCAATGTTGTCTACAGTAAGT 660
Db 1059 CAGATATTATGTGTTCCGCTTGTCTATATGAGACCTGTGGCAATGTTGTCTACAGTAAGT 1118
Oy 661 GAAATTTATGGGCAGTGGGTGATATGAGTGTTGGTTGTGTGTAATTTTTTTTTTAT 720
Db 1119 GAAATTTATGGGCAGTGGGTGATATGAGTGTTGGTTGTGTGTAATTTTTTTTTTAT 1178
Oy 721 TTTTACAGTTTGTGTTTAAAGAAATTTTGTATGTGATTTTAAAGGTCGTGTC 780
Db 1179 TTTTACAGTTTGTGTTTAAAGAAATTTTGTATGTGATTTTAAAGGTCGTGTC 1238
Oy 781 TGAACCTGAGCTGAGCCCGAGCCAGAACCGGAGCTTGCAAGACTTACCCGCTCTTA 840
Db 1239 TGAACCTGAGCTGAGCCCGAGCCAGAACCGGAGCTTGCAAGACTTACCCGCTCTTA 1298
Oy 841 AATGCGGCTGCTATCCGAGACGCGCGACATCACTGTGTCTAGAGATGAATAGTAG 900
Db 1299 AATGCGGCTGCTATCCGAGACGCGCGACATCACTGTGTCTAGAGATGAATAGTAG 1358
Oy 901 TACGATAGCTGTGACTCCGCTCTTCTTAACACACTCTTGAGATACACCGGTGTC 960
Db 1359 TACGATAGCTGTGACTCCGCTCTTCTTAACACACTCTTGAGATACACCGGTGTC 1418
Oy 961 GCTGTGCCCATTAACAGATTGCCGTGAGAGATTGTGGCGCTCGCAAGGCTGTGAAATG 1020
Db 1419 GCTGTGCCCATTAACAGATTGCCGTGAGAGATTGTGGCGCTCGCAAGGCTGTGAAATG 1478
Oy 1021 TATGAGAGACTTGTCTTAACGAGCCTGGGCAACTTTTGAATTGAGCTTAAACGCCCGAG 1080
Db 1479 TATGAGAGACTTGTCTTAACGAGCCTGGGCAACTTTTGAATTGAGCTTAAACGCCCGAG 1538
Oy 1081 GCAATTAAGGTGTAACCTGTGATTGCTGTGTTAGCTTACGCTTGTGCTGATGAGT 1140
Db 1539 GCAATTAAGGTGTAACCTGTGATTGCTGTGTTAGCTTACGCTTGTGCTGATGAGT 1598
Oy 1141 TGATTAATATGTTAAATGAAGGTGAGATATGTTTAACTTGCAATGCGGTAAATGGGCG 1200
Db 1599 TGATTAATATGTTAAATGAAGGTGAGATATGTTTAACTTGCAATGCGGTAAATGGGCG 1658

Oy 1201 GGGGCTTAAAGGATATTAATGCGCGTGGGCTAATCTTGTTACATCTGACCTCATGGA 1260
Db 1659 GGGGCTTAAAGGATATTAATGCGCGCTGGGCTAATCTTGTTACATCTGACCTCATGGA 1718
Oy 1261 GGGTGGAGGTGTTTGGAAATTTTCTGCTGTGCTGATCTTGTGTGAACAGAGCTCTTA 1320
Db 1719 GGGTGGAGGTGTTTGGAAATTTTCTGCTGTGCTGATCTTGTGTGAACAGAGCTCTTA 1778
Oy 1321 CAGTACTCTTGGTTTGGAGTTTCTGTGGGCTCATCCAGGCAAAATGATGCTGAG 1380
Db 1779 CAGTACTCTTGGTTTGGAGTTTCTGTGGGCTCATCCAGGCAAAATGATGCTGAG 1838
Oy 1381 AATTAAGAGGATTAACAAGTGGGAATTTTGAAGACTTTTGAATCTCTGTGTGACTGTT 1440
Db 1839 AATTAAGAGGATTAACAAGTGGGAATTTTGAAGACTTTTGAATCTCTGTGTGACTGTT 1898
Oy 1441 TGATTTCTTGAATCTGGGTCAACAGGCGCTTTTCCAAAGAAAGTCAATCAAGCTTTGA 1500
Db 1899 TGATTTCTTGAATCTGGGTCAACAGGCGCTTTTCCAAAGAAAGTCAATCAAGCTTTGA 1958
Oy 1501 TTTTTCACACCGGGGCGCGCTGCGCTGTGCTTTTGTAGTTTATTAAGATTA 1560
Db 1959 TTTTTCACACCGGGGCGCGCTGCGCTGTGCTTTTGTAGTTTATTAAGATTA 2018
Oy 1561 ATGAGCGAAGAAACCCATCTGAGCGGGGGTACCTGCTGGAATTTTCTGCGCATGCACT 1620
Db 2019 ATGAGCGAAGAAACCCATCTGAGCGGGGGTACCTGCTGGAATTTTCTGCGCATGCACT 2078
Oy 1621 GTGAGAGCGGTTGTGAGACCAAGAAATCGCTGCTAATGTTGCTTCCGTCGCGCGGC 1680
Db 2079 GTGAGAGCGGTTGTGAGACCAAGAAATCGCTGCTAATGTTGCTTCCGTCGCGCGGC 2138
Oy 1681 GATTAATCCGACGAGAGACGACGACGACGACGAGAGAAACCGCGCGCGCAGAGA 1740
Db 2139 GATTAATCCGACGAGAGACGACGACGACGACGAGAGAAACCGCGCGCGCAGAGA 2198
Oy 1741 GCAGAGCCCATGGAACCCGAGAGCGGCTGTGACCTCGGGAATGAATGTTGTACAGGTG 1800
Db 2199 GCAGAGCCCATGGAACCCGAGAGCGGCTGTGACCTCGGGAATGAATGTTGTACAGGTG 2258
Oy 1801 GCTGAACCTGATCCAGAACTGAGACGCAATTTTGAATTAACAGAGATGGCAGGGCTA 1860
Db 2259 GCTGAACCTGATCCAGAACTGAGACGCAATTTTGAATTAACAGAGATGGCAGGGCTA 2318
Oy 1861 AAGGGGTAAAGAGAGAGCGGGGGCTTGTGAGGCTACAGAGAGGCTTAAGAACTTACT 1920
Db 2319 AAGGGGTAAAGAGAGAGCGGGGGCTTGTGAGGCTACAGAGAGGCTTAAGAACTTACT 2378
Oy 1921 TTTAGCTTAATGACCAAGACCGTCTGAGTGATTTACTTTTCAACAGATCAAGGATTAAT 1980
Db 2379 TTTAGCTTAATGACCAAGACCGTCTGAGTGATTTACTTTTCAACAGATCAAGGATTAAT 2438
Oy 1981 TGCCTAATGAGCTTGAATCTGTGGCGCAAGATTAATCCATAGAGCACTGACCACTTAC 2040
Db 2439 TGCCTAATGAGCTTGAATCTGTGGCGCAAGATTAATCCATAGAGCACTGACCACTTAC 2498
Oy 2041 TGGCTGACGCGAGGAGATGATTTTGAAGAGCTATTAGGGTATATGCAAGGTGGCACTT 2100
Db 2499 TGGCTGACGCGAGGAGATGATTTTGAAGAGCTATTAGGGTATATGCAAGGTGGCACTT 2558
Oy 2101 AGGCGAGTTTGCAAGTCAAGATCAGCAAACTTGTAAATACAGAAATGTGTGCTACATT 2160
Db 2559 AGGCGAGTTTGCAAGTCAAGATCAGCAAACTTGTAAATACAGAAATGTGTGCTACATT 2618
Oy 2161 TCTGGGAAACGGGGCGAGGTGAGATTAATCGAGAGATAGGGTGGCTTTTATGATGAGC 2220
Db 2619 TCTGGGAAACGGGGCGAGGTGAGATTAATCGAGAGATAGGGTGGCTTTTATGATGAGC 2678
Oy 2221 ATGATTAATATGTGGCGGGGGTGTCTTGCAATGAGCGGGGTGTTATTAATGATTAAG 2280
Db 2679 ATGATTAATATGTGGCGGGGGTGTCTTGCAATGAGCGGGGTGTTATTAATGATTAAG 2738

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Oy 2281 TTTACTGSCCCCAATTTAGGGTACGGTTTTCTGSCCAATACCAACTTATCTTACAC 2340
Db 2739 TTTACTGSCCCCAATTTAGGGTACGGTTTTCTGSCCAATACCAACTTATCTTACAC 2798
Oy 2341 GGTGTAAAGCTTCTATAGGTTTAAACATACCTGTGTGAAGCGCTGGACCGATGTAAAGGTT 2400
Db 2799 GGTGTAAAGCTTCTATAGGTTTAAACATACCTGTGTGAAGCGCTGGACCGATGTAAAGGTT 2858
Oy 2401 CGGGGCTGTGCTTTTACTGCTGTGAAGGGGGGTGTGTGTGCGCCCAAAAGCAGGGCT 2460
Db 2859 CGGGGCTGTGCTTTTACTGCTGTGAAGGGGGGTGTGTGTGCGCCCAAAAGCAGGGCT 2918
Oy 2461 TCAATTAGAAATGCTCTTTGAAAGGTATCCTTGGGTATCCTGTCTGAGGGTAACTCC 2520
Db 2919 TCAATTAGAAATGCTCTTTGAAAGGTATCCTTGGGTATCCTGTCTGAGGGTAACTCC 2978
Oy 2521 AGGGTGCSCCAAAATGATGGCTCCGACTGTGTTGCTTCACTAGTAAAGCGTGGCT 2580
Db 2979 AGGGTGCSCCAAAATGATGGCTCCGACTGTGTTGCTTCACTAGTAAAGCGTGGCT 3038
Oy 2581 GTGATTAAGCATTAACATGATATGTGGCAACTGCGAGACAGGGGCTCTCAGATGCTGACC 2640
Db 3039 GTGATTAAGCATTAACATGATATGTGGCAACTGCGAGACAGGGGCTCTCAGATGCTGACC 3098
Oy 2641 TGTCTGAGCGGCAACTGTCACTGTGTGAAGCAATTCAGTACCGCACTCTTCGCAAG 2700
Db 3099 TGTCTGAGCGGCAACTGTCACTGTGTGAAGCAATTCAGTACCGCACTCTTCGCAAG 3158
Oy 2701 GCTGTGCGCAAGTGTGTGAACATTAACATCTGACCGCGTGTCTTGGATTTGGATTAACAG 2760
Db 3159 GCTGTGCGCAAGTGTGTGAACATTAACATCTGACCGCGTGTCTTGGATTTGGATTAACAG 3218
Oy 2761 AGGGGGGTGTCTTCACTTACCAATGCAATTGAGTCACTAAGATTTGCTTGAAGCCC 2820
Db 3219 AGGGGGGTGTCTTCACTTACCAATGCAATTGAGTCACTAAGATTTGCTTGAAGCCC 3278
Oy 2821 GAGAGCATGTCACAGGTGAACCTGAACGGGGTGTGTGATGACATGACCAATGAATCTGGAAG 2880
Db 3279 GAGAGCATGTCACAGGTGAACCTGAACGGGGTGTGTGATGACATGACCAATGAATCTGGAAG 3338
Oy 2881 GTGCTGAGGTACGATGAGACCCGACCAAGGTGCAAGCCCTGCAAGTGTGGGGTAAACAT 2940
Db 3339 GTGCTGAGGTACGATGAGACCCGACCAAGGTGCAAGCCCTGCAAGTGTGGGGTAAACAT 3398
Oy 2941 ATTAGGAACCAAGCTGTGATGCTGATGTGAACCAAGAGCTGAGGCCGATCACTTGGTG 3000
Db 3399 ATTAGGAACCAAGCTGTGATGCTGATGTGAACCAAGAGCTGAGGCCGATCACTTGGTG 3458
Oy 3001 CTGGGCTGCAACCGCGCTGATTTGGCTTACGATGAAGATTAAGATTGAG 3052
Db 3459 CTGGGCTGCAACCGCGCTGATTTGGCTTACGATGAAGATTAAGATTGAG 3510

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RESULT 4
AB282331 standard; DNA; 35934 BP.

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XX ID AB282331 standard; DNA; 35934 BP.
XX AC AB282331;
XX DT 14-MAY-2003 (first entry)
XX DE Human adenovirus type 5 genome.
XX KM Adenovirus; PIX; protein IX; gene delivery efficiency; haemostatic;
XX cytoabatic; anti-HIV; virucide; gene therapy; genome; de.
XX OS Human adenovirus type 5.
XX PN W0200296939-A2.
XX PD 05-DEC-2002.
XX PF 29-MAY-2002; 2002MO-EP005942.

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XX 30-MAY-2001; 2001US-029374P.
XX (TRGE ) TRANSGENE SA.
XX Rosa Calatrava M;
XX WPI: 2003-18388/18.
XX Novel modified adenovirus protein IX and its presence in virus or virus-
XX PT like particle, useful for improving gene delivery efficiency in target
XX cell of virus or virus-like particle.
XX Disclosure; Fig 6; 126pp; English.
XX
XX The invention relates to a novel adenovirus protein IX (PIX) modified by
XX mutation of one or more amino acids of PIX as compared to corresponding
XX wild-type PIX and/or to comprise a binding moiety. The presence of
XX modified PIX in a virus or virus-like particle (VLP) results in improved
XX gene delivery efficiency in the target cell of a virus or VLP as compared
XX to the gene delivery efficiency of a virus or VLP containing wild-type
XX PIX. The protein of the invention has haemostatic, cytoabatic, anti-HIV,
XX and virucide activity. The sequence may have a use in gene therapy. The
XX present sequence represents the human adenovirus type 5 genome
XX
XX Sequence 35934 BP; 8367 A; 10072 C; 9761 G; 7734 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 3052; DB 8; Length 35934;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 1 CGTGTAGTATTTTAAACCCGGTGAAGTTCTCAAGAGGCCACTTTAGTCCAGCAGT 60
Db 459 CGTGTAGTATTTTAAACCCGGTGAAGTTCTCAAGAGGCCACTTTAGTCCAGCAGT 518
Oy 61 AGAGTTTTCCTCCCGAGCGGCTCCGACACCGGACGTAAGAAATGACATTTATCTGCC 120
Db 519 AGAGTTTTCCTCCCGAGCGGCTCCGACACCGGACGTAAGAAATGACATTTATCTGCC 578
Oy 121 ACGGAGGTGTTATTAACGAAGAAATGAGCCGCACTTTTGAACCACTGATCGAAGAG 180
Db 579 ACGGAGGTGTTATTAACGAAGAAATGAGCCGCACTTTTGAACCACTGATCGAAGAG 638
Oy 181 TACTGGCTGATATCTTCAACTCTTACCAATTTTGAACCACTTACCAACTGT 240
Db 639 TACTGGCTGATATCTTCAACTCTTACCAATTTTGAACCACTTACCAACTGT 698
Oy 241 ATGATTTAGACGTGACGGCCCGGAAATCCCAACGAGAGGGGCTTTCGAGATTTTC 300
Db 699 ATGATTTAGACGTGACGGCCCGGAAATCCCAACGAGAGGGGCTTTCGAGATTTTC 758
Oy 301 CCGACTCTGATATGTTGGCGGTGACAGAGGAGATTGACTTACTCTTCCGCGGCG 360
Db 759 CCGACTCTGATATGTTGGCGGTGACAGAGGAGATTGACTTACTCTTCCGCGGCG 818
Oy 361 CCGGTTTCCGAGACCGCTTACTTTCCGCGAGCCGAGACCGGAGACGAGACCT 420
Db 819 CCGGTTTCCGAGACCGCTTACTTTCCGCGAGCCGAGACCGGAGACGAGACCT 878
Oy 421 TGGGTCCGGTTTCTATGSCCAAACTTGTACCGGAGGTGATGATCTTACCGGCAAGG 480
Db 879 TGGGTCCGGTTTCTATGSCCAAACTTGTACCGGAGGTGATGATCTTACCGGCAAGG 938
Oy 481 CTGGCTTTTCAACCAAGTACGACGAGGATGAAGAGGTGAGATTGTGTAGATTATG 540
Db 939 CTGGCTTTTCAACCAAGTACGACGAGGATGAAGAGGTGAGATTGTGTAGATTATG 998
Oy 541 TGGAGCACCCCGGACAGGTTGACAGGTTCTTGTATTATCACCGAGGAATACGGGGGAC 600
Db 999 TGGAGCACCCCGGACAGGTTGACAGGTTCTTGTATTATCACCGAGGAATACGGGGGAC 1058
Oy 601 CAGATATTATGTGTGCTTGTGATATTAGGACCTTGGCATGTTGTCTACAGTAAGT 660

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Db	1059	CAGATATTATGTGTCCTGTTGCTATATAGAGAACTGTGGCATGTTGTCTACAGTAAGT	1118
Oy	661	GAATAATTATGGGCAAGTGGGTGATAGAGTGTGGGTTTGGTGTGTAAATTTTTTTTTTAAT	720
Db	1119	GAATAATTATGGGCAAGTGGGTGATAGAGTGTGGGTTTGGTGTGTAAATTTTTTTTTTAAT	1178
Oy	721	TTTTTACAGTTTGTGGTTTAAAGAAATTTTGTATTGTGATTTTTTTTAAAGGTCCTGTGTC	780
Db	1179	TTTTTACAGTTTGTGGTTTAAAGAAATTTTGTATTGTGATTTTTTTTAAAGGTCCTGTGTC	1238
Oy	781	TGAACCTGAGCGCTGAGCCCGAGCCAGAAACCGAGACCTGCAAGACCTACCCGCGCTCTAA	840
Db	1239	TGAACCTGAGCGCTGAGCCCGAGCCAGAAACCGAGACCTGCAAGACCTACCCGCGCTCTAA	1298
Oy	841	AATGGCGCCTGCTATCTCGAGACGGCCGACATCACTGTGTCTAGAGATATGCATATAGAG	900
Db	1299	AATGGCGCCTGCTATCTCGAGACGGCCGACATCACTGTGTCTAGAGATATGCATATAGAG	1358
Oy	901	TACGGATATGCTGTGACTCCGGTCTCTTCTTAAACAACCTCTGAGATPACACCCGGTGTGCC	960
Db	1359	TACGGATATGCTGTGACTCCGGTCTCTTCTTAAACAACCTCTGAGATPACACCCGGTGTGCC	1418
Oy	961	GCTGGCCCCCATTTAAACCAAGTTGCGGTGAGAGTTGGTGGGGGTGGCCAGGCTGTGGAGTG	1020
Db	1419	GCTGGCCCCCATTTAAACCAAGTTGCGGTGAGAGTTGGTGGGGGTGGCCAGGCTGTGGAGTG	1478
Oy	1021	TATCGAGACTTGTCTTAAACGAGCCTGGCAACCTTTGACCTTGAGACTGTAAACGCCACAG	1080
Db	1479	TATCGAGACTTGTCTTAAACGAGCCTGGCAACCTTTGAGACTTGAGACTGTAAACGCCACAG	1538
Oy	1081	GCCATATAGCTGTAAACCTGTGATTTGCGTGTGGTTAAACGCTTTTGTGCTGATATGACT	1140
Db	1539	GCCATATAGCTGTAAACCTGTGATTTGCGTGTGGTTAAACGCTTTTGTGCTGATATGACT	1598
Oy	1141	TGATGTAGTTTAAATTAAGGGTGAGATATGTTTAAACCTGATGGCGGTAAATGGGGC	1200
Db	1599	TGATGTAGTTTAAATTAAGGGTGAGATATGTTTAAACCTGATGGCGGTAAATGGGGC	1658
Oy	1201	GGGGCTTAAAGGATATATATGCGCGGTGGCTATCTTGCTTACATCTGACCTCATGSA	1260
Db	1659	GGGGCTTAAAGGATATATATGCGCGGTGGCTATCTTGCTTACATCTGACCTCATGSA	1718
Oy	1261	GCGTTGGGAGTGTGGAAATTTTTCTGCTGTGCTTAACTTGCTGGAAACAGACTCTTAA	1320
Db	1719	GCGTTGGGAGTGTGGAAATTTTTCTGCTGTGCTTAACTTGCTGGAAACAGACTCTTAA	1778
Oy	1321	CAGTACCTCTGTGTTTGGAGAGTTTCTGTGGGGCTCAATCCAGGCAAAAGTATAGTCTGAG	1380
Db	1779	CAGTACCTCTGTGTTTGGAGAGTTTCTGTGGGGCTCAATCCAGGCAAAAGTATAGTCTGAG	1838
Oy	1381	AATTATAGAGAGATTACAAGTGGGAATTTGAAGAGCTTTTGAATTCCTGTGTGAGCTGTT	1440
Db	1839	AATTATAGAGAGATTACAAGTGGGAATTTGAAGAGCTTTTGAATTCCTGTGTGAGCTGTT	1898
Oy	1441	TGATTCTTTGAATCTGGGTCAACAGGCGCTTTTCAAGAGAAAGTCATCAAGACTTTGGA	1500
Db	1899	TGATTCTTTGAATCTGGGTCAACAGGCGCTTTTCAAGAGAAAGTCATCAAGACTTTGGA	1958
Oy	1501	TTTTTCCACACCGGGGCGCGCTGGCGTGTGCTTTTGTGAGTTTATTAAGAGATPA	1560
Db	1959	TTTTTCCACACCGGGGCGCGCTGGCGTGTGCTTTTGTGAGTTTATTAAGAGATPA	2018
Oy	1561	ATGAGAGCAAGAAACCATCTGAGCGGGGGAGATACCTGTGGAATTTTCTGGCCATGACATCT	1620
Db	2019	ATGAGAGCAAGAAACCATCTGAGCGGGGGAGATACCTGTGGAATTTTCTGGCCATGACATCT	2078
Oy	1621	GTGAGAGCGGTTGTGAGACACAAGAAATCGCTGTGCTATCTGTTGTCTTCCGTCGCGCGGC	1680
Db	2079	GTGAGAGCGGTTGTGAGACACAAGAAATCGCTGTGCTATCTGTTGTCTTCCGTCGCGCGGC	2138
Oy	1681	GATTAATACCGACGAGACGACGACGACGACGACGACGAGGCGGCGGCGGACGSA	1740
Db	2139	GATTAATACCGACGAGACGACGACGACGACGACGAGGCGGCGGCGGCGGACGSA	2198

QY	1741	GCAGAGCCCATGGAATCCCGAGAGCCCGGCTCTGGACCTTCGGGAATGAAATGTTTGTACAGCTG	1800
Db	2199	GCAGAGCCCATGGAATCCCGAGAGCCCGGCTCTGGACCCCTCGGGAAATGAAATGTTTGTACAGCTG	2258
QY	1801	GCAGAACTGTATCCAGAACTGAGACGCAATTTTGACATTAATACAGAGATGGGACAGGGCTCTA	1860
Db	2259	GCTGAACTGTATCCAGAACTGAGACGCAATTTTGACATTAATACAGAGATGGGACAGGGCTCTA	2318
QY	1861	AAAGGGGTAAAGAGAGAGCGGGGGGCTTGTGAGGCTACAGAGAGGCTAGGAATCTAGCT	1920
Db	2319	AAAGGGGTAAAGAGAGAGCGGGGGGCTTGTGAGGCTACAGAGAGGCTAGGAATCTAGCT	2378
QY	1921	TTTAACTTAATGACCGAGACCGGCTCGATGTATTAATCTTTCAACAGATCAAGATTAAT	1980
Db	2379	TTTAACTTAATGACCGAGACCGGCTCGATGTATTAATCTTTCAACAGATCAAGATTAAT	2438
QY	1981	TGCGCTAATGAGCTTGAATCTGTGCGCAGAAATTAATCCATAGACAGCTGACCACTTAC	2040
Db	2439	TGCGCTAATGAGCTTGAATCTGTGCGCAGAAATTAATCCATAGACAGCTGACCACTTAC	2498
QY	2041	TGCGTGAAGCCAGGGAGTGAATTTTGAGAGGCTAATTAAGGTTAATGCAAGGTGGCACTT	2100
Db	2499	TGCGTGAAGCCAGGGAGTGAATTTTGAGAGGCTAATTAAGGTTAATGCAAGGTGGCACTT	2558
QY	2101	AGGCGAATGTCAGAAATGCAAGATCAGCAAACTTGAATATCAGAAATTTGTTGCTACATT	2160
Db	2559	AGGCGAATGTCAGAAATGCAAGATCAGCAAACTTGAATATCAGAAATTTGTTGCTACATT	2618
QY	2161	TCCTGGGAACGGGGCCGAGGTGAGATGATACGAGAGATAGGCTGGCTTTAGATGTAGC	2220
Db	2619	TCCTGGGAACGGGGCCGAGGTGAGATGATACGAGAGATAGGCTGGCTTTAGATGTAGC	2678
QY	2221	ATGATTAATATATGTGGCCGGGGGGTGCTGGATGGAACGGGGTGCTTAATTAAGATGTAAAG	2280
Db	2679	ATGATTAATATATGTGGCCGGGGGGTGCTGGATGGAACGGGGTGCTTAATTAAGATGTAAAG	2738
QY	2281	TTTAACTGGCCCAATTTTAAACGGGTACGGTTTTCTGTGCCAATACCAACTTATCTACAC	2340
Db	2739	TTTAACTGGCCCAATTTTAAACGGGTACGGTTTTCTGTGCCAATACCAACTTATCTACAC	2798
QY	2341	GGGTGTAAGCTTCTAATGGGTTTAAACAATCCTGTGTGGAACCTGGACCGAATGTAAAGGTT	2400
Db	2799	GGGTGTAAGCTTCTAATGGGTTTAAACAATCCTGTGTGGAACCTGGACCGAATGTAAAGGTT	2858
QY	2401	CGGGGCTGTGCTTTTAACTGCTGTGGAAGGGGGTGTGTGTGCGCCCAAAAGCAGGGCT	2460
Db	2859	CGGGGCTGTGCTTTTAACTGCTGTGGAAGGGGGTGTGTGTGCGCCCAAAAGCAGGGCT	2918
QY	2461	TCATTTAAGAAATGCGCTCTTTGAAAGGTGTACCTTGGGTATCCTGTGTGAGGGTAACTCC	2520
Db	2919	TCATTTAAGAAATGCGCTCTTTGAAAGGTGTACCTTGGGTATCCTGTGTGAGGGTAACTCC	2978
QY	2521	AGGGTGGCCACAATGTGGGCTCCGACGTGTGTTGCTTAATGCTAGTGAAGAAAGCGTGGCT	2580
Db	2979	AGGGTGGCCACAATGTGGGCTCCGACGTGTGTTGCTTAATGCTAGTGAAGAAAGCGTGGCT	3038
QY	2581	GTTGATTAAGCAATAATGTATGTGTGCACTGCGAGGACAGGGCTCTTCAAGATGCTACCC	2640
Db	3039	GTTGATTAAGCAATAATGTATGTGTGCACTGCGAGGACAGGGCTCTTCAAGATGCTACCC	3098
QY	2641	TGCTCGGACGGCAACTGTCACTGCTGTGAAGCAATTAACGTTAGCAACCACTCTCGCAAG	2700
Db	3099	TGCTCGGACGGCAACTGTCACTGCTGTGAAGCAATTAACGTTAGCAACCACTCTCGCAAG	3158
QY	2701	GCCTGGCCAGTGTGTTGAGCAATACTAGACCCGCTGTTCTCTGCAATTTGGGTAAACAGG	2760
Db	3159	GCCTGGCCAGTGTGTTGAGCAATACTAGACCCGCTGTTCTCTGCAATTTGGGTAAACAGG	3218
QY	2761	AGGGGGGTGTTCCTAATCTTAACCAATGCAATTTGAGTCACTAAGATATTGCTTGACCCC	2820
Db	3219	AGGGGGGTGTTCCTAATCTTAACCAATGCAATTTGAGTCACTAAGATATTGCTTGACCCC	3278

QY 2821 GAGGCAATGTCAGGTGAACCTGAACGGGGTGTGTCATGACCATGAAGATCTGGAG 2880
DB 3279 GAGGCAATGTCAGGTGAACCTGAACGGGGTGTGTCATGACCATGAAGATCTGGAG 3338
QY 2881 GTGCTGAGTACGATGAGACCCGACCAAGGTGACAGACCTGCGAGTGGCGGTAAACAT 2940
DB 3339 GTGCTGAGTACGATGAGACCCGACCAAGGTGACAGACCTGCGAGTGGCGGTAAACAT 3398
QY 2941 ATTGAGAACCAAGCTGTGATGCTGATGTGACCGAGAGACTGAGACCCGATCACTTG3TG 3000
DB 3399 ATTGAGAACCAAGCTGTGATGCTGATGTGACCGAGAGACTGAGACCCGATCACTTG3TG 3458
QY 3001 CTGGCGCTGACCCGCGCTGAGTTGGCTCTAGCGATGAAGAATAGATTGAG 3052;
DB 3459 CTGGCGCTGACCCGCGCTGAGTTGGCTCTAGCGATGAAGAATAGATTGAG 3510;
RESULT 5
AAV07258
ID AAV07258 standard; DNA, 35935 BP.
AC AAV07258;
XX 17-OCT-2003 (revised)
DT 26-SEP-1998 (first entry)
XX Adenovirus 5 genome.
DE Adenovirus 5 genome.
XX Adenovirus 5; Ad5; vector; gene therapy; de.
OS Human adenovirus type 5.
XX MO9817783-A1.
XX 30-APR-1998.
XX 23-OCT-1997; 97MO-US019541.
XX 23-OCT-1996; 96US-00735609.
XX 23-OCT-1996; 96US-00735609.
XX (UNMI) UNIV MICHIGAN.
XX Chamberlain JS, Amalfitano A, Hauser MA, Kumar-Singh R;
PI Hartigan-O'Connor DJ;
XX WPI, 1998-261485/23.
XX New adeno-viral recombinant plasmid(s) - comprise sequences provided for
PT expression of large foreign DNA fragments, used for, e.g. gene therapy of
PT Genetic disease(s).
XX Disclosure; Page 69-86; 139pp; English.
XX This nucleotide sequence comprises the adenovirus 5 (Ad5) genome. The
XX invention provides improved adenoviral vectors and packaging cell lines.
XX One type of improved vector comprises deletions within the E2b region of
XX the adenoviral genome (see also AAV07261). These E2b-deleted virus are
XX used in conjunction with novel cell lines that constitutively express E2b
XX gene products. The invention also provides vectors deleted for all viral
XX coding regions. These 'gutted' vectors permit the transfer of large genes
XX (e.g. up to 35 kb) to cells, as demonstrated by the transfer of the
XX dystrophin gene to the muscle of mice. The E2b-deleted and gutted vectors
XX provide improved adenoviral vectors useful for a wide variety of gene
XX therapy applications. (Updated on 17-OCT-2003 to standardise OS field)
XX
QY Sequence 35935 BP, 8367 A; 10074 C; 9760 G; 7734 T; 0 U; 0 Other;
Query Match 100.0%; Score 3052; DB 2; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGTAGTGTATTATACCGGTGAGTTCTCAAGAGGCCACTCTTGAGTGCAGCAGT 60
|||||

DB 459 CGGTAGTGTATTATACCGGTGAGTTCTCAAGAGGCCACTCTTGAGTGCAGCAGT 518
QY AGATTTTCTCTCCGAGCCGCTCCGACACCGGACTGAAATGAGACATATTCTGCC 120
DB 519 AGATTTTCTCTCCGAGCCGCTCCGACACCGGACTGAAATGAGACATATTCTGCC 578
QY 121 ACGGAGGTGTTATTACCGAAAGAAATGCGCCGACTCTTTGGACACAGTGTGCAAGAG 180
DB 579 ACGGAGGTGTTATTACCGAAAGAAATGCGCCGACTCTTTGGACACAGTGTGCAAGAG 638
QY 181 TACTGGCTGTAATCTTCCACTCTCTAGCAATTTGAACCACTTACCTTACAGACGT 240
DB 639 TACTGGCTGTAATCTTCCACTCTCTAGCAATTTGAACCACTTACCTTACAGACGT 698
QY 241 ATGATTTAGACGTGACCGGCCCGGAGATCCCAAGAGAGCGGTTTCGAGATTTTTC 300
DB 699 ATGATTTAGACGTGACCGGCCCGGAGATCCCAAGAGAGCGGTTTCGAGATTTTTC 758
QY 301 CCGACTCTGTAATGTTGGCGGTGACGAGAGGATTTGACTTACTACTTTTCCGCGGC 360
DB 759 CCGACTCTGTAATGTTGGCGGTGACGAGAGGATTTGACTTACTACTTTTCCGCGGC 818
QY 361 CCGGTTCTCGGAGCGGCTCACCTTTCCGGGACCGCGAGCGGAGAGAGAGCT 420
DB 819 CCGGTTCTCGGAGCGGCTCACCTTTCCGGGACCGCGAGCGGAGAGAGAGCT 878
QY 421 TGGGTCGGTTTCTATGCAAACTTGTACCGAGGTGATGATCTTACCTGCCACAGG 480
DB 879 TGGGTCGGTTTCTATGCAAACTTGTACCGAGGTGATGATCTTACCTGCCACAGG 938
QY 481 CTGGCTTCCACCGACGATGACGAGAGATGAAGAGGTGAGAGTTGTGTAGATTATG 540
DB 939 CTGGCTTCCACCGACGATGACGAGAGATGAAGAGGTGAGAGTTGTGTAGATTATG 998
QY 541 TGGAGCACCCCGGAGCGGTTGCGAGCTTGTCTATTCACCGAGGAAATACGGGGAGC 600
DB 999 TGGAGCACCCCGGAGCGGTTGCGAGCTTGTCTATTCACCGAGGAAATACGGGGAGC 1058
QY 601 CAGATATTATGTTGCTTGTCTATTAAGAGACTGTGCAATGTTTGTCTACAGTAAGT 660
DB 1059 CAGATATTATGTTGCTTGTCTATTAAGAGACTGTGCAATGTTTGTCTACAGTAAGT 1118
QY 661 GAAATTTATGCGAGAGGTGATGAGATGAGTGGTTTGTGTGTATTTTTTTTAAAT 720
DB 1119 GAAATTTATGCGAGAGGTGATGAGATGAGTGGTTTGTGTGTATTTTTTTTAAAT 1178
QY 721 TTTTACAGTTTGTGTTTAAAGAAATTTGTATGTATTTTTTTTAAAGTCTGTGTC 780
DB 1179 TTTTACAGTTTGTGTTTAAAGAAATTTGTATGTATTTTTTTTAAAGTCTGTGTC 1238
QY 781 TGAACCTGAGCTGAGCCGAGCCAGAACCGAGCTGCAAGACTTACCCGCTCTTAA 840
DB 1239 TGAACCTGAGCTGAGCCGAGCCAGAACCGAGCTGCAAGACTTACCCGCTCTTAA 1298
QY 841 AATGCGGCTCTGATCTGAGAGCGCCGACATCACTGTGTCTAGAGAAATGCAATATAG 900
DB 1299 AATGCGGCTCTGATCTGAGAGCGCCGACATCACTGTGTCTAGAGAAATGCAATATAG 1358
QY 901 TACGAGATGCTGAGCTCGGCTCTTCTAAGACACCTCGAGATACACCGGAGTCC 960
DB 1359 TACGAGATGCTGAGCTCGGCTCTTCTAAGACACCTCGAGATACACCGGAGTCC 1418
QY 961 GCTGTGCCCATTTAAACCACTTCCGTGAGAGTTGTGGCGTCCGAGCTGTGAATG 1020
DB 1419 GCTGTGCCCATTTAAACCACTTCCGTGAGAGTTGTGGCGTCCGAGCTGTGAATG 1478
QY 1021 TATCGAGATTTGCTTAAACGAGCTGAGCACTTTTGAATTTGAGCTGTAAAGCCCCAG 1080
DB 1479 TATCGAGATTTGCTTAAACGAGCTGAGCACTTTTGAATTTGAGCTGTAAAGCCCCAG 1538
QY 1081 GCCATAGGTGTAAACCTGTGATTTGCGTGTGTGTTAAACCTTTGTTGCTGAATAGT 1140
DB 1539 GCCATAGGTGTAAACCTGTGATTTGCGTGTGTGTTAAACCTTTGTTGCTGAATAGT 1598

OY	1141	TCATGTAAATTTAATAAAGGTGAGATATATGTTTAACTTGATGAGCGCTGTAAATGGGGC	1200
DB	1599	TGATGTAAATTTAATAAAGGTGAGATATATGTTTAACTTGATGAGCGCTGTAAATGGGGC	1658
OY	1201	GGGGCTTAAAGGATATATATATGAGCGCGGAGGCTAATCTGTGGTACATCTGACCTCAATGA	1260
DB	1659	GGGGCTTAAAGGATATATATATGAGCGCGGAGGCTAATCTGTGGTACATCTGACCTCAATGA	1718
OY	1261	GGCTTGGGAGTGTTTGGAGATTTTTTCTGCTGTGCGTAACCTTGTGAGCAAGAGCTCTAA	1320
DB	1719	GGCTTGGGAGTGTTTGGAGATTTTTTCTGCTGTGCGTAACCTTGTGAGCAAGAGCTCTAA	1778
OY	1321	CAGTAACTCTTGTTTTGGAGGTTTCTGTGGGCTCATCCAGGCAAAATTAATGTTCTGAG	1380
DB	1779	CAGTAACTCTTGTTTTGGAGGTTTCTGTGGGCTCATCCAGGCAAAATTAATGTTCTGAG	1838
OY	1381	AATTAAGGAGATTAACAAGTGGGAATTTGAAGAGCTTTGAAATCCTGTGGTGAAGCTTT	1440
DB	1839	AATTAAGGAGATTAACAAGTGGGAATTTGAAGAGCTTTGAAATCCTGTGTGAGCTGTT	1898
OY	1441	TGATTTCTTGAATCTGGTCAACAGCGCTTTTCCAAGAGAGGTCAATCAAGCTTTTGA	1500
DB	1899	TGATTTCTTGAATCTGGTCAACAGCGCTTTTCCAAGAGAGGTCAATCAAGCTTTTGA	1958
OY	1501	TTTTTCCACACCGGGGCGCGCTGGGCGTGTGCTTTTGTGATTTTATAAAGATTA	1560
DB	1959	TTTTTCCACACCGGGGCGCGCTGGGCGTGTGCTTTTGTGATTTTATAAAGATTA	2018
OY	1561	ATGAGGCAAAAGAAACCCATCTGAGCGGGGGGTACTGCTGATATTTTCTGGCATGATCT	1620
DB	2019	ATGAGGCAAAAGAAACCCATCTGAGCGGGGGGTACTGCTGATATTTTCTGGCATGATCT	2078
OY	1621	GTGAGAGCGGTTGTGAGACACAAGAAATGCGCTGTCACTGTTGTCTTCGTCGCGCCGCG	1680
DB	2079	GTGAGAGCGGTTGTGAGACACAAGAAATGCGCTGTCACTGTTGTCTTCGTCGCGCCGCG	2138
OY	1681	GATATATACCGACGAGAGGACGACGACACACAGAGAAACCCAGCGCGCGCGGCAAGGA	1740
DB	2139	GATATATACCGACGAGAGGACGACGACACACAGAGAAACCCAGCGCGCGCGGCAAGGA	2198
OY	1741	GCAGAGCCCATGGAACCCGAGAGCGCGGCTGGAACCTTGCGGGAATGAATGTTGTACAGGTG	1800
DB	2199	GCAGAGCCCATGGAACCCGAGAGCGCGGCTGGAACCTTGCGGGAATGAATGTTGTACAGGTG	2258
OY	1801	GCTGAACCTGTATCCGAACCTGAGACGATTTTGAACAATTACAGAGATGGGCAAGGGCTA	1860
DB	2259	GCTGAACCTGTATCCGAACCTGAGACGATTTTGAACAATTACAGAGATGGGCAAGGGCTA	2318
OY	1861	AAGGGGATTAAGAGAGGAGCGGGGGCTTGTATAGGCTACAGAGGAGCTTAAGAAATCTAGCT	1920
DB	2319	AAGGGGATTAAGAGAGGAGCGGGGGCTTGTATAGGCTACAGAGGAGCTTAAGAAATCTAGCT	2378
OY	1921	TTTAACTTAATGACACAGACACCGTCTGAGTGTATTACTTTTCAACAGATCAAGATTAAT	1980
DB	2379	TTTAACTTAATGACACAGACACCGTCTGAGTGTATTACTTTTCAACAGATCAAGATTAAT	2438
OY	1981	TGCGCTAATGAGCTTGAATCTGTGCGGCGAGAAATTCATATAGACAGCTGACCACTTAC	2040
DB	2439	TGCGCTAATGAGCTTGAATCTGTGCGGCGAGAAATTCATATAGACAGCTGACCACTTAC	2498
OY	2041	TGCGTGCAGCCAGAGGGATGATTTTGAAGAGGCTATTAAGGATATATGCAAAAGTGGCACTT	2100
DB	2499	TGCGTGCAGCCAGAGGGATGATTTTGAAGAGGCTATTAAGGATATATGCAAAAGTGGCACTT	2558
OY	2101	AGGCGAGATTGCAATATACAGATCAGCAAACTTGTAAATATCAGAAATGTGTCTTAATTT	2160
DB	2559	AGGCGAGATTGCAATATACAGATCAGCAAACTTGTAAATATCAGAAATGTGTCTTAATTT	2618
OY	2161	TCTGAGAAACGGGGCCGAGGTGAGATTAATACGAGATTAAGGCTTGTGATGTATGAC	2220
DB	2619	TCTGAGAAACGGGGCCGAGGTGAGATTAATACGAGATTAAGGCTTGTGATGTATGAC	2678

QY	2221	ATGATAAATATGTGGCCGGGGGGTCTTGGATGGA	CGGGGGTGGTATTAATGAATGTAAAG	2280
Db	2679	ATGATAAATATGTGGCCGGGGGGTCTTGGATGGA	CGGGGGTGGTATTAATGAATGTAAAG	2738
QY	2281	TTTACTGAGCCCAATTTTAAACGGGATCGGTTTTC	CTGGCCAAATACCACTTATCTTACAC	2340
QY	2341	GGTGTAAAGCTTCTATGGGTTTAAACATACCTGT	GTGGAGCCGTGACCGATGTAAAGGTT	2400
Db	2739	GGTGTAAAGCTTCTATGGGTTTAAACATACCTGT	GTGGAGCCGTGACCGATGTAAAGGTT	2858
QY	2401	CGGGGCTGTGCTTTTACTGCTGTGGA	AAAGGGGTGGTGTGTGGCCCAAAAGAGGGCT	2460
Db	2859	CGGGGCTGTGCTTTTACTGCTGTGGA	AAAGGGGTGGTGTGTGGCCCAAAAGAGGGCT	2918
QY	2461	TCAATTAAAGAAATGCTCTTTGAAAAGGTATAC	CTTGGGTTATCCGTCTGAGGGTAACTCC	2520
Db	2919	TCAATTAAAGAAATGCTCTTTGAAAAGGTATAC	CTTGGGTTATCCGTCTGAGGGTAACTCC	2978
QY	2521	AGGGTGGCCCAAAATGTGGCCTCCGACTGTGTG	TTGCTTTCATGTCTAATGTAAAGCGTGGCT	2580
Db	2979	AGGGTGGCCCAAAATGTGGCCTCCGACTGTGTG	TTGCTTTCATGTCTAATGTAAAGCGTGGCT	3038
QY	2581	GTGATTAAGCATTAACATGTATGTGGGA	CTTGGCAGGACAGGGGCTCTTGAGTCTAAC	2640
Db	3039	GTGATTAAGCATTAACATGTATGTGGGA	CTTGGCAGGACAGGGGCTCTTGAGTCTAAC	3098
QY	2641	TGCTTCGAGACGGCACTGTCACTGTCTGAA	AGCACTTACAGTAGCCAGCCACTCTCGCAAG	2700
Db	3099	TGCTTCGAGACGGCACTGTCACTGTCTGAA	AGCACTTACAGTAGCCAGCCACTCTCGCAAG	3158
QY	2701	GCCGTGGCCAGTGTTTGAGCATTAACATACTGA	CCCGCTGTTCCTTGCAATTTGGGTAAACAG	2760
Db	3159	GCCGTGGCCAGTGTTTGAGCATTAACATACTGA	CCCGCTGTTCCTTGCAATTTGGGTAAACAG	3218
QY	2761	AGGGGGGTGTTCCTCACTTACCAATGCAATTTGA	GTGACACTAAGATATTCCTTGAAGCC	2820
Db	3219	AGGGGGGTGTTCCTCACTTACCAATGCAATTTGA	GTGACACTAAGATATTCCTTGAAGCC	3278
QY	2821	GAGAGCATGTGCCAAGGTGAACCTGAA	CGGGGTGTTTGACATGACATGAAGATCTGAA	2880
Db	3279	GAGAGCATGTGCCAAGGTGAACCTGAA	CGGGGTGTTTGACATGACATGAAGATCTGAA	3338
QY	2881	GTGCTGAGGTACGATGAGACCCCGACAGGTG	CAGACCTTCGAGTGTGGCGGTAAACAT	2940
Db	3339	GTGCTGAGGTACGATGAGACCCCGACAGGTG	CAGACCTTCGAGTGTGGCGGTAAACAT	3398
QY	2941	ATTATGGAACACAGCTGTGATGTCTGATGTGA	ATCCAGAGAGCTGAGAGCCCGATCATTTGGTG	3000
Db	3399	ATTATGGAACACAGCTGTGATGTCTGATGTGA	ATCCAGAGAGCTGAGAGCCCGATCATTTGGTG	3458
QY	3001	CTGGCGCTGACACCGCGCGTGAAGTTTGGCTTA	AGCATGAAGATACAGATTGAG	3052
Db	3459	CTGGCGCTGACACCGCGCGTGAAGTTTGGCTTA	AGCATGAAGATACAGATTGAG	3510
RESULT 6				
AAC85026				
ID	AAC85026 standard; DNA; 35935 BP.			
XX	AAC85026;			
XX	08-MAY-2001 (first entry)			
DT				
XX	Complete nucleotide sequence of the genome of Ad5.			
DE				
XX	Adenovirus death protein; ADP; neoplastic; cell death; cancer therapy;			
KW	anti-cancer; gene therapy; cytosstatic; Ad5; de.			
XX				
OS	Mastadenovirus.			
XX				
PN	WO200104282-A2.			

XX PD 18-JAN-2001.
XX XX 12-JUL-2000; 2000WO-US018971.
XX PR 12-JUL-1999; 99US-00351778.
XX PA (UYSL-) UNIV SAINT LOUIS.
XX P1 Wold WSM, Toth K, Doronin K, Tollefson AE;
XX DR WPI; 2001-103079/11.
XX PT Recombinant vector which is replication-competent in a neoplastic cell
XX PT and overexpresses an adenovirus death protein, useful in cancer therapy
XX PT when used together with replication-defective adenovirus which expresses
XX PT an anti-cancer gene.
XX PS
XX PS Disclosure; Fig 21; 196pp; English.
XX CC The invention relates to a recombinant vector (V1) which is replication-
XX CC competent in a neoplastic cell and which overexpresses an adenovirus
XX CC death protein (ADP). The vector can be used in a method for promoting
XX CC death of a neoplastic cell that comprises contacting the neoplastic cell
XX CC with at least one V1; and a composition comprising V1 and a second
XX CC recombinant virus which is: (a) replication defective and which
XX CC expresses an anti-cancer gene product, where V1 complements replication
XX CC of the second recombinant virus; or (b) replication-competent in a
XX CC neoplastic cell. V1, together with one or more replication-defective
XX CC adenovirus which expresses an anti-cancer gene product, are useful in
XX CC cancer therapy. Overexpression of ADP by V1 results in faster lysis of
XX CC cells and spread of the virus throughout a cell monolayer than viruses
XX CC expressing wild-type levels of ADP. The present sequence represents the
XX CC complete nucleotide sequence of the genome of human adenovirus Ad5.
XX CC
XX Sequence 35935 BP; 8367 A; 10073 C; 9761 G; 7734 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 3052; DB 4; Length 35935;
Best Local Similarly 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGTAGTATGATTAATACCGGTGAGTTCCTCAAGAGGCCACTTGTAGTCCGAGAGT 60
DB 459 CGGTAGTATGATTAATACCGGTGAGTTCCTCAAGAGGCCACTTGTAGTCCGAGAGT 518
QY 61 AGAGTTTCTCTCCGAGCCGCTCCGACACCGGAGCTGAATAATGACATATTAATCTGCC 120
DB 519 AGAGTTTCTCTCCGAGCCGCTCCGACACCGGAGCTGAATAATGACATATTAATCTGCC 578
QY 121 ACGGAGGTGTTATTAACGGAATAATGGCCGCGCAGTCTTTTGGACCAAGTCGAAGAG 180
DB 579 ACGGAGGTGTTATTAACGGAATAATGGCCGCGCAGTCTTTTGGACCAAGTCGAAGAG 638
QY 181 TACTGGGTGAATATCTTCCACTCTAGCCATTTTGAACCACTACCTTACAGAACTGT 240
DB 639 TACTGGGTGAATATCTTCCACTCTAGCCATTTTGAACCACTACCTTACAGAACTGT 698
QY 241 ATGATTTAGACGTGACGCGCCCGCAAGATCCCAACGAGAGGCGTTTGGAGATTTTTC 300
DB 699 ATGATTTAGACGTGACGCGCCCGCAAGATCCCAACGAGAGGCGTTTGGAGATTTTTC 758
QY 301 CCGACTCTGTAATGTTGGCGGTGACGAGAGGATTTGACTTACCTTTTCCGCGCGGC 360
DB 759 CCGACTCTGTAATGTTGGCGGTGACGAGAGGATTTGACTTACCTTTTCCGCGCGGC 818
QY 361 CCGGTTCTCCGAGACCGCTCACTTTCCGCGACCGCGAGCCGCGAGAGAGAGAGCT 420
DB 819 CCGGTTCTCCGAGACCGCTCACTTTCCGCGACCGCGAGCCGAGAGAGAGAGCT 878
QY 421 TGGGTCCGGTTTCTATGCAAACTTGTATCCGAGAGGTATGATCTTACCTGCCACGAG 480
DB 879 TGGGTCCGGTTTCTATGCAAACTTGTATCCGAGAGGTATGATCTTACCTGCCACGAG 938

QY 481 CTGGCTTTCCACCCGAGTACGACGAGAGTGAAGGGGTGAGAGTGTGTGTTAATATG 540
DB 939 CTGGCTTTCCACCCGAGTACGACGAGAGTGAAGGGGTGAGAGTGTGTGTTAATATG 998
QY 541 TGGAGCACCCCGGACAGGTTGACAGTCTGTCAATTATCACCGAGAGAAATCGGGGAGCC 600
DB 999 TGGAGCACCCCGGACAGGTTGACAGTCTGTCAATTATCACCGAGAGAAATCGGGGAGCC 1058
QY 601 CAGATATTAATGTTGCTTGTGCTATATGAGAGACTGTGCAATTTGTCTACAGTAAGT 660
DB 1059 CAGATATTAATGTTGCTTGTGCTATATGAGAGACTGTGCAATTTGTCTACAGTAAGT 1118
QY 661 GAAATATGAGGACGATGAGGTATGAGTGTGGTGTGTGTGTTATTTTATTTTAT 720
DB 1119 GAAATATGAGGACGATGAGGTATGAGTGTGGTGTGTGTGTTATTTTATTTTAT 1178
QY 721 TTTTACAGTTTGTGTTTAAAGAAATTTGTATGTATTTTAAAGGTCCGTGTC 780
DB 1179 TTTTACAGTTTGTGTTTAAAGAAATTTGTATGTATTTTAAAGGTCCGTGTC 1238
QY 781 TGAACCTGAGCTGAGCCCGAGCCGAGAACCGAGCTGCAAGACTACCCGCGCTCTAA 840
DB 1239 TGAACCTGAGCTGAGCCCGAGCCGAGAACCGAGCTGCAAGACTACCCGCGCTCTAA 1298
QY 841 AATGGCGCTGCTATCTTGAGACGCGCCGACATCACTGTGTCTAGAGATGCAATAGTAG 900
DB 1299 AATGGCGCTGCTATCTTGAGACGCGCCGACATCACTGTGTCTAGAGATGCAATAGTAG 1358
QY 901 TAGGATAGCGTGAACCTCGGCTCTTAAACACCTCTGAGATACACCGGAGTCCC 960
DB 1359 TAGGATAGCGTGAACCTCGGCTCTTAAACACCTCTGAGATACACCGGAGTCCC 1418
QY 961 GCTGTGCCCATTTAAACAGTTGCGGTGAGAGTTGTGGGCGTCCAGAGCTGTGATG 1020
DB 1419 GCTGTGCCCATTTAAACAGTTGCGGTGAGAGTTGTGGGCGTCCAGAGCTGTGATG 1478
QY 1021 TATCGAGACTTGCTTAAACGAGCTTGAGCAACTTTGAGCTTGAACGCCCCAG 1080
DB 1479 TATCGAGACTTGCTTAAACGAGCTTGAGCAACTTTGAGCTTGAACGCCCCAG 1538
QY 1081 GCCATAGGTGAACCTGTGATGCGGTGTGTGTTAACCTTGTGTGTAATAGT 1140
DB 1539 GCCATAGGTGAACCTGTGATGCGGTGTGTGTTAACCTTGTGTGTAATAGT 1598
QY 1141 TGATGTAAGTTTAAAGGCTGAGATATGTTTAACTTGCATGCGCTGTTAAATGGGCGC 1200
DB 1599 TGATGTAAGTTTAAAGGCTGAGATATGTTTAACTTGCATGCGCTGTTAAATGGGCGC 1658
QY 1201 GGGGCTTAAAGGCTATTAATATGCGCGCTGAGCTTAATCTTGATTAATCTGATGGA 1260
DB 1659 GGGGCTTAAAGGCTATTAATATGCGCGCTGAGCTTAATCTTGATTAATCTGATGGA 1718
QY 1261 GGGTGGGAGTGTGGAAGATTTTCTGCTGTCGTAATCTGTGGAACAGAGCTTAA 1320
DB 1719 GGGTGGGAGTGTGGAAGATTTTCTGCTGTCGTAATCTGTGGAACAGAGCTTAA 1778
QY 1321 CAGTACCTTGTGTTTGAAGAGTTTCTGTGGGCTCATCCAGGCAAGTTAGTCTGAG 1380
DB 1779 CAGTACCTTGTGTTTGAAGAGTTTCTGTGGGCTCATCCAGGCAAGTTAGTCTGAG 1838
QY 1381 AATTAAGAGAGATTAACAAGTGGGAATTTGAAGAGCTTTGAATCTGTGGTGAAGCTTT 1440
DB 1839 AATTAAGAGAGATTAACAAGTGGGAATTTGAAGAGCTTTGAATCTGTGGTGAAGCTTT 1898
QY 1441 TGATTTCTTAATCTGGGTGACACGAGGCTTTTCCAAAGAGAGTCAAGACTTTTGA 1500
DB 1899 TGATTTCTTAATCTGGGTGACACGAGGCTTTTCCAAAGAGAGTCAAGACTTTTGA 1958
QY 1501 TTTTTCACACCGGGGCGCTGCGGTGCTGTGCTTTTGAAGTTTAAAGATTA 1560
DB 1959 TTTTTCACACCGGGGCGCTGCGGTGCTGTGCTTTTGAAGTTTAAAGATTA 2018

(NS) having 5' and 3' end, left and right inverted terminal repeat of
adenovirus flanking NS, adenovirus packaging sequence linked to inverted
terminal repeat, and adeno-associated virus terminal repeat linked to 3'
end of NS, into cell expressing adenovirus early gene lacking from vector
/ and culturing cell to produce another vector. The method is useful for
generating vectors, especially mad vectors. The method is useful in
transferring nucleotide sequences of interest into a cell, for gene
transfer applications (e.g. gene therapy) in vitro, ex vivo and in vivo.
The nucleotide sequences are useful for treating diseases associated with
1c, 1.e. adenosine deaminase gene associated with adenosine deaminase
deficiency with severe combined immune deficiency, beta-chain of
hemoglobin gene associated with beta-thalassemia and sickle cell
disease, receptor for low density lipoprotein gene associated with
familial hypercholesterolemia, hypoxanthine-guanine
phosphoribosyltransferase associated with Lesch-Nyhan syndrome,
phenylalanine hydroxylase (PAH) gene associated with phenylketonuria,
dystrophin gene associated with muscular dystrophy, and human cystic
fibrosis transmembrane conductance regulator gene associated with cystic
fibrosis. The present nucleic acid sequence represents a human adenovirus
genome sequence that was used in the methods of the invention

XX Sequence 35935 BP; 8367 A; 10073 C; 9761 G; 7734 T; 0 U; 0 Other;

Query Match 100.0%; Score 3052; DB 6; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CGTGTAGTATTTATACCCGGTGAAGTCTCTCAAGAGCCACTCTTAGTGCCAGCAGT 60
459 CGTGTAGTATTTATACCCGGTGAAGTCTCTCAAGAGCCACTCTTAGTGCCAGCAGT 518
61 AGAGTTTCTCTCCGAGCCGCTCCGACACCGGACCTGAATAATGACATTTATCTGCC 120
519 AGAGTTTCTCTCCGAGCCGCTCCGACACCGGACCTGAATAATGACATTTATCTGCC 578
121 ACGGAGTGTATTAACGAGAAATGCGCGCAGTCTTTTGACACAGTGTGCAAGAG 180
579 ACGGAGTGTATTAACGAGAAATGCGCGCAGTCTTTTGACACAGTGTGCAAGAG 638
181 TACTGCTGATTAATCTTCACTCTCTCACTTGAACACCTACCTTCAACGACCTGT 240
639 TACTGCTGATTAATCTTCACTCTCTCACTTGAACACCTACCTTCAACGACCTGT 698
241 ATGATTTAGACGTGACGCGCCCGAAGATCCGACGAGAGCGGTTTCGACATTTTC 300
699 ATGATTTAGACGTGACGCGCCCGAAGATCCGACGAGAGCGGTTTCGACATTTTC 758
301 CCGACTCTGATTAATGTCGCGGTGACGAGAGGATTAAGTCACTTTCGCGCGGCG 360
759 CCGACTCTGATTAATGTCGCGGTGACGAGAGGATTAAGTCACTTTCGCGCGGCG 818
361 CCGGTTCTCCGAGCCGCTCACTTTCGCGGACCCGAGACCCGAGACGAGACCT 420
819 CCGGTTCTCCGAGCCGCTCACTTTCGCGGACCCGAGACCCGAGACGAGACCT 878
421 TGGGTCCGCTTCTATATCCCAACTTGTACCGAGGTGATGATCTTAAGTCCAGAG 480
879 TGGGTCCGCTTCTATATCCCAACTTGTACCGAGGTGATGATCTTAAGTCCAGAG 938
481 CTGCTTTCCACCCGAGGACGAGAGATGAAGAGGATGAGAGATTTGTGTGAATTATG 540
939 CTGCTTTCCACCCGAGGACGAGAGATGAAGAGGATGAGAGATTTGTGTGAATTATG 998
541 TGAAGACCCCGGACGAGTGTGACAGTCTTGTCTATATCAACCGAGAGATTAACGGGAC 600
999 TGAAGACCCCGGACGAGTGTGACAGTCTTGTCTATATCAACCGAGAGATTAACGGGAC 1058
601 CAGATATTAATGTGTGCTTGTCTATATGAGACCTGTGAGATTTGTCTACAGTAAGT 660
1059 CAGATATTAATGTGTGCTTGTCTATATGAGACCTGTGAGATTTGTCTACAGTAAGT 1118
661 GAAATATATGAGGAGTGTGATAGAGTGTGAGTGTGTGTAATTTTTTTTAAAT 720

1119 GAAATATATGAGGAGTGTGATAGAGTGTGAGTGTGTGTAATTTTTTTTAAAT 1178
721 TTTTACAGTTTGTGTTTAAAGAAATTTGTATGATTTTAAAGATCTGTGTC 780
1179 TTTTACAGTTTGTGTTTAAAGAAATTTGTATGATTTTAAAGATCTGTGTC 1238
781 TGAACCTGACCTGAGCCGACCGAGCAACCGGAGCTGCAAGACTTCCGCGCTCTAA 840
1239 TGAACCTGACCTGAGCCGACCGAGCAACCGGAGCTGCAAGACTTCCGCGCTCTAA 1298
841 AATGCGCCTGCTATCTCTGAGACGCGGACATCACTGTGCTGAGAAATGCAATAGAG 900
1299 AATGCGCCTGCTATCTCTGAGACGCGGACATCACTGTGCTGAGAAATGCAATAGAG 1358
901 TACGATAGCTGTGACCTCCGCTCTTCTAAACACACTCTGAGATACACCGGAGTCTCC 960
1359 TACGATAGCTGTGACCTCCGCTCTTCTAAACACACTCTGAGATACACCGGAGTCTCC 1418
961 GCTGTGCCCCATTAACCAAGTGTGCGTGAAGTGTGCGGCTGCGACGCTGTGAAATG 1020
1419 GCTGTGCCCCATTAACCAAGTGTGCGTGAAGTGTGCGGCTGCGACGCTGTGAAATG 1478
1021 TATGAGACCTGCTTACGAGCCCTGAGCAACCTTTGAGACTGATGATTAACGCCCCAG 1080
1479 TATGAGACCTGCTTACGAGCCCTGAGCAACCTTTGAGACTGATGATTAACGCCCCAG 1538
1081 GCCATTAAGTGTAAACCTGTGATTCGCTGTGTGTTAAACGCTTTGTGTGTAATAGT 1140
1539 GCCATTAAGTGTAAACCTGTGATTCGCTGTGTGTTAAACGCTTTGTGTGTAATAGT 1598
1141 TGAATGATTTTAAAGGATGAGATTAATGTTAACTTGTGATGCGCTGTTAAATGGGCG 1200
1599 TGAATGATTTTAAAGGATGAGATTAATGTTAACTTGTGATGCGCTGTTAAATGGGCG 1658
1201 GGGGCTTAAAGGATTAATGAGCGGTGAGCTTAATCTTGTGATTAATGAGCTGATGAG 1260
1659 GGGGCTTAAAGGATTAATGAGCGGTGAGCTTAATCTTGTGATTAATGAGCTGATGAG 1718
1261 GGCCTGGAGATGTTTGGAGATTTTCTGCTGTGCGTAATCTGTGAGACGAGCTTAA 1320
1719 GGCCTGGAGATGTTTGGAGATTTTCTGCTGTGCGTAATCTGTGAGACGAGCTTAA 1778
1321 CAGTACTCTTGTGTTTGAAGTTCGTGTGAGGCTCATCCAGCAAAATTAATGCTGAG 1380
1779 CAGTACTCTTGTGTTTGAAGTTCGTGTGAGGCTCATCCAGCAAAATTAATGCTGAG 1838
1381 AATTAAGAGAGATTAACAGTGGGAAATTAAGAGCTTTGAAATCCGTGTGAGCTGTT 1440
1839 AATTAAGAGAGATTAACAGTGGGAAATTAAGAGCTTTGAAATCCGTGTGAGCTGTT 1898
1441 TGAATCTTTGAAATCTGTGTACACGAGGCTTTTCAAGAGAGTCAATCAAGCTTTGGA 1500
1899 TGAATCTTTGAAATCTGTGTACACGAGGCTTTTCAAGAGAGTCAATCAAGCTTTGGA 1958
1501 TTTTTCACACCGGGGCGGCTGCGCTGCTGTGCTTTTGAAGTTTAAAGATTA 1560
1959 TTTTTCACACCGGGGCGGCTGCGCTGCTGTGCTTTTGAAGTTTAAAGATTA 2018
1561 ATGAGGAGAAATCAATCATGACCGGGGGTACCTGCTGAGATTTTCTGACATGACATCT 1620
2019 ATGAGGAGAAATCAATCATGACCGGGGGTACCTGCTGAGATTTTCTGACATGACATCT 2078
1621 GTGAGAGCGGTTGTGAGACACAAAGATGCGCTGCTAATGTTGCTTCCGTCGCGCCGCG 1680
2079 GTGAGAGCGGTTGTGAGACACAAAGATGCGCTGCTAATGTTGCTTCCGTCGCGCCGCG 2138
1681 GATTAATCCGAGGAGAGACGACGACGACGACGAGAGAGAGCCAGGCGGCGGCGGACGGA 1740
2139 GATTAATCCGAGGAGAGACGACGACGACGAGAGAGAGAGCCAGGCGGCGGCGGACGGA 2198
1741 GCAGAGCCATGGAACCCGAGACCCGCGCTGACCTCTCGGGAATGATGTTGTACAGGTG 1800
2199 GCAGAGCCATGGAACCCGAGACCCGCGCTGACCTCTCGGGAATGATGTTGTACAGGTG 2258

1801 GCTGAACCTGATCCAGAACCTGAGACGCAATTTTGAACAATTACAGAGAGATGGGACAGGGGCTA 1860
2259 GCTAACTGATCCAGAACCTGAGACGCAATTTTGAACAATTACAGAGAGATGGGACAGGGGCTA 2318
1861 AAGGGGGTAAAGAGAGAGAGCGGGGGGCTTGTAGAGCTACAGAGAGAGCTAGAGATCTAGCT 1920
2319 AAGGGGGTAAAGAGAGAGAGCGGGGGGCTTGTAGAGCTACAGAGAGAGCTAGAGATCTAGCT 2378
1921 TTTAGCTTAATGACACACACCGCTCTGAGTGTATTAATCTTTCAACAGATCAAGATTAAT 1980
2379 TTTAGCTTAATGACACACACCGCTCTGAGTGTATTAATCTTTCAACAGATCAAGATTAAT 2438
1981 TGCGCTAATGAGCTTGAATCTGCTGGCGCAGAGATTTCCATAGAGAGCTGACCACTTAC 2040
2439 TGCGCTAATGAGCTTGAATCTGCTGGCGCAGAGATTTCCATAGAGAGCTGACCACTTAC 2498
2041 TGCGCTGACCGAGGGGATGATTTTGAAGAGCTATTAGGGTATATGCAAGGTGGCACTT 2100
2499 TGCGCTGACCGAGGGGATGATTTTGAAGAGCTATTAGGGTATATGCAAGGTGGCACTT 2558
2101 AGGCCAGTTGCAAGTACAAATCAGCAACTTGTAAATATCAGGAATTTGTTCTACTT 2160
2559 AGGCCAGTTGCAAGTACAAATCAGCAACTTGTAAATATCAGGAATTTGTTCTACTT 2618
2161 TCTGGGAACCGGGGCGGAGGTGAGATGATACGAGAGATAGGGTGGCTTTAGATGATGAC 2220
2619 TCTGGGAACCGGGGCGGAGGTGAGATGATACGAGAGATAGGGTGGCTTTAGATGATGAC 2678
2221 ATGATAAATATGTGGCCGGGGGGTGTGGCAATGCAACGGGGTGTATTATATGAAATGTAAAG 2280
2679 ATGATAAATATGTGGCCGGGGGGTGTGGCAATGCAACGGGGTGTATTATGAAATGTAAAG 2728
2281 TTTACTGGCCCCCAATTTTAAAGGGGTACGGTTTTTCTGGGCAATACCAACTTATCTTACAC 2340
2739 TTTACTGGCCCCCAATTTTAAAGGGGTACGGTTTTTCTGGGCAATACCAACTTATCTTACAC 2798
2341 GGTGTAAGCTTCTATGAGGTTTAAACAATCCTGTGAGAGAGCTGGACGATGTAAGGGTT 2400
2799 GGTGTAAGCTTCTATGAGGTTTAAACAATCCTGTGAGAGAGCTGGACGATGTAAGGGTT 2858
2401 CGGGGCTGTGCTTTTAACTGTGCTGAGAAAGGGGGTGTGTGTGCGCCCAAAAGCAGGGCT 2460
2859 CGGGGCTGTGCTTTTAACTGTGCTGAGAAAGGGGGTGTGTGTGCGCCCAAAAGCAGGGCT 2918
2461 TCAATTAAAGAAATGCTCTTTGAAAGGTGTACCTTGGGTATCTGTCTGAGGGTAACTCC 2520
2919 TCAATTAAAGAAATGCTCTTTGAAAGGTGTACCTTGGGTATCTGTCTGAGGGTAACTCC 2978
2521 AGGGGCGCCCAATGTGGCCCTCCGACTGTGGTGTCTTCACTGATGTAAGAAAGCGTGGCT 2580
2979 AGGGGCGCCCAATGTGGCCCTCCGACTGTGGTGTCTTCACTGATGTAAGAAAGCGTGGCT 3038
2581 GTGATTTAAGCAATTAACATGATGTGTGCAACTGCGAGACAGGGGCTCTCAGATGCTGACC 2640
3039 GTGATTTAAGCAATTAACATGATGTGTGCAACTGCGAGACAGGGGCTCTCAGATGCTGACC 3098
2641 TGCTGGAACGGCACTGTCACTGTGTAAGACATTTACAGTACAGGCACTCTTGGCAG 2700
3099 TGCTGGAACGGCACTGTCACTGTGTAAGACATTTACAGTACAGGCACTCTTGGCAG 3158
2701 GCGTGGCCAGTGTGAGCATTAACATACCTGACCGCTGTTCTTCCATTTGGGTAAACAG 2760
3159 GCGTGGCCAGTGTGAGCATTAACATACCTGACCGCTGTTCTTCCATTTGGGTAAACAG 3218
2761 AGGGGGGTGTTCTTCACTTAACATGCAATTTAGTCACTAAGATATTTGCTGAGCC 2820
3219 AGGGGGGTGTTCTTCACTTAACATGCAATTTAGTCACTAAGATATTTGCTGAGCC 3278
2821 GAGAGCATGTCCAAAGGTGAACCTGAACGGGGTGTGACATGACATGAAGATCTGGAAG 2880
3279 GAGAGCATGTCCAAAGGTGAACCTGAACGGGGTGTGACATGACATGAAGATCTGGAAG 3338

2881 GTGCTGAGTACGATGAGACCCCGACAGAGTGCAGACCTCTGCGAGTGTGGCGTAAACAT 2940
3339 GTGCTGAGTACGATGAGACCCCGACAGAGTGCAGACCTCTGCGAGTGTGGCGTAAACAT 3398
2941 ATTAGAACAACCTCTGATGCTGATGATGATGACCGAGAGCTGAGGCCCGATCACTTGCTG 3000
3399 ATTAGAACAACCTCTGATGCTGATGATGATGACCGAGAGCTGAGGCCCGATCACTTGCTG 3458
3001 CTGGCCCTGCAACCGCGCTGAGTGTGGCTCTAGCGATGAAGATACAGATTGAG 3052
3459 CTGGCCCTGCAACCGCGCTGAGTGTGGCTCTAGCGATGAAGATACAGATTGAG 3510

RESULT 8
ABS69883
ID ABS69883 standard; DNA, 35935 BP.
XX
AC ABS69883;
XX
DT 21-NOV-2002 (first entry)
XX
DE Human adenovirus type 5 genome sequence #2.
XX
XX Vector; adenovirus; adeno-associated; adenosine deaminase gene; receptor;
KW adenosine deaminase deficiency; severe combined immune deficiency; PAB;
KW beta-chain; haemoglobin gene; beta-thalassemia; sickle cell disease;
KW low density lipoprotein gene; familial hypercholesterolemia;
KW hypoxanthine-guanine phosphoribosyltransferase; Lesch-Nyhan syndrome;
KW phenylalanine hydroxylase gene; gene therapy; phenylketonuria;
KW dystrophin gene; muscular dystrophy; cystic fibrosis; immunostimulant;
KW human cystic fibrosis transmembrane conductance regulator gene;
KW antianaemic; antileptemic; nontropic; cytostatic; dermatological;
KW human adenovirus genome; de.
XX
OS Human adenovirus type 5.
XX
PN US2002102731-A1.
XX
PD 01-AUG-2002.
XX
PF 12-FEB-2001, 2001US-00782378.
XX
PR 02-OCT-2000; 2000US-0237747P.
XX
PA (UNIV) UNIV NEW YORK STATE RES FOUND.
XX
P1 Hearing P, Bahou WF, Sandalon Z, Gnatenko DV;
XX
XX WPI; 2002-690619/74.
XX
XX
XX Producing vector, by introducing vector having nucleotide sequence,
PT adenovirus inverted terminal repeats and packaging sequence, and adeno-
PT associated virus terminal repeat, into cell, and culturing cell.
XX
XX
XX Disclosure; Page 56-72; 191pp; English.
XX
XX The present invention relates to a new method of producing a vector. The
CC method involves introducing recombinant vector having nucleotide sequence
CC (NS) having 5' and 3' end, left and right inverted terminal repeats of
CC adenovirus flanking NS, adenovirus packaging sequence linked to inverted
CC terminal repeat, and adeno-associated virus terminal repeat linked to 3'
CC end of NS, into cell expressing adenovirus early gene lacking from vector
CC and culturing cell to produce another vector. The method is useful for
CC generating vectors, especially md vectors. The method is useful in
CC transferring nucleotide sequences of interest into a cell, for gene
CC transfer applications (e.g. gene therapy) in vitro, ex vivo and in vivo.
CC The nucleotide sequences are useful for treating diseases associated with
CC it, i.e. adenosine deaminase gene associated with adenosine deaminase
CC deficiency with severe combined immune deficiency, beta-chain of
CC haemoglobin gene associated with beta-thalassemia and sickle cell
CC disease, receptor for low density lipoprotein gene associated with
CC familial hypercholesterolemia, hypoxanthine-guanine
CC phosphoribosyltransferase associated with Lesch-Nyhan syndrome,

CC phenylalanine hydroxylase (PAH) gene associated with phenylketonuria,
CC dystrophin gene associated with muscular dystrophy, and human cystic
CC fibrosis transmembrane conductance regulator gene associated with cystic
CC fibrosis. The present nucleic acid sequence represents a human adenovirus
CC genome sequence that was used in the methods of the invention

XX Sequence 35935 BP; 8367 A; 10073 C; 9761 G; 7734 T; 0 U; 0 Other;

Query Match 100.0%; Score 3052; DB 6; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 CGTATAGATATTAATACCCGATGAGTCTCTCAAGAGGCACTCTTGATGCGACGAGT 60
Db 459 CGTATAGATATTAATACCCGATGAGTCTCTCAAGAGGCACTCTTGATGCGACGAGT 518
QY 61 AGAGTTTCTCTCCGAGCGCTCCGACACCGGGACTGAAAATGACATATTAATCTGCC 120
Db 519 AGAGTTTCTCTCCGAGCGCTCCGACACCGGGACTGAAAATGACATATTAATCTGCC 578
QY 121 ACCGAGGTGTTATTAACCGAAGAAATGGCCGCACTTTTGACCAAGTGAATCGAAGG 180
Db 579 ACCGAGGTGTTATTAACCGAAGAAATGGCCGCACTTTTGACCAAGTGAATCGAAGG 638
QY 181 TACTGAGCTGATATCTTCCACCTCTAGCAATTTGAACCACTAACCTTCAGCACTGT 240
Db 639 TACTGAGCTGATATCTTCCACCTCTAGCAATTTGAACCACTAACCTTCAGCACTGT 698
QY 241 ATGATTTAGACGTACCGGCCCCCGAAGATCCCAACGAGAGCGGTTTCGACATTTTC 300
Db 699 ATGATTTAGACGTACCGGCCCCCGAAGATCCCAACGAGAGCGGTTTCGACATTTTC 758
QY 301 CCGACTCTGATATGTGGCGGTGACGAGAGGATTTGACTTCACTTTCCGCGCGGC 360
Db 759 CCGACTCTGATATGTGGCGGTGACGAGAGGATTTGACTTCACTTTCCGCGCGGC 818
QY 361 CCGGTTCTCCGAGCGGCTCACCTTTCCGCGAGCCGAGACCCGAGAGAGAGGCT 420
Db 819 CCGGTTCTCCGAGCGGCTCACCTTTCCGCGAGCCGAGACCCGAGAGAGAGGCT 878
QY 421 TGGGTCGGGTTTCTATGCAAACTTTGACCGGAGTGATGATCTTACCTGCCACGAG 480
Db 879 TGGGTCGGGTTTCTATGCAAACTTTGACCGGAGTGATGATCTTACCTGCCACGAG 938
QY 481 CTGCTTTCCACCGACGTACGACGAGATGAAGAGGTGAGAGATTGTGTAATATG 540
Db 939 CTGCTTTCCACCGACGTACGACGAGATGAAGAGGTGAGAGATTGTGTAATATG 998
QY 541 TGGAGCAACCCGAGGACGAGTTGACAGTCTTGTCAATTACCGGAGAAATCGGGGAGC 600
Db 999 TGGAGCAACCCGAGGACGAGTTGACAGTCTTGTCAATTACCGGAGAAATCGGGGAGC 1058
QY 601 CAGATATTAATGTGTCGTTTGTCTATATGAGACCTGTGATTTGTCTACAGTAAGT 660
Db 1059 CAGATATTAATGTGTCGTTTGTCTATATGAGACCTGTGATTTGTCTACAGTAAGT 1118
QY 661 GAAATTAATGAGGCAATGAGTGTGAGTGTGAGTGTGTAATTTTATTTTAT 720
Db 1119 GAAATTAATGAGGCAATGAGTGTGAGTGTGAGTGTGTAATTTTATTTTAT 1178
QY 721 TTTTACAGTTTGTGTTTAAAGAAATTTGATATGATTTTAAAGTCTGTGTC 780
Db 1179 TTTTACAGTTTGTGTTTAAAGAAATTTGATATGATTTTAAAGTCTGTGTC 1238
QY 781 TGAACCTGAGCTGAGCCGACGACGAGAACCGAGACCTGCAAGACTACCCGCGTCTTAA 840
Db 1239 TGAACCTGAGCTGAGCCGACGACGAGAACCGAGACCTGCAAGACTACCCGCGTCTTAA 1298
QY 841 AATGGCGCTGCTATCTCTGAGACGCGGACATCACTGTGTCTAGAGATCAATAGTAG 900
Db 1299 AATGGCGCTGCTATCTCTGAGACGCGGACATCACTGTGTCTAGAGATCAATAGTAG 1358
QY 901 TAGGATAGCTGTGATCTCCGCTCTTCAACACACTCTCTGAGATACACCCGCGTCTCC 960
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Db 1359 TAGGATAGCTGTGATCTCCGCTCTTCAACACACTCTCTGAGATACACCCGCGTCTCC 1418
QY 961 GCTGTGCCCATTAACCAAGTTCGAGAGTTGTGGCGGTGCGAGGCTGTGAATG 1020
Db 1419 GCTGTGCCCATTAACCAAGTTCGAGAGTTGTGGCGGTGCGAGGCTGTGAATG 1478
QY 1021 TATGAGAGACTTGTCTTACAGACCTGAGCAACTTTTGGACTTGAAGCTTAAACGCCCAG 1080
Db 1479 TATGAGAGACTTGTCTTACAGACCTGAGCAACTTTTGGACTTGAAGCTTAAACGCCCAG 1538
QY 1081 GCCATTAAGTGTAAACCTGTGATTTGCGTGTGATTAAGCTTTGTTGCTGAATAGT 1140
Db 1539 GCCATTAAGTGTAAACCTGTGATTTGCGTGTGATTAAGCTTTGTTGCTGAATAGT 1598
QY 1141 TGATGTAAGTTTAAATAAGGCTGATTAATGTTTAACTTGATGATGCGTGTAAATGGGCG 1200
Db 1599 TGATGTAAGTTTAAATAAGGCTGATTAATGTTTAACTTGATGATGCGTGTAAATGGGCG 1658
QY 1201 GGGGCTTAAAGGATTAATATGCGCGGTGAGCTTATCTTGTTTCAATCTGACCTATGGA 1260
Db 1659 GGGGCTTAAAGGATTAATATGCGCGGTGAGCTTATCTTGTTTCAATCTGACCTATGGA 1718
QY 1261 GCGTTGGAGATGTTTGAAGATTTTCTGCTGTGCGTAACTTGCTGGAACGAGCTCTAA 1320
Db 1719 GCGTTGGAGATGTTTGAAGATTTTCTGCTGTGCGTAACTTGCTGGAACGAGCTCTAA 1778
QY 1321 CAGTACCTCTTGTGTTTGAAGGTTCTGTGGGCTCATCCACGACAAAGTTAGTCTGACG 1380
Db 1779 CAGTACCTCTTGTGTTTGAAGGTTCTGTGGGCTCATCCACGACAAAGTTAGTCTGACG 1838
QY 1381 AATTAAAGAGATTTCAAGTGGGAATTTGAAGCTTTTGAATCTGTGTGAGCTGTT 1440
Db 1839 AATTAAAGAGATTTCAAGTGGGAATTTGAAGCTTTTGAATCTGTGTGAGCTGTT 1898
QY 1441 TGATTTTGAATCTGTGATCACGAGGCTTTTCCAGAGAGGTCATCAAGCTTTGGA 1500
Db 1899 TGATTTTGAATCTGTGATCACGAGGCTTTTCCAGAGAGGTCATCAAGCTTTGGA 1958
QY 1501 TTTTTCACACCGGGGCGCTGCGGCTGTGCTTTTGTGAGTTTAAAGGATTA 1560
Db 1959 TTTTTCACACCGGGGCGCTGCGGCTGTGCTTTTGTGAGTTTAAAGGATTA 2018
QY 1561 ATGAGGGAAGAAACCATCTGAGCGGGGGTACCTGTGATTTTGTGGCATGACTCT 1620
Db 2019 ATGAGGGAAGAAACCATCTGAGCGGGGGTACCTGTGATTTTGTGGCATGACTCT 2078
QY 1621 GTGAGAGCGGTTGTGAGACAAAGAAATGCTGTGCTTCTGCTCCGCGCCGCGC 1680
Db 2079 GTGAGAGCGGTTGTGAGACAAAGAAATGCTGTGCTTCTGCTCCGCGCCGCGC 2138
QY 1681 GATTAATACCGACGAGAGAGACGACGACGAGAGAGAAACGAGCGGGCGGACAGA 1740
Db 2139 GATTAATACCGACGAGAGAGACGACGACGAGAGAGAAACGAGCGGGCGGACAGA 2198
QY 1741 GCAAGGCCATGGAACCGAGAGCGGCTGTGACCTTGGGAAATGAATGTTGTACAGGTG 1800
Db 2199 GCAAGGCCATGGAACCGAGAGCGGCTGTGACCTTGGGAAATGAATGTTGTACAGGTG 2258
QY 1801 GCTGAAGTATCCAGAACTGAGACGATTTTGACAAATTAACAGAGATGAGGCGGGGCTA 1860
Db 2259 GCTGAAGTATCCAGAACTGAGACGATTTTGACAAATTAACAGAGATGAGGCGGGGCTA 2318
QY 1861 AAGGGGTTAAAGAGAGCGGGGGCTTGTGAGGCTTACAGAGAGGCTAGAAATTAAGCT 1920
Db 2319 AAGGGGTTAAAGAGAGCGGGGGCTTGTGAGGCTTACAGAGAGGCTAGAAATTAAGCT 2378
QY 1921 TTTTACCTTAATGACCAAGACCGCTCTGAGTATTAATTTTAAAGATCAAGATTAAT 1980
Db 2379 TTTTACCTTAATGACCAAGACCGCTCTGAGTATTAATTTTAAAGATCAAGATTAAT 2438
QY 1981 TGGGCTTAATGAGCTTAATCTGTGCGGAGAGATTAATTTTCAATAAGAGCTGAACACTTAC 2040
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Db 2439 TGCCTAATGAGCTTGATCTGCTGCGCAGAAATATTCATAGAGCAGCTGACCACTTAC 2498
Qy 2041 TGGCTGACGACGGGGGATGATTTTGAAGGAGCTATTAGGGTATATGCAAGGTGGCACTT 2100
Db 2499 TGGCTGACGACGGGGGATGATTTTGAAGGAGCTATTAGGGTATATGCAAGGTGGCACTT 2558
Qy 2101 AGGCCAGATTGCAAGTACAGATCAGCAAACTTGTAAATATCAGAAATTTGTTGCTACATT 2160
Db 2559 AGGCCAGATTGCAAGTACAGATCAGCAAACTTGTAAATATCAGAAATTTGTTGCTACATT 2618
Qy 2161 TCTGGGAAACGGGGCCGAGAGTGAATAGATACCGAGAGATTAGGGTGGCTTTAGATGTRGC 2220
Db 2619 TCTGGGAAACGGGGCCGAGAGTGAATAGATACCGAGAGATTAGGGTGGCTTTAGATGTRGC 2678
Qy 2221 ATGATTAATATATGTCGCGGGGGTGTCTTGGCATGAGCGGGGTGTTATTAATGAAAGTAAAG 2280
Db 2679 ATGATTAATATATGTCGCGGGGGTGTCTTGGCATGAGCGGGGTGTTATTAATGAAAGTAAAG 2738
Qy 2281 TTTACTGGCCCAATTTTATGCGGTACCGTTTTTCTGGCCAAATACCAACTTATCTTACAC 2340
Db 2739 TTTACTGGCCCAATTTTATGCGGTACCGTTTTTCTGGCCAAATACCAACTTATCTTACAC 2798
Qy 2341 GGTGTAGCTTCTATGGGTTTAAACAATCTGTGTGGAAGCCTTGAACCGATGTAAGGTT 2400
Db 2799 GGTGTAGCTTCTATGGGTTTAAACAATCTGTGTGGAAGCCTTGAACCGATGTAAGGTT 2858
Qy 2401 CGGGGCTGTGCTTTTACTGCTGTGAGAGGGGGGTGTGTGCGCCCAAAAGAGAGGCT 2460
Db 2859 CGGGGCTGTGCTTTTACTGCTGTGAGAGGGGGGTGTGTGCGCCCAAAAGAGAGGCT 2918
Qy 2461 TCAATTAAGAAATGCTCTTTTGAAGGTGTACCTTGGGTATCTGTCTGAGGGTAACTCC 2520
Db 2919 TCAATTAAGAAATGCTCTTTTGAAGGTGTACCTTGGGTATCTGTCTGAGGGTAACTCC 2978
Qy 2521 AGGGTGGCCCAATGTGAGCTCCGACCTGTGTGCTTCAATGCTAATGTAAAGGTGGCT 2580
Db 2979 AGGGTGGCCCAATGTGAGCTCCGACCTGTGTGCTTCAATGCTAATGTAAAGGTGGCT 3038
Qy 2581 GTGATTAAGCATATCATGTATGTGGCAACTGCGAGAGCAGAGGCTCTCAGATGCTGACC 2640
Db 3039 GTGATTAAGCATATCATGTATGTGGCAACTGCGAGAGCAGAGGCTCTCAGATGCTGACC 3098
Qy 2641 TGCTCGAAGCGCAACTGTACCTGTGAGAACCAATTCAGTACGAGCCACTCTCGCAG 2700
Db 3099 TGCTCGAAGCGCAACTGTACCTGTGAGAACCAATTCAGTACGAGCCACTCTCGCAG 3158
Qy 2701 GCTTGGCCAGTGTGTGAGCATAACTATGACCCGCTGTCTTGTGATTTGGGTAAACAG 2760
Db 3159 GCTTGGCCAGTGTGTGAGCATAACTATGACCCGCTGTCTTGTGATTTGGGTAAACAG 3218
Qy 2761 AGGGGGGTGTTCTTACCTTACCAATGCAATTGTGATCACAATAAGATTTTCTTGAGGCC 2820
Db 3219 AGGGGGGTGTTCTTACCTTACCAATGCAATTGTGATCACAATAAGATTTTCTTGAGGCC 3278
Qy 2821 GAGAGCATGTCCAAAGTGAACCTGAAACGGGGTGTTTGACATGACCATGAAAGATCTGAA 2880
Db 3279 GAGAGCATGTCCAAAGTGAACCTGAAACGGGGTGTTTGACATGACCATGAAAGATCTGAA 3338
Qy 2881 GTGCTGAGTACGATGAGAACCCGACCCAGGTGACAGACCTTCCGAGTGTGGGGGTAAACAT 2940
Db 3339 GTGCTGAGTACGATGAGAACCCGACCCAGGTGACAGACCTTCCGAGTGTGGGGGTAAACAT 3398
Qy 2941 ATTAGGAACAGAGCTGTGATCTGGATGTGACCGAGAGAGCTGAGAGCCGATCACTTGGTG 3000
Db 3399 ATTAGGAACAGAGCTGTGATCTGGATGTGACCGAGAGAGCTGAGAGCCGATCACTTGGTG 3458
Qy 3001 CTGGCTTGACCCGCGCTGAGTTTGGCTCTAGCCATGAAATACAGATTGAG 3052
Db 3459 CTGGCTTGACCCGCGCTGAGTTTGGCTCTAGCCATGAAATACAGATTGAG 3510

RESULT 9
ACA61116

ID ACA61116 standard; DNA; 35935 BP.
XX
AC ACA61116;
XX
DT 09-JUN-2003 (first entry)
XX
DE Adenovirus serotype 6 genome.
XX
KW ds; non-structural protein; NS3; NS4A; NS4B; NS5A; NS5B; genome;
XX adenoviral vector; HCV infection; vaccine; gene therapy; protease.
XX
OS Adenovirus serotype 6.
XX
PN MO2003031588-A2.
XX
PD 17-APR-2003.
XX
PF 10-OCT-2002; 2002MO-US032512.
XX
PR 11-OCT-2001; 2001US-0328655P.
PR 13-MAR-2002; 2002US-0363774P.
XX
PA (MERCK) MERCK & CO INC.
PA (RICE-) 1ST RICERCHER BIOL MOLECOLARE ANGELETTI.
PI Emami EA, Kaslow DC, Bett AJ, Shiver JW, Nicolson A, Lahm A;
PI Luzzagio A, Correse R, Colloca S;
XX WPI; 2003-381708/36.
XX
PT New nucleic acid encoding a Met-NS3-NS4A-NS4B-NS5A-NS5B polypeptide,
PT useful as a component of an adenovector or DNA plasmid vaccine for
PT preventing or treating hepatitis C virus.
XX
PS Claim 19; Fig 7; 231pp; English.
XX
XX The invention relates to a nucleic acid encoding a Met-NS3-NS4A-NS4B-NS5A-NS5B (NS strands for non-structural protein from HCV) polypeptide appearing as AB009574. The encoded polypeptide has sufficient protease activity to process itself to produce an NS5B protein that is enzymatically inactive. Also included are a cultured recombinant cell comprising the novel nucleic acid, making an adenovector (comprising: (a) producing an adenovirus genome plasmid comprising a gene expression cassette by homologous recombination between the novel nucleic acid and a nucleic acid comprising a first adenovirus region from base pair 1-450 corresponding to either Ad5 or Ad6, a second adenovirus region from base pair 3511-5548 corresponding to Ad5 or from base pair 3508-5541 corresponding to Ad6, joined to the first region, a third adenovirus region from base pair 5545-28133 corresponding to Ad5 or from base pair 5542-28156 corresponding to Ad6, joined to the second region, a fourth adenovirus region from base pair 30818-33966 corresponding to Ad5 or from base pair 30789-33784 corresponding to Ad6, joined to the third region, and a fifth adenovirus region from base pair 33967-35935 corresponding to Ad5 or from base pair 33785-35759 corresponding to Ad6, joined to the fourth region; and (b) rescuing the recombinant adenovirus from the recombinant adenovirus plasmid), an adenoviral vector that is produced by the method above appearing as ACA61113 which has a humanised version of the polynucleotide of the invention and encodes the HCV inactivated polypeptide, a recombinant nucleic acid comprising one or more Ad6 regions and a region not present in Ad6, where at least one Ad6 region is selected from E1A, E1B, E2B, E2A, E4, E1, E2, E4 and E5. The nucleic acid is useful as a component of an adenoviral vector or a DNA plasmid vaccine providing a broad range of antigens for generating an HCV-specific cell mediated immune response. The nucleic acid may also be used in treating patients infected with HCV. The present sequence is the Ad6 genome
XX
SQ Sequence 35935 BP; 8367 A; 10073 C; 9761 G; 7734 T; 0 U; 0 Other;

Query Match 100.0%; Score 3052; DB 8; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGTGTACTGATATTATACCCGGTGAGTTCTTCAAGAGGCCACTTGTAGTCCAGCGAGT 60

Db 459 CCGTAAAGTATTAATCCGGTGAAGTCTCTCAAGAGCCACTCTTGAGTCCAGCGAGT 518
Qy 61 AGAGTTTCTCTCCGAGCCGCTCCGACACCGGGAGTGAATATAGACATATATCTGCC 120
Db 519 AGAGTTTCTCTCCGAGCCGCTCCGACACCGGGAGTGAATATAGACATATATCTGCC 578
Qy 121 AGGAGGTGTATTAACGAGAAATGGCCGCACTCTTTGACCAAGCTGATCGAAGGG 180
Db 579 ACGGAGGTGTATTAACGAGAAATGGCCGCACTCTTTGACCAAGCTGATCGAAGGG 638
Qy 181 TACTGGCGATATCTTCCACTCTAGCCATTTTGAACCACTTACCCTTACGAACTGT 240
Db 639 TACTGGCGATATCTTCCACTCTAGCCATTTTGAACCACTTACCCTTACGAACTGT 698
Qy 241 ATGATTTAGACGTACGCGCCCGGAGATCCCAACGAGAGCGGTTCGACGATTTTTC 300
Db 699 ATGATTTAGACGTACGCGCCCGGAGATCCCAACGAGAGCGGTTCGACGATTTTTC 758
Qy 301 CCGACTCTGATATGTGGCGGTGACGAGAGGATTTGACTTACTCATTTTCCGCGCGC 360
Db 759 CCGACTCTGATATGTGGCGGTGACGAGAGGATTTGACTTACTCATTTTCCGCGCGC 818
Qy 361 CCGGTTCTCCGAGCCGCTCACCTTCCGCGAGCCGAGCCGAGAGAGAGCCT 420
Db 819 CCGGTTCTCCGAGCCGCTCACCTTCCGCGAGCCGAGCCGAGAGAGAGCCT 878
Qy 421 TGGGTCCGTTCTATGCAAACTTGTACCGAGTGAATGATCTTACTCTGCCAGAG 480
Db 879 TGGGTCCGTTCTATGCAAACTTGTACCGAGTGAATGATCTTACTCTGCCAGAG 938
Qy 481 CTGGCTTCCACCGACGTACGACGAGATGAAGAGGTGAGAGATTGTGTAAATTATG 540
Db 939 CTGGCTTCCACCGACGTACGACGAGATGAAGAGGTGAGAGATTGTGTAAATTATG 998
Qy 541 TGGAGACCCCGGGGACGGTTGACAGTCTTGTCAATATCACCGAGGAAATCGGGGGAC 600
Db 999 TGGAGACCCCGGGGACGGTTGACAGTCTTGTCAATATCACCGAGGAAATCGGGGGAC 1058
Qy 601 CAGATATTAATGTGTGCTTGTCTATATAGAGACCTGTGCAATTTTCTACAGTAA 660
Db 1059 CAGATATTAATGTGTGCTTGTCTATATAGAGACCTGTGCAATTTTCTACAGTAA 1118
Qy 661 GAAATTAATGGGCGAGTGGTATAGAGTGTGGTTTGTGTGTAATTTTTTTTAA 720
Db 1119 GAAATTAATGGGCGAGTGGTATAGAGTGTGGTTTGTGTGTAATTTTTTTTAA 1178
Qy 721 TTTTACAGTTTGTGTTTAAAGAAATTTGTATGTGATTTTTTTTAAAGGTCCTGTCT 780
Db 1179 TTTTACAGTTTGTGTTTAAAGAAATTTGTATGTGATTTTTTTTAAAGGTCCTGTCT 1238
Qy 781 TGAACCTGAGCCTGAGCCGAGCAGAACCGGAGCTTCAAGACTTACCCGCTCTTAA 840
Db 1239 TGAACCTGAGCCTGAGCCGAGCAGAACCGGAGCTTCAAGACTTACCCGCTCTTAA 1298
Qy 841 AATGGCCCTGCTATCTGAGACCGCCGACATCACTGTGTCTAGAGATCAATAGTAG 900
Db 1299 AATGGCCCTGCTATCTGAGACCGCCGACATCACTGTGTCTAGAGATCAATAGTAG 1358
Qy 901 TAGGGATAGCTGTAACCTCCGCTCTTCAACAACCTCTGAGATACCCGCGGTGCTCC 960
Db 1359 TAGGGATAGCTGTAACCTCCGCTCTTCAACAACCTCTGAGATACCCGCGGTGCTCC 1418
Qy 961 GCTGTGCCCATTAACAGTTGCGTGAAGATTGTGTGGCGTCCGACAGGCTGTGATG 1020
Db 1419 GCTGTGCCCATTAACAGTTGCGTGAAGATTGTGTGGCGTCCGACAGGCTGTGATG 1478
Qy 1021 TATGAGAGACTTGTCTTAAAGAGCTGCGCAACTTTGACTTGAAGCTTAAACGCCAG 1080
Db 1479 TATGAGAGACTTGTCTTAAAGAGCTGCGCAACTTTGACTTGAAGCTTAAACGCCAG 1538
Qy 1081 GCGTAAGGTGTAACCTGTGATTTGCGTGTGTTAGGCTTTTGTGCGATGAGT 1140
Db 1140 GCGTAAGGTGTAACCTGTGATTTGCGTGTGTTAGGCTTTTGTGCGATGAGT 1140

Db 1539 GCGTAAGGTGTAACCTGTGATTTGCGTGTGTTAGGCTTTTGTGCGATGAGT 1598
Qy 1141 TGATGTAAGTTTAAATAAGGTGAGATATGTTTAACTTGATGGCGTTAAATGGGCG 1200
Db 1599 TGATGTAAGTTTAAATAAGGTGAGATATGTTTAACTTGATGGCGTTAAATGGGCG 1658
Qy 1201 GGGGCTTAAAGGTTTAAATGCGCCGTTGGCTTAACTTGTGTAATCTGACCTCA 1260
Db 1659 GGGGCTTAAAGGTTTAAATGCGCCGTTGGCTTAACTTGTGTAATCTGACCTCA 1718
Qy 1261 GGGTGGAGGTGTTGGAAGATTTTTCGCTGTCGTAATCTTGCGGAACAGAGCTTAA 1320
Db 1719 GGGTGGAGGTGTTGGAAGATTTTTCGCTGTCGTAATCTTGCGGAACAGAGCTTAA 1778
Qy 1321 CAGTACCTTTGTTTGAAGTTTCTGTGGGCTCATCCAGGCAAGTTAGTCTGAG 1380
Db 1779 CAGTACCTTTGTTTGAAGTTTCTGTGGGCTCATCCAGGCAAGTTAGTCTGAG 1838
Qy 1381 AATTAAAGAGATTAACAAGTGGAAATTTGAAGAGCTTTGAAATCCTGTGTGAGCT 1440
Db 1839 AATTAAAGAGATTAACAAGTGGAAATTTGAAGAGCTTTGAAATCCTGTGTGAGCT 1898
Qy 1441 TGATTTCTTGAATCTGGGTCAACAGGCTTTTCAAGAGAGGTCAATCAAGCTTTGA 1500
Db 1899 TGATTTCTTGAATCTGGGTCAACAGGCTTTTCAAGAGAGGTCAATCAAGCTTTGA 1958
Qy 1501 TTTTTCACACCGGGGGCGCGTGGGCTGTGTTGCTTTTGAAGTTTAAAGATTA 1560
Db 1959 TTTTTCACACCGGGGGCGCGTGGGCTGTGTTGCTTTTGAAGTTTAAAGATTA 2018
Qy 1561 ATGAGCGGAAGAAACCCATCTGAGCGGGGGTACTCTGATTTTCTGCGCATGCACT 1620
Db 2019 ATGAGCGGAAGAAACCCATCTGAGCGGGGGTACTCTGATTTTCTGCGCATGCACT 2078
Qy 1621 GTGAGAGCGGTTGTGAGACCAAGAAATGCTCTGATGTTGTTCCGTCGCGCCG 1680
Db 2079 GTGAGAGCGGTTGTGAGACCAAGAAATGCTCTGATGTTGTTCCGTCGCGCCG 2138
Qy 1681 GATTAATCCGACGGAGAGCAGCAGCAGCAGAGAGAAACAGCGCGCGCGAGGA 1740
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Qy 1741 GCAGAGCCCATGGAACCCGAGAGCCGCTGAGACCTCGGAAATGAATGTTGTAAG 1800
Db 2199 GCAGAGCCCATGGAACCCGAGAGCCGCTGAGACCTCGGAAATGAATGTTGTAAG 2258
Qy 1801 GCTGAACGTATCCAGAACTGAGACGCAATTTGACAAATTAAGAGATGGCAGGGCT 1860
Db 2259 GCTGAACGTATCCAGAACTGAGACGCAATTTGACAAATTAAGAGATGGCAGGGCT 2318
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2859 CGGGGCTGTGCTTTTCTGCTGCGAAGGGGGGTGTGTGCGCCCAAAAGAGGGCT 2918
2461 TCAATTAAGAAATGCTCTTTGAAAGGTGTACCTTGGGTATCTGTCTAGAGGTAACTCC 2520
2919 TCAATTAAGAAATGCTCTTTGAAAGGTGTACCTTGGGTATCTGTCTAGAGGTAACTCC 2978
2521 AGGGTGGCCCAATGTGCGCTCCGACTGTGCTTCAATGCTAATGTAAGAGGTGGCT 2580
2979 AGGGTGGCCCAATGTGCGCTCCGACTGTGCTTCAATGCTAATGTAAGAGGTGGCT 3038
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3099 TGCTCGACCGCAACTGTACCTGCTGTAAGACCAATTCAGTACGACCACTCTTCGCAAG 3158
2701 GCCTGGCCAGTGTGTAGCAATACACTGACCGGCTGTCTTGCATTTGGGTAAACAGG 2760
3159 GCCTGGCCAGTGTGTAGCAATACACTGACCGGCTGTCTTGCATTTGGGTAAACAGG 3218
2761 AGGGGGGGTCTTCAACCTTACCAATGCAATTGAGTCACATGAGATTTGCTGAGGCC 2820
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2821 GAGAGCATGTCCAAAGTGAACCTGAAACCGGGGTGTGTAATGATGACCATGAAATCTGGAAG 2880
3279 GAGAGCATGTCCAAAGTGAACCTGAAACCGGGGTGTGTAATGATGACCATGAAATCTGGAAG 3338
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2941 ATTAGGAACCAAGCTGTGATGCTGATGTGACCGGAGAGCTGAGGCCCGGATCACTGGTG 3000
3399 ATTAGGAACCAAGCTGTGATGCTGATGTGACCGGAGAGCTGAGGCCCGGATCACTGGTG 3458
3001 CTGGCTTGACACCGCGCTGAGTGTGGCTCTAGCGATGAAGATACGATTTGAG 3052
3459 CTGGCTTGACACCGCGCTGAGTGTGGCTCTAGCGATGAAGATACGATTTGAG 3510

PN WO2003031588-A2.
XX 17-APR-2003.
PD 10-OCT-2002; 2002WO-US032512.
XX 11-OCT-2001; 2001US-0328655P.
XX 13-MAR-2002; 2002US-0363774P.
PR (MERI) MERCK & CO INC.
PA (RICE-) IST RICERCHIE BIOL MOLECOLARE ANGELETTI.
PI Eminl EA, Kaslow DC, Belt AJ, Shiver JW, Nicosia A, Lahm A;
PI Luzzago A, Corese R, Colloca S;
DR WPI; 2003-381708/36.
XX
XX
XX New nucleic acid encoding a Met-NS3-NS4A-NS4B-NS5A-NS5B polypeptide,
PT useful as a component of an adenovector or DNA plasmid vaccine for
PT preventing or treating hepatitis C virus.
XX
XX
XX Claim 19, Fig 8; 231pp; English.
XX
XX The invention relates to a nucleic acid encoding a Met-NS3-NS4A-NS4B-NS5A
CC -NS5B (NS strands for non-structural protein from HCV) polypeptide
CC appearing as AB099574. The encoded polypeptide has sufficient protease
CC activity to process itself to produce an NS5B protein that is
CC enzymatically inactive. Also included are a cultured recombinant cell
CC comprising the novel nucleic acid, making an adenovector (comprising: (a)
CC producing an adenovirus genome plasmid comprising a gene expression
CC cassette by homologous recombination between the novel nucleic acid and a
CC nucleic acid comprising a first adenovirus region from base pair 1-450
CC corresponding to either Ad5 or Ad6, a second adenovirus region from base
CC pair 3511-5548 corresponding to Ad5 or from base pair 3508-5541
CC corresponding to Ad6, joined to the first region, a third adenovirus
CC region from base pair 5549-2813 corresponding to Ad5 or from base pair
CC 5542-28156 corresponding to Ad6, joined to the second region, a fourth
CC adenovirus region from base pair 30818-33966 corresponding to Ad5 or from
CC base pair 30789-33784 corresponding to Ad6, joined to the third region,
CC and a fifth adenovirus region from base pair 33967-35935 corresponding to
CC Ad5 or from base pair 33785-35759 corresponding to Ad6, joined to the
CC fourth region; and (b) rescuing the recombinant adenovirus from the
CC recombinant adenovirus plasmid), an adenoviral vector that is produced by
CC method above appearing as ACA61113 which has a humanised version of the
CC polynucleotide of the invention and encodes the HCV inactivated
CC polypeptide, a recombinant nucleic acid comprising one or more Ad6
CC regions and a region not present in Ad6, where at least one Ad6 region is
CC selected from E1A, E1B, E2A, E2A, E4, E4, E1, E2, E4 and E5. The nucleic acid
CC is useful as a component of an adenoviral vector or a DNA plasmid vaccine
CC providing a broad range of antigens for generating an HCV-specific cell
CC mediated immune response. The nucleic acid may also be used in treating
CC patients infected with HCV. The present sequence is the Ad5 genome
XX
XX Sequence 35935 BP; 8367 A; 10073 C; 9761 G; 7734 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 3052; DB 8; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGTAGTGTATTATTAACCGGGTGTCTCTCAAGAGGCCACTTTGATGCGACGAGT 60
DB 459 CGGTAGTGTATTATTAACCGGGTGTCTCTCAAGAGGCCACTTTGATGCGACGAGT 518
QY 61 AGAGTTTTCCTCCCGAGCCGCTCCGACACCGGGAACGTAATGATTTATCTGCC 120
DB 519 AGAGTTTTCCTCCCGAGCCGCTCCGACACCGGGAACGTAATGATTTATCTGCC 578
QY ACGAGGTGTATTATTAACGAAATGCGCGCACTTTTGTGACCACTGATCGAAGAG 180
DB 579 ACGAGGTGTATTATTAACGAAATGCGCGCACTTTTGTGACCACTGATCGAAGAG 638
QY TACTGGCTGATTAATCTTCACTTCTAGCAATTTGAAACCACTTACCTTGACGAACGT 240

Db 639 TACTGGCTGATTAATCTTCCACTCTCCTAGSCATTTTGAAACACTACCTTCCAGCACTGT 698
Qy 241 ATGATTTTAGAGTGAACGGCCCCCGAAGATCCCAACGAGAGAGCGGTTTCCGAGATTTTTC 300
Db 699 ATGATTTAGAGTGAACGGCCCCCGAAGATCCCAACGAGAGAGCGGTTTCCGAGATTTTTC 758
Qy 301 CCGACTCTGTAAATGTTGGCGGTGACGAAAGGAAATTGACTTACTCACTTTTCCGCGCGGC 360
Db 759 CCGACTCTGTAAATGTTGGCGGTGACGAAAGGAAATTGACTTACTCACTTTTCCGCGCGGC 818
Qy 361 CCGGTTCTCCGAGACCGGCTCACTTTCCCGCAGACCCGAGACCCGAGAGAGAGGCT 420
Db 819 CCGGTTCTCCGAGACCGGCTCACTTTCCCGCAGACCCGAGACCCGAGAGAGAGGCT 878
Qy 421 TGGGTCGGGTTTCTATGCAAACTTTGTAACGAGAGTGAATGATCTTAACTTGCAACGAG 480
Db 879 TGGGTCGGGTTTCTATGCAAACTTTGTAACGAGAGTGAATGATCTTAACTTGCAACGAG 938
Qy 481 CTGGCTTTTCCAACGAGTGAACGAGGATGAAAGGAGTGAAGAGTTTGTATGATTAATG 540
Db 939 CTGGCTTTTCCAACGAGTGAACGAGGATGAAAGGAGTGAAGAGTTTGTATGATTAATG 998
Qy 541 TGGAGCAACCCGGGCAACGGTTGCAAGTCTTGTCAATTAACCGAGAGAAATCCGGGGAC 600
Db 999 TGGAGCAACCCGGGCAACGGTTGCAAGTCTTGTCAATTAACCGAGAGAAATCCGGGGAC 1058
Qy 601 CAGATTAATATGTTTCCGTTTGTCTATATGAGAACCTGTGACATGTTGTCTACAGTAAGT 660
Db 1059 CAGATTAATATGTTTCCGTTTGTCTATATGAGAACCTGTGACATGTTGTCTACAGTAAGT 1118
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Qy 1321 CAGTACCTTTGTTTGGAGGTTTCTGTGGGCTCATCCGAGCAAGTATGTTGTCAG 1380
Db 1779 CAGTACCTTTGTTTGGAGGTTTCTGTGGGCTCATCCGAGCAAGTATGTTGTCAG 1838
Qy 1381 AATTAAGAGATTAACAAGTGGAAATTGAAAGCTTTTGAATTCCTGTGTGAGCTGT 1440
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Qy 1441 TGATTTCTTGAATCTGGGTCAACGAGCGCTTTTCAAGAGAGTCAATCAAGCTTTTGA 1500
Db 1899 TGATTTCTTGAATCTGGGTCAACGAGCGCTTTTCAAGAGAGTCAATCAAGCTTTTGA 1958
Qy 1501 TTTTTCACACCGGGGCGCGCTGTGCTGTGCTTTTGTAGTTTATTAAGATTA 1560
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Db 2319 AAGGGGTAAAGAGAGAGCGGGGGCTTGTGAGGCTAACAGAGAGGCTAAGAACTAGCT 2378
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    |||||
Db 3459 CTGGCCTGACCCCGGCTGAGTTGGCTCTGACCGATGAAGATACAGATTGAG 3510
    |||||

RESULT 11
ACA60761 standard; DNA; 35935 BP.
XX ACA60761;
XX
DT 11-AUG-2003 (first entry)
XX
XX Human adenovirus type 5 DNA sequence.
XX
XX Neoplasm; ds; tumour; malignant tumour; metastatic tumour; cancer;
KM liver tumour; colorectal cancer; melanoma.
XX
XX Human adenovirus type 5.
OS
XX
XX
XX Key location/Qualifiers
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    /note= "E1A promoter"
    /tag= b
    /rpt_type= OTHER
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    /tag= C
    /note= "Region of max DNA replication"
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FT      /tag= z
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FT      /rpt_type= OTHER
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XX
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XX
XX      12-JUL-2002; 2002WO-GB003211.
XX
XX      13-JUL-2001; 2001GB-00017198.
XX
XX      (BTGI-) BTG INT LTD.
XX
XX      I990 RD, Fuierer C, Homicsko KG;
XX
XX      WPI; 2003-221752/21.
XX
XX      New viral DNA construct having one or more tumor specific transcrip
PT      tion factor binding sites controlling expression of the E1A open reading
PT      frame, useful in the treatment of malignant and metastatic tumors of the
PT      colon.
XX
XX      Disclosure; Page 70-87; 97BP; English.
XX
XX      The invention relates to a new viral DNA construct encoding for an
CC      adenovirus capable of replication in a human or animal tumour cell, that
CC      comprises one or more transcription factor (TF) binding sites operatively
CC      positioned together with the E1A open reading frame to promote expression
CC      of E1A proteins in the presence of the TF. The viral construct and/or
CC      virus is useful in the manufacture of a medicament in the therapy of
CC      patients having neoplasm, where they are capable of causing death to
CC      tumour cell. They are useful in treating malignant and metastatic tumours
CC      derived from colon cells particularly liver tumours also for treating
CC      colorectal cancers and melanomas. The present sequence represents the DNA
CC      sequence of human adenovirus type 5
XX
XX      Sequence 35935 BP; 8367 A; 10073 C; 9761 G; 7734 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 3052; DB 10; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 CGGTAGTATTTATATACCGGATGAGTTCCTCAAGAGCCACTCTTGAGTCCAGCGAGT 60
DB      459 CGGTAGTATTTATATACCGGATGAGTTCCTCAAGAGCCACTCTTGAGTCCAGCGAGT 518
QY      61 AGAGTTTCTCTCGAGAGCCGCTCCGACACCGGAGCTGAAAATGAGACATTTATCTGCC 120
DB      519 AGAGTTTCTCTCGAGAGCCGCTCCGACACCGGAGCTGAAAATGAGACATTTATCTGCC 578
QY      121 ACGGAGGTGTTATTAACGAATAATGCGCGACGCTTTTGACACGAGCTGATCGAAGAG 180
DB      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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DB      579 ACGGAGGTGTTATTAACGAATAATGCGCGCGACGCTTTTGACACGAGCTGATCGAAGAG 638
QY      181 TACTGCTGATTAATCTTCAACTCTAGCCATTTTGAACCACTAACCTTTCAGCAACTGT 240
DB      639 TACTGCTGATTAATCTTCAACTCTAGCCATTTTGAACCACTAACCTTTCAGCAACTGT 698
QY      241 ATGATTTAGAGTACGCGCCCGCGAAGATCCCAACGAGAGAGCGGTTCCGAGATTTTTC 300
DB      699 ATGATTTAGAGTACGCGCCCGCGAAGATCCCAACGAGAGAGCGGTTCCGAGATTTTTC 758
QY      301 CCGACTCTGTAATGTTGGCGGTGAGAGAAAGGATTGACTTACTACTTTTCCGCGCGGC 360
DB      759 CCGACTCTGTAATGTTGGCGGTGAGAGAAAGGATTGACTTACTACTTTTCCGCGCGGC 818
QY      361 CCGGTTCTCCGAGACCGGCTTCACTTTTCCCGGACCCCGAGACCCGAGAGAGAGCT 420
DB      819 CCGGTTCTCCGAGACCGGCTTCACTTTTCCCGGACCCCGAGAGAGAGAGCT 878
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DB      879 TGGGTCGGGTTCTATATGCCAAACCTTGTAACGAGGTGATGATCTTAACCTGCCACGAG 938
QY      481 CTGGCTTTCCACCCGAGTACGAGAGTGAAGAGGATGAGAGGTTGTGTAGATTATG 540
DB      939 CTGGCTTTCCACCCGAGTACGAGAGTGAAGAGGATGAGAGGTTGTGTAGATTATG 998
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DB      999 TGAGACACCCCGGACGAGGTTGACAGTCTTGTCTATATCAACCGAGAAATACGGGGAGC 1058
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DB      1059 CAGATATTATATGTTCCGCTTGTCTATATGAGAGACTGTGGATGTTGTCTACAGTAAGT 1118
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DB      1119 GAAATATTATGAGCAGTGGTGTATAGAGTGTGGGTTGTGTGTGTAATTTTTTTTAT 1178
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QY      841 AATGGCGCTGCTATCTCGTGAAGCCCGGACATCACTGTGCTAGAGATCAATATGATG 900
DB      1299 AATGGCGCTGCTATCTCGTGAAGCCCGGACATCACTGTGCTAGAGATCAATATGATG 1358
QY      901 TACGATAGCTGTGACTCCGCTCTTCTTAACACACTCTTGAGATACACCCCGTGTGCC 960
DB      1359 TACGATAGCTGTGACTCCGCTCTTCTTAACACACTCTTGAGATACACCCCGTGTGCC 1418
QY      961 GCTGTGCCCCCTTAACCAAGTGGCCGTGAGAGTGTGGGCGTGGCCAGGCTGTGGATG 1020
DB      1419 GCTGTGCCCCCTTAACCAAGTGGCCGTGAGAGTGTGGGCGTGGCCAGGCTGTGGATG 1478
QY      1021 TATGAGAGACTTGTCTTAACGAGCTTGGGCAACTTTTGAAGCTTGAAGCTTAAACGCCAG 1080
DB      1479 TATGAGAGACTTGTCTTAACGAGCTTGGGCAACTTTTGAAGCTTGAAGCTTAAACGCCAG 1538
QY      1081 GCGATTAAGGTGTAACCTGTGATTTGCGTGTGTGTTAAACGCTTTTGTGTGATGATG 1140
DB      1539 GCGATTAAGGTGTAACCTGTGATTTGCGTGTGTGTTAAACGCTTTTGTGTGATGATG 1598
QY      1141 TGATGTAAGTTTAAATGAAGGTGATATGTTTAACTTGAATGCGCGTAAATATGGGCC 1200
DB      1599 TGATGTAAGTTTAAATGAAGGTGATATGTTTAACTTGAATGCGCGTAAATATGGGCC 1658
QY      1201 GGGGCTTAAAGGATTAATATGCGCGTGGGCTAATCTTGGTTACATCTGACTCATGGA 1260
DB      1659 GGGGCTTAAAGGATTAATATGCGCGTGGGCTAATCTTGGTTACATCTGACTCATGGA 1718
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QY	1261	GGCTTTGGAGAGCTTTGGAAAGATTTTCTGCTGTGACGTAACCTTGTGGAAAGAGACTTTAA	1320
Db	1719	GGCTTTGGAGAGCTTTGGAAAGATTTTCTGCTGTGACGTAACCTTGTGGAAAGAGACTTTAA	1778
QY	1321	CAGTACCTCTTGATTTTGGAGGTTCTGTGGGGCTCACTCCAGGCAAAAGTTAGTCTGAG	1380
Db	1779	CAGTACCTCTTGATTTTGGAGGTTCTGTGGGGCTCACTCCAGGCAAAAGTTAGTCTGAG	1838
QY	1381	AATTAAAGAGAGATTACAAGTGGGAATTTGAAAGACTTTTGAAATCTGTGTGAGCTGTT	1440
Db	1839	AATTAAAGAGAGATTACAAGTGGGAATTTGAAAGACTTTTGAAATCTGTGTGAGCTGTT	1898
QY	1441	TGATTTCTTGGATCTGGGCTCAACAGGCGCTTTTCCAAGAGAAGGTCATCAAGACTTTGGA	1500
Db	1899	TGATTTCTTGGATCTGGGCTCAACAGGCGCTTTTCCAAGAGAAGGTCATCAAGACTTTGGA	1958
QY	1501	TTTTTCCACACCGGGGCGGCTGCGGCTGCTGTTGCTTTTGTAGTTTATTAAGATTA	1560
Db	1959	TTTTTCCACACCGGGGCGGCTGCGGCTGCTGTTGCTTTTGTAGTTTATTAAGATTA	2018
QY	1561	ATGAGAGCAAGAAACCCATCTGAGCGGGGGGTAACCTGTGGATTTCTGGCGATGACACT	1620
Db	2019	ATGAGAGCAAGAAACCCATCTGAGCGGGGGGTAACCTGTGGATTTCTGGCGATGACACT	2078
QY	1621	GTGGAGAGCGGTTGTGAGACACAAAGAAATCGCTGTACTGTGTCTTCCGTCGCGCCGCG	1680
Db	2079	GTGGAGAGCGGTTGTGAGACACAAAGAAATCGCTGTACTGTGTCTTCCGTCGCGCCGCG	2138
QY	1681	GATTAATACCGAGCGAGAGACAGACAGACAGACAGAGAGAACCCAGCGCGCGCCGACAGA	1740
Db	2139	GATTAATACCGAGCGAGAGACAGACAGACAGACAGAGAGAACCCAGCGCGCGCCGACAGA	2198
QY	1741	GCAGAGCCCATGAGAACCCGAGAGCGCGGCTGAGACCTCGGGGAATGAATGTTGTACAGTGTG	1800
Db	2199	GCAGAGCCCATGAGAACCCGAGAGCGCGGCTGAGACCTCGGGGAATGAATGTTGTACAGTGTG	2258
QY	1801	GCTGAACGTGATCCAGAACTGAGACGCAATTTTGACAAATTACAGAGATGGGCGAGGGCTTA	1860
Db	2259	GCTGAACGTGATCCAGAACTGAGACGCAATTTTGACAAATTACAGAGATGGGCGAGGGCTTA	2318
QY	1861	AAAGGGGTGAAGAGAGGAGCGGGGGGCTTGTAGAGCTACAGAGAGGGCTAGGAATCTAGCT	1920
Db	2319	AAAGGGGTGAAGAGAGGAGCGGGGGGCTTGTAGAGCTACAGAGAGGGCTAGGAATCTAGCT	2378
QY	1921	TTTACCTTAATGACACAGACACCGTCTGTAAGTGTATTACTTTTCAACAGATCAAGATTAAT	1980
Db	2379	TTTACCTTAATGACACAGACACCGTCTGTAAGTGTATTACTTTTCAACAGATCAAGATTAAT	2438
QY	1981	TGCGCTAATGAGCTTGATGCTGTGCGCGAGAAATTTCCATTAAGACAGCTGACCACTTAC	2040
Db	2439	TGCGCTAATGAGCTTGATGCTGTGCGCGAGAAATTTCCATTAAGACAGCTGACCACTTAC	2498
QY	2041	TGGCTGACAGCCAGGGGATGATTTTGAAGAGGCTATTAGAGTATATATGCAAAAGTGGCACTT	2100
Db	2499	TGGCTGACAGCCAGGGGATGATTTTGAAGAGGCTATTAGAGTATATATGCAAAAGTGGCACTT	2558
QY	2101	AGGCCAGATTGCAAGTACAAAGATCAGCAAACTGTAAATATCAGGAATGTGTGCTACATT	2160
Db	2559	AGGCCAGATTGCAAGTACAAAGATCAGCAAACTGTAAATATCAGGAATGTGTGCTACATT	2618
QY	2161	TCTGGGAAACGGGCGGAGGTGAGATTAATATACGAGAGATAGAGGTGGCCTTTAGATGATAC	2220
Db	2619	TCTGGGAAACGGGCGGAGGTGAGATTAATATACGAGAGATAGAGGTGGCCTTTAGATGATAC	2678
QY	2221	ATGATAAATATGTGCGCGGGGCTGCTTGAGCAATGACAGGGGTGTGTTATTAATGAATGTAAGG	2280
Db	2679	ATGATAAATATGTGCGCGGGGCTGCTTGAGCAATGACAGGGGTGTGTTATTAATGAATGTAAGG	2738
QY	2281	TTTATCGGCCCCCAATTTTAAGCGGTACGGTTTTCTCGGCCAATACCAACTTATCTTACAC	2340
Db	2739	TTTATCGGCCCCCAATTTTAAGCGGTACGGTTTTCTCGGCCAATACCAACTTATCTTACAC	2798

OY	2341	GGTGTAAAGCTTCTATGGGCTTTAAACAATACCTGTGTGGAACCTGGACCGATGTAAAGGTT	2400
Db	2799	GGTGTAAAGCTTCTATGGGCTTTAAACAATACCTGTGTGGAAGCTGGACCGATGTAAAGGTT	2858
OY	2401	CGGGGCTGTGCTTTTACTGCTGCTGGAAGGGGGGTGTGTGTGCGCCCAAAAGCAGGGCT	2460
Db	2859	CGGGGCTGTGCTTTTACTGCTGCTGGAAGGGGGGTGTGTGTGCGCCCAAAAGCAGGGCT	2918
OY	2461	TCAATTAAAGAAATGCGCTCTTTGAAAAGGTGATCCTTGGGTATCCTGTGTAGGGTTAATCC	2520
Db	2919	TCAATTAAAGAAATGCGCTCTTTGAAAAGGTGATCCTTGGGTATCCTGTGTAGGGTTAATCC	2978
OY	2521	AGGGTGGGCGCCAAATGTGGGCTCCGATCTGTGTGTTCTCAATGCAATGAAAAGGTGGCT	2580
Db	2979	AGGGTGGGCGCCAAATGTGGGCTCCGATCTGTGTGTTCTCAATGCAATGAAAAGGTGGCT	3038
OY	2581	GTCATTAAAGCAATAACATGATGTGTGGGAACTGCGAGGACAGGGGCTCTCAGATCTGACC	2640
Db	3039	GTCATTAAAGCAATAACATGATGTGTGGGAACTGCGAGGACAGGGGCTCTCAGATCTGACC	3098
OY	2641	TGCTCGGACGGCAACTGTCACTGTGTAAGACATTCAAGGCAAGCACTCTGCAAG	2700
Db	3099	TGCTCGGACGGCAACTGTCACTGTGTAAGACATTCAAGGCAAGCACTCTGCAAG	3158
OY	2701	GCCCTGGCCACAGTGTGTGAGCATTAATACTAGACCCGCTGTTCCTTGCAATTTGGGTAAACAG	2760
Db	3159	GCCCTGGCCACAGTGTGTGAGCATTAATACTAGACCCGCTGTTCCTTGCAATTTGGGTAAACAG	3218
OY	2761	AGGGGGGGTGTTCTTACCTTACCTTACCAATGCAATTTGAGTCAACATAAGATATTTGCTTGAGCC	2820
Db	3219	AGGGGGGGTGTTCTTACCTTACCTTACCAATGCAATTTGAGTCAACATAAGATATTTGCTTGAGCC	3278
OY	2821	GAGAGCATGTTCACAGGTGAACCTGGAACGGGGTGTTTGAATGACATGAACATGAAGATCTGAAAG	2880
Db	3279	GAGAGCATGTTCACAGGTGAACCTGGAACGGGGTGTTTGAATGACATGAACATGAAGATCTGAAAG	3338
OY	2881	GTCGTGAAGTACGATGAGACCCCGCACAGGTGTGCAGACCTTCGAGTGTGGCGGTAAACAT	2940
Db	3339	GTCGTGAAGTACGATGAGACCCCGCACAGGTGTGCAGACCTTCGAGTGTGGCGGTAAACAT	3398
OY	2941	ATTAGGAACCAAGCCCTGTGATGTGCAATGTGACGAGAGGCTGAGGCCGATCACTTGGTG	3000
Db	3399	ATTAGGAACCAAGCCCTGTGATGTGCAATGTGACGAGAGGCTGAGGCCGATCACTTGGTG	3458
OY	3001	CTGGCCTTGACACCCGCGCTGAGTGTGGCTTACGCGATGAAGATACAGATTGAG	3052
Db	3459	CTGGCCTTGACACCCGCGCTGAGTGTGGCTTACGCGATGAAGATACAGATTGAG	3510
RESULT 12			
ADRA41672			
ID	ADRA41672 standard; DNA; 35935 BP.		
AC	ADRA41672;		
DT	04-NOV-2004 (first entry)		
XX			
XX			
DE	Wild type ADS adenovirus.		
XX			
KM	Lytic agent; ds; chaperone; heat shock protein; stimulus;		
KM	tumour shrinkage; oncolysis; HSP; HSP-CRA; cancer reactive antigen;		
KM	nasopharyngeal carcinoma; chondrosarcoma; colon cancer; breast; prostate;		
KM	ovarian; stomach carcinoma; rectum; malignant hepatoma; melanoma; p53;		
KM	tumour suppressor gene; Ad5; S98-002; E1b region; E3; E1b-55KD; gene;		
XX	access.		
OS	Human adenovirus type 5.		
FH	Key		
FT	misc_feature		
FT	location/Qualifiers		
FT	2501..3328		
FT	/*tag=		
FT	/note="Partial E1b region"		
FT	misc_feature		
FT	27865..30995		

FT /tag= b
FT /note= "E3 region"
XX
XX
XX WO2004066947-A2.
XX
XX 12-AUG-2004.
XX
XX 28-JAN-2004; 2004WO-US002330.
XX
XX 28-JAN-2003; 2003US-0443095P.
XX
XX (SHAN-) SHANGHAI SUNWAY BIOTECH CO LTD.
XX
XX Hu F, Wu B;
XX
XX WPI; 2004-580848/56.
XX
XX Abilating tumor cells in a subject having at least one tumor site by
PT connecting the tumor cells in at least one tumor with a lytic agent in
PT vivo and applying a sufficient in vivo stimulus to the treated tumor
PT forming a stimulated tumor.
XX
XX Example 1; SEQ ID NO 4; 129bp; English.
XX
XX The present invention relates to the compositions and methods for
XX ablating tumor cells in a subject having one or more tumor sites. The
XX method includes introduction of a lytic agent into a tumor (which forms
XX a treated tumor) and application of stimulus to the treated tumor. The
XX stimulus (physical, chemical or biological) induces the level of
XX chaperone proteins (heat shock proteins) in the tumor cells. The
XX combination of the lytic agent and tumor cell stimulus leads to tumor
XX shrinkage. The invention relates to the synchronization between oncolysis
XX and elevated expression of a heat shock protein (HSP), which results in
XX sufficient release of HSP-CRA (cancer reactive antigen). The sufficient
XX levels of HSP-CRA exhibit a signal immunogenic enough to the immune
XX system in order to elicit an immune response against the cancer. The
XX method of the invention is useful in ablating tumor cells for treating
XX nasopharyngeal carcinoma, chondrosarcoma, colon cancer, breast cancer,
XX prostate cancer, ovarian cancer, stomach carcinoma, rectum cancer,
XX malignant hepatoma, melanoma, ascites etc. Mutations of the p53 gene
XX exist in more than half of cancer cases. The treated or non-treated
XX cancers which consist of a defective p53 tumor suppressor gene or an
XX activated oncogene are good candidates for this method of therapy. The
XX oncolytic viruses of this invention comprise genetically modified Ad5
XX variants. This oncolytic adenovirus selectively replicates in cancer
XX cells with a p53 mutation and lyses cancer cells with high specificity.
XX The genome of a wild type Ad5 is composed of 35,935 bps. Genetically
XX modified variant Ad5 (598-001) has an extra stop codon at position 2025
XX (E1b region) and possesses deletions in E1b region (in between 2,501 and
XX 3,328) and in E3 (in between 27865 and position 30,995) region. In normal
XX cells E1b-55KD binds and inactivates the protein encoded by the p53 gene
XX and initiates viral replication. The 598-001 variant is not able to
XX replicate in normal cells, but replicates rapidly in cancer cells in
XX which the p53 protein is dysfunctional. The function of E3 is related to
XX the ability of an adenovirus to escape from the surveillance of the
XX immune system. The complete deletion of the E3 region in 598-001 enables
XX the immune system easier recognition and elimination of this virus. 598
XX -002 is another genetically modified variant Ad5. It has deletions in the
XX region encoding E1b-55KD (in between 2,501 and 3,328) and of the entire
XX E3 region (in between 27865 and position 30,995). The variant sequences
XX of Ad5 are unable to integrate into the human genome, but selectively
XX replicate in cancer cells. So, 598-001 and 598-002 are safe for use in
XX humans and animals. The presented sequence is shown as SEQ ID NO 4 in the
XX adenovirus DNA. Note: This sequence is shown as SEQ ID NO 4 in the
XX sequence listing, however, this does not correspond to the description of
XX the sequence in example 1 of the specification. This sequence is referred
XX as SEQ ID NO 3 in example 1.
XX
XX Sequence 35935 BP; 8367 A; 10073 C; 9761 G; 7734 T; 0 U; 0 Other;
Query Match 100.0%; Score 3052; DB 13; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTGTAGTATTTTAAACCCGCTGAGTTCCTCAAGAGCCACTCTTGAGTGCAGCAGT 60
DB 459 CGTGTAGTATTTTAAACCCGCTGAGTTCCTCAAGAGCCACTCTTGAGTGCAGCAGT 518
QY 61 AGAGTTTTCCTCCGAGCCGCTCCGACACCGGAGCTGAAATGAGCATATTTCTGCC 120
DB 519 AGAGTTTTCCTCCGAGCCGCTCCGACACCGGAGCTGAAATGAGCATATTTCTGCC 578
QY 121 ACGAGGTGTTATTAACGAAAGAAATGAGCCGACAGTCTTTTGAACCACTGATCGAAGG 180
DB 579 ACGAGGTGTTATTAACGAAAGAAATGAGCCGACAGTCTTTTGAACCACTGATCGAAGG 638
QY 181 TACTGCTGATATCTTCAACTCTTACATTTTGAACCACTTCCCTTCAGACTGT 240
DB 639 TACTGCTGATATCTTCAACTCTTACATTTTGAACCACTTCCCTTCAGACTGT 698
QY 241 ATGATTTAGACGTGACGCCCCGAGAGATCCCAACGAGGAGCGGTTTCCAGATTTTTC 300
DB 699 ATGATTTAGACGTGACGCCCCGAGAGATCCCAACGAGGAGCGGTTTCCAGATTTTTC 758
QY 301 CCGACTCTGTAATGTTGGCGGTGACGAGAGGATTTGACTTACTCTTTCCGCGGCGC 360
DB 759 CCGACTCTGTAATGTTGGCGGTGACGAGAGGATTTGACTTACTCTTTCCGCGGCGC 818
QY 361 CCGGTTCTCCGAGCCGCTTCACTTTCCGCGAGCCCGAGACCGGAGAGAGCCT 420
DB 819 CCGGTTCTCCGAGCCGCTTCACTTTCCGCGAGCCCGAGAGAGAGAGCCT 878
QY 421 TGGGTCCGTTTCTATGCGCAACCTTTGACCGAGGATCGATCTTACCTGACCAAGG 480
DB 879 TGGGTCCGTTTCTATGCGCAACCTTTGACCGAGGATCGATCTTACCTGACCAAGG 938
QY 481 CTGGCTTTCACCAAGAGAGAGAGAGAGAGAGGTTGTTGATTAATG 540
DB 939 CTGGCTTTCACCAAGAGAGAGAGAGAGAGAGGTTGTTGATTAATG 998
QY 541 TGGAGCAACCCCGGAGCGGTTGACAGTCTTGTCTATTCACCGAGAAATGCGGGAGC 600
DB 999 TGGAGCAACCCCGGAGCGGTTGACAGTCTTGTCTATTCACCGAGAAATGCGGGAGC 1058
QY 601 CAGATTAATGTTGCTTGTGATATGAGACCTGTCAGTGTCTACAGTAAGT 660
DB 1059 CAGATTAATGTTGCTTGTGATATGAGACCTGTCAGTGTCTACAGTAAGT 1118
QY 661 GAAATATGAGGACAGTGGATATGAGTGTGGTTGTGTGTAATTTTTTTTAAAT 720
DB 1119 GAAATATGAGGACAGTGGATATGAGTGTGGTTGTGTGTAATTTTTTTTAAAT 1178
QY 721 TTTTACAGTTTGTGTTTAAAGAAATTTGTATTTTAAAGAGTCTCTGTGC 780
DB 1179 TTTTACAGTTTGTGTTTAAAGAAATTTGTATTTTAAAGAGTCTCTGTGC 1238
QY 781 TGAACCTGAGCCGTGAGCCGAGCCAGAACCGGAGCCGAAAGCTTCCGCTCTTAA 840
DB 1239 TGAACCTGAGCCGTGAGCCGAGCCAGAACCGGAGCCGAAAGCTTCCGCTCTTAA 1298
QY 841 AATGAGCCCTGATCTCTGAGAGCCCGACATCACTGTGCTTGAAGAAATGCAATAGAG 900
DB 1299 AATGAGCCCTGATCTCTGAGAGCCCGACATCACTGTGCTTGAAGAAATGCAATAGAG 1358
QY 901 TACGATAGCTGTGATCTCGGCTCTTAAACACCTCTGAGATACACCGGCTGCTCC 960
DB 1359 TACGATAGCTGTGATCTCGGCTCTTAAACACCTCTGAGATACACCGGCTGCTCC 1418
QY 961 GCTGTGCCCATTAACACAGTGGCGGAGAGTTGTGGGCGTCCGAGGCTGGAGATG 1020
DB 1419 GCTGTGCCCATTAACACAGTGGCGGAGAGTTGTGGGCGTCCGAGGCTGGAGATG 1478
QY 1021 TATCGAGAGCTTGTATTAACAGAGCTGGGCAACTTTTGAAGCTGTAAACGCCCCAG 1080
DB 1479 TATCGAGAGCTTGTGTAAACAGAGCTGGGCAACTTTTGAAGCTGTAAACGCCCCAG 1538

QY	1081	GCCTAAGGCTTAACCTGCTGATTCGCTGTGTGCTTAACGCTTTGTTGCTGAATGACT	1140
Db	1539	GCCATAAGGGGTAAACCTGATATGGCGTGTGTGCTTAACGCTTTGTTGCTGAATAGT	1598
QY	1141	TGATGTAAAGTTTAAAGGGGTGAGATAATGTTTAACTTGATGAGCGGTAAATGGGAGC	1200
Db	1599	TGATGTAAAGTTTAAAGGGGTGAGATAATGTTTAACTTGATGATGAGCGGTAAATGGGAGC	1658
QY	1201	GGGGCTTAAAGGATATATATATGCGCGGTGGCTAATCTTGTTACATCTGACTCATGGA	1260
Db	1659	GGGGCTTAAAGGATATATATATGCGCGCGGTGGCTAATCTTGTTACATCTGACTCATGGA	1718
QY	1261	GGCTTTGGGAGCTTTTGGAAAGATTTTTCTGCTGTGTGCTTAACCTTGTTGGAACAGAGCTCTAA	1320
Db	1719	GGCTTTGGGAGCTTTTGGAAAGATTTTTCTGCTGTGTGCTTAACCTTGTTGGAACAGAGCTCTAA	1778
QY	1321	CAGTAACTCTTGTTTGGAGGTTTCTGTGGGGCTCAATCCAGGCAAAAGTAAGTCTGAG	1380
Db	1779	CAGTAACTCTTGTTTGGAGGTTTCTGTGGGGCTCAATCCAGGCAAAAGTAAGTCTGAG	1838
QY	1381	AATTAAAGAGGATTTACAAGTGGAAATTTGAAAGACTTTTGAATCTGTGTGAGCTGTT	1440
Db	1839	AATTAAAGAGGATTTACAAGTGGAAATTTGAAAGACTTTTGAATCTGTGTGAGCTGTT	1898
QY	1441	TGATTTCTTTGAATCTGGGTCAACAGCGGCTTTTCCAGAGAAAGTCAATCAAGACTTTTGA	1500
Db	1899	TGATTTCTTTGAATCTGGGTCAACAGCGGCTTTTCCAGAGAAAGTCAATCAAGACTTTTGA	1958
QY	1501	TTTTTCCACACCGGGGGCGCGCTGGGGGCTGTGCTTTTGAAGTTTAAAGAGATAA	1560
Db	1959	TTTTTCCACACCGGGGGCGCGCTGGGGGCTGTGCTTTTGAAGTTTAAAGAGATAA	2018
QY	1561	ATGAGAGGAAGAAACCCATCTGAGCGGGGGGTACTGTGTGATTTTCTGGCCATGACT	1620
Db	2019	ATGAGAGGAAGAAACCCATCTGAGCGGGGGGTACTGTGTGATTTTCTGGCCATGACT	2078
QY	1621	GTGAGAGACGGTTGTGAGACACAGAATTCGCTGTCTACTGTTGTCTTCGTCGCGCCGGC	1680
Db	2079	GTGAGAGACGGTTGTGAGACACAGAATTCGCTGTCTACTGTTGTCTTCGTCGCGCCGGC	2138
QY	1681	GATTAATCCGACGAGAGGAGCAGACAGCAGCAGAGAGAACCCAGCGCGCGCAGAGA	1740
Db	2139	GATTAATCCGACGAGAGGAGCAGACAGCAGCAGAGAGAACCCAGCGCGCGCAGAGA	2198
QY	1741	GCAGAGCCCATGGAACCCGAGAGCCGCGCTTGAACCTTCGGAAATGAATGTTTGAACAAGTGTG	1800
Db	2199	GCAGAGCCCATGGAACCCGAGAGCCGCGCTTGAACCTTCGGAAATGAATGTTTGAACAAGTGTG	2258
QY	1801	GCTGAACCTGTATCCAGAACTGAGACCGCATTTTGAACATTTACAGAGATGGCGAGGGCTTA	1860
Db	2259	GCTGAACCTGTATCCAGAACTGAGACCGCATTTTGAACATTTACAGAGATGGCGAGGGCTTA	2318
QY	1861	AAGGGGGGTAAAGAGGGAGCGGGGGGCTTGTAGGCTACAGAGAGGCTAGGAATCTAGCT	1920
Db	2319	AAGGGGGGTAAAGAGGGAGCGGGGGGCTTGTAGGCTACAGAGAGGCTAGGAATCTAGCT	2378
QY	1921	TTTATGCTTAATAGACAGACACCGTCTGTAAGTATTACTTTTCAACAGATCAAGATTAAT	1980
Db	2379	TTTATGCTTAATAGACAGACACCGTCTGTAAGTATTACTTTTCAACAGATCAAGATTAAT	2438
QY	1981	TGCGCTAATGAGCTTTGATCTGCTGGCGCAAGATTTTCATAGACAGCTGACCACTTAC	2040
Db	2439	TGCGCTAATGAGCTTTGATCTGCTGGCGCAAGATTTTCATAGACAGCTGACCACTTAC	2498
QY	2041	TGCGTGCAACGAGGGAGATTTTGGAGAGGCTATTAGGGATATATGCAAAAGTGGCACTT	2100
Db	2499	TGCGTGCAACGAGGGAGATTTTGGAGAGGCTATTAGGGATATATGCAAAAGTGGCACTT	2558
QY	2101	AGGCGAAGTTTCAAGTACAAATATCAGCAAACTTGTATTAATCAGAGAAATGTTGCTACATT	2160
Db	2559	AGGCGAAGTTTCAAGTACAAATATCAGCAAACTTGTATTAATCAGAGAAATGTTGCTACATT	2618
QY	2161	TCTGGGAACGGGGCCGAGGTGAGATATACGAGAGATTAAGGTGGCTTTTGAATGTAGC	2220

Db	2619	TCGCGGAACGGGGCCGAGGTGAGATGAGATCGAGGATGAGGCTTTAGATGAC	2678
Qy	2221	ATGATTAATATATGTGGCCGGGGGTGCTTGGCATGAGACGGGGTGTATTATGATGATGAAG	2280
Db	2679	ATGATTAATATATGTGGCCGGGGGTGCTTGGCATGAGACGGGGTGTATTATGATGATGAAG	2738
Qy	2281	TTTAATCGGCCCAATTTTAAGCGGTACGGTTTCTCGGCCAATACCACCTTATCTTACAC	2344
Db	2739	TTTAATCGGCCCAATTTTAAGCGGTACGGTTTCTCGGCCAATACCACCTTATCTTACAC	2798
Qy	2341	GGTGTAAAGCTTCATGAGGTTTAAACAATACCTGTGTGGAAGCTGTGACCGATGTAAAGGTT	2400
Db	2799	GGTGTAAAGCTTCATGAGGTTTAAACAATACCTGTGTGGAAGCTGTGACCGATGTAAAGGTT	2858
Qy	2401	CGGGGCTGTGCTTTTACTGTGTGTGGAAGGGGGTGTGTGTGCGCCCAAAAGCAGGGCT	2460
Db	2859	CGGGGCTGTGCTTTTACTGTGTGTGGAAGGGGGTGTGTGTGCGCCCAAAAGCAGGGCT	2918
Qy	2461	TCAATTAAAGAAATCCCTCTTGAAGAGGTGACCTTGGGTATCTGTGTGAGGGTAACTCC	2520
Db	2919	TCAATTAAAGAAATCCCTCTTGAAGAGGTGACCTTGGGTATCTGTGTGAGGGTAACTCC	2978
Qy	2521	AGGGTGGGCCCAATGTGGGCTCCGACCTGTGGTTCCTCATGCTAAGTAAAGCGTGGCT	2580
Db	2979	AGGGTGGGCCCAATGTGGGCTCCGACCTGTGGTTCCTCATGCTAAGTAAAGCGTGGCT	3038
Qy	2581	GTGATTAAGCATTAACATGTATGTGTGGCACTGCGAGGACAGGGCTCTCAGATGCTGAC	2640
Db	3039	GTGATTAAGCATTAACATGTATGTGTGGCACTGCGAGGACAGGGCTCTCAGATGCTGAC	3098
Qy	2641	TGCTCGGACGGCAACTGTCACTGTGTAAGACCAATTCACTGAACCAAGCACTCTTGGCAAG	2700
Db	3099	TGCTCGGACGGCAACTGTCACTGTGTAAGACCAATTCACTGAACCAAGCACTCTTGGCAAG	3158
Qy	2701	GCCGTGGCAGTGTTTGAAGCATTAATATCTGACCCGCTGTTCCTTGATTTGGGTAAACAAG	2760
Db	3159	GCCGTGGCAGTGTTTGAAGCATTAATATCTGACCCGCTGTTCCTTGATTTGGGTAAACAAG	3218
Qy	2761	AGGGGGGTGTCTTACCTTACCAATTCGAAATTGAGTCACTAAGATATTGCTTGAGGCC	2820
Db	3219	AGGGGGGTGTCTTACCTTACCAATTCGAAATTGAGTCACTAAGATATTGCTTGAGGCC	3278
Qy	2821	GAGAGCATGTTCGAAGGTGAACCTGAAACGGGGTGTTTGATGACCATGAAGATCTGGAAG	2880
Db	3279	GAGAGCATGTTCGAAGGTGAACCTGAAACGGGGTGTTTGATGACCATGAAGATCTGGAAG	3338
Qy	2881	GTGCTGAGGTACGATGAGACCCCGGACAGAGGTGACACCCTGCGAGTGGGGGTAAACAT	2940
Db	3339	GTGCTGAGGTACGATGAGACCCCGGACAGAGGTGACACCCTGCGAGTGGGGGTAAACAT	3398
Qy	2941	ATTAGGAACACAGCCTGTGATCTGTGATGTGACCGAGAGACTGAGGCCCGCATCACTTGGTG	3000
Db	3399	ATTAGGAACACAGCCTGTGATCTGTGATGTGACCGAGAGACTGAGGCCCGCATCACTTGGTG	3458
Qy	3001	CTGGCCTTGACACCGCCGCTGAGTTGGCTCTTACGATGAAGATACAGATTGAG 3052	
Db	3459	CTGGCCTTGACACCGCCGCTGAGTTGGCTCTTACGATGAAGATACAGATTGAG 3510	
RESULT 13			
ID	AAD27971	standard; DNA; 35978 BP.	
XX	AAD27971;		
XX	AC		
XX	16-JUN-2002	(first entry)	
DT	XX		
XX	XX		
DE	Recombinant adenovirus vector G23-TERT.		
XX	Recombinant adenovirus vector; adenovirus death protein; ADP; telomerase;		
KM	human; telomerase reverse transcriptase promoter; TERT; neoplastic cell;		
KM	cancer; G23-TERT; E3 region; mutant; ds.		

QY 1441 TGATCTTTGAATCGGGTCACAGGGGCTTTTCCAAAGAGAAGGCATCAAGACTTTTGA 1500
DB 1899 TGATCTTTGAATCTGGGTCCACAGGCGCTTTTCCAAAGAAAGTCATCAAGACTTTGGA 1958
QY 1501 TTTTTCACACCGGGGCGCGCTGCGGCTGCTGTTGCTTTTGAAGTTTATTAAGATTA 1560
DB 1959 TTTTTCACACCGGGGCGCGCTGCGGCTGCTGTTGCTTTTGAAGTTTATTAAGATTA 2018
QY 1561 ATGAGAGCAAAACCCATCTGAAGCGGGGGATCCTGCTGGAATTTTTCGCGCATGCACT 1620
DB 2019 ATGAGAGCAAAACCCATCTGAAGCGGGGGATCCTGCTGGAATTTTTCGCGCATGCACT 2078
QY 1621 GTGAGAGCGGTTGTGAGACAAAGAAATCGCTGCTGCTGTTGCTTCCGTCGCGCGGC 1680
DB 2079 GTGAGAGCGGTTGTGAGACAAAGAAATCGCTGCTGCTGTTGCTTCCGTCGCGCGGC 2138
QY 1681 GATAATACCGACGAGAGAGCAGCAGCAGCAGAGAGAGAGCCAGCGCGCGCAGAGA 1740
DB 2139 GATAATACCGACGAGAGAGCAGCAGCAGCAGAGAGAGAGAGCCAGCGCGCGCAGAGA 2198
QY 1741 GCAGAGCCCATGGAACCCGAGAGCGCGGCTGGAACCTCGGGAATGAATGTTGTACAGGTG 1800
DB 2199 GCAGAGCCCATGGAACCCGAGAGCGCGGCTGGAACCTCGGGAATGAATGTTGTACAGGTG 2258
QY 1801 GCTGAACCTGTATCCAGAACTGAGACGCAATTTTGAACAATTAAGAGATGGCAGGGGCTA 1860
DB 2259 GCTGAACCTGTATCCAGAACTGAGACGCAATTTTGAACAATTAAGAGATGGCAGGGGCTA 2318
QY 1861 AAGGGGGTAAAGAGGAGCGGGGGGCTTTGTAGGCTACAGAGAGGCTAGAGAACTTACCT 1920
DB 2319 AAGGGGGTAAAGAGGAGCGGGGGGCTTTGTAGGCTACAGAGAGGCTAGAGAACTTACCT 2378
QY 1921 TTTAGCTTAAAGACACAGACACGCTCTGAGTGTATTAATTTTCAACAGATCAAGATTAAT 1980
DB 2379 TTTAGCTTAAAGACACAGACACGCTCTGAGTGTATTAATTTTCAACAGATCAAGATTAAT 2438
QY 1981 TGCCTAATGAGCTTGATCTGCTGGCGCAGAGATATTCATAGAGAGCTGACCACTTAC 2040
DB 2439 TGCCTAATGAGCTTGATCTGCTGGCGCAGAGATATTCATAGAGAGCTGACCACTTAC 2498
QY 2041 TGGCTGCACGACGAGGAGATGATTTTGAAGAGGCTATTAAGGTATATGCAAGGTGGCACTT 2100
DB 2499 TGGCTGCACGACGAGGAGATGATTTTGAAGAGGCTATTAAGGTATATGCAAGGTGGCACTT 2558
QY 2101 AGGCGCAATTCAGATCAAAATCAGCAAACTTGAAATATCAGAGAAATTTGCTACACTT 2160
DB 2559 AGGCGCAATTCAGATCAAAATCAGCAAACTTGAAATATCAGAGAAATTTGCTACACTT 2618
QY 2161 TCTGGGAAACGGGGCGGAGGTGAGATAGATACGAGAGATAGGGTGGCTTTAGATGTAGC 2220
DB 2619 TCTGGGAAACGGGGCGGAGGTGAGATAGATACGAGAGATAGGGTGGCTTTAGATGTAGC 2678
QY 2221 ATGATAAATATGTGGCCGGGGGTGCTTGGCATGACGGGGGTGTTATATGATGTAAAG 2280
DB 2679 ATGATAAATATGTGGCCGGGGGTGCTTGGCATGACGGGGGTGTTATATGATGTAAAG 2738
QY 2281 TTTTCTGGCCCCAATTTTGAAGGCTTTCCTGGGCAATTAACCAACCTTATCCTTAC 2340
DB 2739 TTTTCTGGCCCCAATTTTGAAGGCTTTCCTGGGCAATTAACCAACCTTATCCTTAC 2798
QY 2341 GGTGTAAAGCTTCTATAGGTTTAAACAATACCTGTGTGAAGCCTGGACCGATGAAGGTT 2400
DB 2799 GGTGTAAAGCTTCTATAGGTTTAAACAATACCTGTGTGAAGCCTGGACCGATGAAGGTT 2858
QY 2401 CGGGGCTGTGCTTTTACTGCTGTGAAGGGGGGTGTGTGTGCGCCCAAAAAGCAGGCT 2460
DB 2859 CGGGGCTGTGCTTTTACTGCTGTGAAGGGGGGTGTGTGTGCGCCCAAAAAGCAGGCT 2918
QY 2461 TCAATTAAGAAATGCTCTTTGAAGAGGTACCTTGGGTATCCTGCTCAGAGGTAACTCC 2520
DB 2919 TCAATTAAGAAATGCTCTTTGAAGAGGTACCTTGGGTATCCTGCTCAGAGGTAACTCC 2978
QY 2521 AGGGTGCACCAATGTGGCTCCGACTGTGGTGTCTTCACTGTAGTGAAGAGGTGGCT 2580

DB 2979 AGGGTGCACCAATGTGGCTCCGACTGTGTGCTTCACTGTAGTGAAGAGGTGGCT 3038
QY 2581 GTGATTAAGCATTAACATGTATGTGCAACTCGAGAGACAGGGCTTTCAGATGCTGACC 2640
DB 3039 GTGATTAAGCATTAACATGTATGTGCAACTCGAGAGACAGGGCTTTCAGATGCTGACC 3098
QY 2641 TGGCTGGAGCGGCAACCTGTGCACTGCTGTAAGACCAATTGACGTAGGACGCACTCGGCAAG 2700
DB 3099 TGGCTGGAGCGGCAACCTGTGCACTGCTGTAAGACCAATTGACGTAGGACGCACTCGGCAAG 3158
QY 2701 GCTTGGCCAGTGTGTTGAGCATTAACATTACTGACCCGCTGTTCTTGAATTTGGGTTAACAG 2760
DB 3159 GCTTGGCCAGTGTGTTGAGCATTAACATTACTGACCCGCTGTTCTTGAATTTGGGTTAACAG 3218
QY 2761 AGGGGGGTGTTCTTCACTTTCATTAATGATGATACCTAAGATTAATGCTTTGAGCCCC 2820
DB 3219 AGGGGGGTGTTCTTCACTTTCATTAATGATGATACCTAAGATTAATGATGCTTTGAGCCCC 3278
QY 2821 GAGAGCATGTCCAAGGTGAACCTGAACGGGGGTGTTTGAAGTGAACCATGAAGATCTGGAAG 2880
DB 3279 GAGAGCATGTCCAAGGTGAACCTGAACGGGGGTGTTTGAAGTGAACCATGAAGATCTGGAAG 3338
QY 2881 GTGCTGAGTACAGATGAGACCCGACCAAGGTGACAGACCTTGCGAGTGTGGCGGTAAACAT 2940
DB 3339 GTGCTGAGTACAGATGAGACCCGACCAAGGTGACAGACCTTGCGAGTGTGGCGGTAAACAT 3398
QY 2941 ATTAAGAACCAAGCTGTGATGCTGATGTGATGACCGAGAGAGCTGAGGCCCGATCACTTGGTG 3000
DB 3399 ATTAAGAACCAAGCTGTGATGCTGATGTGATGACCGAGAGAGCTGAGGCCCGATCACTTGGTG 3458
QY 3001 CTGGCTGACACCGCGCTGAGTGTGGCTTACGAGTGAAGTACAGATTGAG 3052
DB 3459 CTGGCTGACACCGCGCTGAGTGTGGCTTACGAGTGAAGTACAGATTGAG 3510

RESULT 14
AAH20746
ID AAH20746 standard; DNA: 7090 BP.
XX
AC AAH20746;
XX
DT 13-AUG-2001 (first entry)
XX
DE Plasmid STK146 DNA fragment.
XX
KW Gene therapy; amniocyte; cytostatic; Ad5; E1A region; E1B region;
XX modified tropism; tumor; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200136615-A2.
XX
PD 25-MAY-2001.
XX
PF 07-NOV-2000; 2000WO-EP010992.
XX
PR 18-NOV-1999; 99DE-0105558.
XX
PA (KOCH/) KOCHANNEK S.
XX
PI KoehaneK S, Schiedner G;
XX
DR WPI: 2001-343817/36.
XX
PT New permanent amniocyte cell lines, useful for producing viral gene
PT therapy vectors or mutant adenoviruses, express the adenoviral E1A and
PT E1B gene products.
XX
PS Example 1; Page 67-72; 72pp; German.
XX
CC This invention describes novel permanent amniocyte cell lines (A), the
CC containing at least one nucleic acid (I) that causes expression of the

CC gene products (II) of the adenoviral E1A and E1B regions. (A) are used to
CC produce gene therapy vectors, especially adeno, adeno-associated, retro
CC or lentiviral vectors, particularly first- or second generation, large-
CC capacity or deleted adenoviral vectors. (A) are also used to produce
CC adenoviral mutants, optionally with modified tropism. The vectors may
CC express a wide range of therapeutic proteins or antisense RNAs.
CC Adenoviral mutants, unable to express the E1B 55 kDa protein, are useful
CC for treating tumors, they replicate in the cells but not significantly in
CC normal primary cells. (A) can be made efficiently, simply and
CC reproducibly. The products of the invention have cytosolic activity.
CC This sequence represents a PCR primer used in the amplification of
CC Adenovirus A45 DNA which is described in the method of the invention
XX

Sequence 7090 BP, 1696 A, 1685 C, 1882 G, 1827 T, 0 U, 0 Other:

Query Match 98.5%; Score 3006.8; DB 5; Length 7090;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3008; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 43 TCTTGATGCGCAGGAGTGAAGTTTCTCTCCGAGCCGCTCCGACACCGGAGCTGAAA 102
D 2749 TATGAGAGCCAGGAGTGAAGTTTCTCTCCGAGCCGCTCCGACACCGGAGCTGAAA 2808
D 103 TGAACATATTATCTGCGCAGGAGTGTATTATCCGAAAGAAATGGCGCCAGCTTTGG 162
D 2809 TGAACATATTATCTGCGCAGGAGTGTATTATCCGAAAGAAATGGCGCCAGCTTTGG 2868
QY 163 ACAGCTGATGAAGAGGTACTGCTGATTAATCTTCCACCTCTAGCCATTTTGAACAC 222
D 2869 ACAGCTGATGAAGAGGTACTGCTGATTAATCTTCCACCTCTAGCCATTTTGAACAC 2928
QY 223 CTACCTTCACGAACTGTATATTTAGAGTGAAGCGGCCCGGAAAGATCCCAACAGAGG 282
D 2929 CTACCTTCACGAACTGTATATTTAGAGTGAAGCGGCCCGGAAAGATCCCAACAGAGG 2988
QY 283 CGGTTTGCAGATTTTCCGACCTGTATATTTGGCGGTGACAGAAAGGATTAAGTTAC 342
D 2989 CGGTTTGCAGATTTTCCGACCTGTATATTTGGCGGTGACAGAAATGAATTAAGTTAC 3048
QY 343 TCACCTTTCCGCGCGCGCCGGTCTCCGAGCCGCTCACTTTCCGCGAGCCGAGC 402
D 3049 TCACCTTTCCGCGCGCGCCGGTCTCCGAGCCGCTCACTTTCCGCGAGCCGAGC 3168
QY 403 AGCCGAGACAGAGGCTTGGGTCCGGTTCTATGCGCAAACTTTGATCCGAGGTGATCG 462
D 3109 AGCCGAGACAGAGGCTTGGGTCCGGTTCTATGCGCAAACTTTGATCCGAGGTGATCG 3168
QY 463 ATCTTACCTGCGCAGGAGCTGGCTTTCCACCAGTGAACGAGAGATGAAGAGGTGAG 522
D 3169 ATCTTACCTGCGCAGGAGCTGGCTTTCCACCAGTGAACGAGAGATGAAGAGGTGAG 3228
QY 523 AGTTTGTGTAGATTATGTGAGACACCCCGGCAAGTTTGAGGTCTTGTGATTAAC 582
D 3229 AGTTTGTGTAGATTATGTGAGACACCCCGGCAAGTTTGAGGTCTTGTGATTAAC 3288
QY 583 GAGAGATACGGGGGAGCCAGATATTAATGTGTGCTTGTGCTATATAGAGACTGTGCA 642
D 3289 GAGAGATACGGGGGAGCCAGATATTAATGTGTGCTTGTGCTATATAGAGACTGTGCA 3348
QY 643 TGTGTGTACAGTGAAGTGAAGTGAAGGAGGTGATGAGTGGTGGTGGTGGT 702
D 3349 TGTGTGTACAGTGAAGTGAAGTGAAGGAGGTGATGAGTGGTGGTGGTGGTGGT 3408
QY 703 GGTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 762
D 3409 GGTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 3468
QY 763 TTTTAAAGTCTCTGTCTGAACCTGAGCTGAGCCGAGCCAGAACCCGAGCTGCAAG 822
D 3469 TTTTAAAGTCTCTGTCTGAACCTGAGCCGAGCCAGAACCCGAGCTGCAAG 3528
QY 823 ACCTACCGCGCTCTAAATATGGCGCTGTACTGTAGAGCGCCGACATACCTGTGTC 882
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D 3529 ACCTACCGCGCTCTAAATATGGCGCTGTACTGTAGAGCGCCGACATACCTGTGTC 3588
QY 883 TAGAAGATGCAATAGTAGTACGATAGCTGATCTCCGCTCTTCTTAACACACCTCTGA 942
D 3589 TAGAAGATGCAATAGTAGTACGATAGCTGATCTCCGCTCTTCTTAACACACCTCTGA 3648
QY 943 GATACACCCGGTGTCCCGCTGTGCCCCCATTAACCAAGTTCGGTGAAGTTGGTGGCG 1002
D 3649 GATACACCCGGTGTCCCGCTGTGCCCCCATTAACCAAGTTCGGTGAAGTTGGTGGCG 3708
QY 1003 TCGCAGCTGTGAAGTATGAGAGCTTGCTTAAGAGCTGGGAACTTTTGAATT 1062
D 3709 TCGCAGCTGTGAAGTATGAGAGCTTGCTTAAGAGCTGGGAACTTTTGAATT 3768
QY 1063 GAGCTGTAAACGCCCAAGCCATTAAGGTGAACCTGTGATTTGCTGTGTGAAGCC 1122
D 3769 GAGCTGTAAACGCCCAAGCCATTAAGGTGAACCTGTGATTTGCTGTGTGAAGCC 3828
QY 1123 TTTGTTGCTGAATGAGTTGATGATTAATTAAGGCTGAATATGTTAACTTGCA 1182
D 3829 TTTGTTGCTGAATGAGTTGATGATTAATTAAGGCTGAATATGTTAACTTGCA 3888
QY 1183 TGGCGTGTAAATGGGGCGGGGCTTAAGGGTATATATGCGCGGTGAATCTTGGT 1242
D 3889 TGGCGTGTAAATGGGGCGGGGCTTAAGGGTATATATGCGCGGTGAATCTTGGT 3948
QY 1243 TACATCTGACCTCAATGAGGCTTGGAGTGTGGAAGATTTTCTGCTGTGCTAACTT 1302
D 3949 TACATCTGACCTCAATGAGGCTTGGAGTGTGGAAGATTTTCTGCTGTGCTAACTT 4008
QY 1303 GCTGGAACAGAGCTTACAGATCTTGGTTTGAAGTTTCTGAGGCTTATCCCA 1362
D 4009 GCTGGAACAGAGCTTACAGATCTTGGTTTGAAGTTTCTGAGGCTTATCCCA 4068
QY 1363 GGCAAGTTAGTCTGCAAGTATTAAGAGATTAACAGTGGAAATTTGAAGCTTTTGA 1422
D 4069 GGCAAGTTAGTCTGCAAGTATTAAGAGATTAACAGTGGAAATTTGAAGCTTTTGA 4128
QY 1423 ATCTGTGTGAGTGTGTTGATTTCTTGAATCTGAGTCAACAGGCTTTTCAAGAA 1482
D 4129 ATCTGTGTGAGTGTGTTGATTTCTTGAATCTGAGTCAACAGGCTTTTCAAGAA 4188
QY 1483 GGTCAATCAAGCTTTGATTTTCCACACCGGGCGGCTGCTGTGCTTTT 1542
D 4189 GGTCAATCAAGCTTTGATTTTCCACACCGGGCGGCTGCTGTGCTTTT 4248
QY 1543 GAGTTTATTAAGATTAATGAGACGAAGAAACCATCTGAGCGGGGGTACCTGTGA 1602
D 4249 GAGTTTATTAAGATTAATGAGACGAAGAAACCATCTGAGCGGGGGTACCTGTGA 4308
QY 1603 TTTTCTGGCATGATCTGTGAGAGCGGTTGTGAGACACAAGATGCTGTACTGTT 1662
D 4309 TTTTCTGGCATGATCTGTGAGAGCGGTTGTGAGACACAAGATGCTGTACTGTT 4368
QY 1663 GTCTTCCGTCCGCGCCGCAATATCCGACGAGAGCAGACAGACAGACAGAGAGAGC 1722
D 4369 GTCTTCCGTCCGCGCCGCAATATCCGACGAGAGCAGACAGACAGACAGAGAGAGC 4428
QY 1723 CAGCGCGCGCGGAGAGAGAGCCCATGAACCCGAGACCGGCTGTGACCTCGGGA 1782
D 4429 CAGCGCGCGCGGAGAGAGAGCCCATGAACCCGAGACCGGCTGTGACCTCGGGA 4488
QY 1783 ATGAATGTTGAACGTTGCTGAATCTGATCCAGAACTGAGACGCAATTTTGA 1842
D 4489 ATGAATGTTGAACGTTGCTGAATCTGATCCAGAACTGAGACGCAATTTTGA 4548
QY 1843 GAGGATGGGAGGGGCTTAAGGGGCTTAAGGGGCTTAAGGGGCTTAAGGGCTTA 1902
D 4549 GAGGATGGGAGGGGCTTAAGGGGCTTAAGGGGCTTAAGGGGCTTAAGGGCTTA 4608
QY 1903 GAGGCTAGAAATCTAGCTTTTGAATGACCAAGACAGCTGTGATTAATTA 1962
D 4609 GAGGCTAGAAATCTAGCTTTTGAATGACCAAGACAGCTGTGATTAATTA 4668
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Oy 1963 CAAGAGATCAAGGATTAATTGGGCTTAATGAGCTTGA TCTGCTGGGCGAGAGATTTCATA 2022
Db 4669 CAACGATCAAGGATTAATTGGGCTTAATGAGCTTGA TCTGCTGGGCGAGAGATTTCATA 4728
Oy 2023 GAGCAGCTGACCACTTA CTGGCTGAGCCAGGGAGTGA TTTTGAAGAGGCTATTAGGCTA 2082
Db 4729 GAGCAGCTGACCACTTA CTGGCTGAGCCAGGGAGTGA TTTTGAAGAGGCTATTAGGCTA 4788
Oy 2083 TATGCAAGGTGGGCACTTAAGCCAGATTGCAAGTCA AAGATCAGCAAACTTGTAATATTC 2142
Db 4789 TATGCAAGGTGGGCACTTAAGCCAGATTGCAAGTCA AAGATCAGCAAACTTGTAATATTC 4848
Oy 2243 AGGATTGTGCTCATTTCTGGGAGCGGGCCGAGGTGA GATTAGATAGACGAGGATAGG 2202
Db 4849 AGGATTGTGCTCATTTCTGGGAGCGGGCCGAGGTGA GATTAGATAGACGAGGATAGG 4908
Oy 2203 GTGGCCTTTAGATGATGATGATTAATAATATGTGG CCGGGGTGCTTGGCATGGA CCGGGGTG 2262
Db 4909 GTGGCCTTTAGATGATGATGATTAATAATATGTGG CCGGGGTGCTTGGCATGGA CCGGGGTG 4968
Oy 2263 GTTATTATGAATGTAAGGTTTACTGCGCCCAATTTT ACGGGTACGGTTTCTCTGGCCAAAT 2322
Db 4969 GTTATTATGAATGTAAGGTTTACTGCGCCCAATTTT ACGGGTACGGTTTCTCTGGCCAAAT 5028
Oy 2323 ACCAACCCTTATCTTACACAGGTGTAAGCTTCTATGG GGTTTAA CAATACCTGTGTGGAAGCC 2382
Db 5029 ACCAACCCTTATCTTACACAGGTGTAAGCTTCTATGG GGTTTAA CAATACCTGTGTGGAAGCC 5088
Oy 2383 TGAACCGATGTAAGGGTTCGGGGCTGTGCTCTTTTA CTGCTGCTGGAGGGGGTGTGTGT 2442
Db 5089 TGAACCGATGTAAGGGTTCGGGGCTGTGCTCTTTTA CTGCTGCTGGAGGGGGTGTGTGT 5148
Oy 2443 CGCCCCCAAAACAGAGGGCTTCAATTAAGAAATGCCC TTTGAAAAGGTGTA CTTTGGGATTC 2502
Db 5149 CGCCCCCAAAACAGAGGGCTTCAATTAAGAAATGCCC TTTGAAAAGGTGTA CTTTGGGATTC 5208
Oy 2503 CTGCTGAGGGTAACTCCAGGGTGGCCACAATGTGGCC TCGACTGTGTTGCTTCATG 2562
Db 5209 CTGCTGAGGGTAACTCCAGGGTGGCCACAATGTGGCC TCGACTGTGTTGCTTCATG 5268
Oy 2563 CTAGTAAAGCGTGGCTGTGATTAAGCATTAACATGTG TATGTGGCAACTGGCAGACAGG 2622
Db 5269 CTAGTAAAGCGTGGCTGTGATTAAGCATTAACATGTG TATGTGGCAACTGGCAGACAGG 5328
Oy 2623 GCCTCTCAGATGCTGACCTGTGCTCGGACGGCAACTG TCACTGCTGGAAGACCAATTCACGTA 2682
Db 5329 GCCTCTCAGATGCTGACCTGTGCTCGGACGGCAACTG TCACTGCTGGAAGACCAATTCACGTA 5388
Oy 2683 GCCAGCCACTCTCGCAAGGCTGGCCAGTGTGTTGAGCA TTAACATPACTGACCCGCTGTTC 2742
Db 5389 GCCAGCCACTCTCGCAAGGCTGGCCAGTGTGTTGAGCA TTAACATPACTGACCCGCTGTTC 5448
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Db 5449 TTGCAATTTGGGTAAACAGAGGGGGGTGTTCTTA CTTAACCAATGCAATTTGAGTCAACT 5508
Oy 2803 AAGATATTGCTTGAAGCCGAGAGATGTCACCAAGTGAA CTTGAAACGGGGTATTGACATG 2862
Db 5509 AAGATATTGCTTGAAGCCGAGAGATGTCACCAAGTGAA CTTGAAACGGGGTATTGACATG 5568
Oy 2863 ACCATGAAGATCTGGAAAGTCTGAGTACGATGAGAGAC CCGCACCAGAGTGGACACCTGCG 2922
Db 5569 ACCATGAAGATCTGGAAAGTCTGAGTACGATGAGAGAC CCGCACCAGAGTGGACACCTGCG 5628
Oy 2923 GAGTGTGGCGGTAAACATATTAGGAACCAAGCCTGTG ATGCTGAGATGTAACGAGAGAGCTG 2982
Db 5629 GAGTGTGGCGGTAAACATATTAGGAACCAAGCCTGTG ATGCTGAGATGTAACGAGAGAGCTG 5688
Oy 2983 AGGCCCGGATCACTTGGTGTCTGGCCGTCGACCCGCG TGAAGTTGGCTTAAGGATGAANAAT 3042
Db 5689 AGGCCCGGATCACTTGGTGTCTGGCCGTCGACCCGCG TGAAGTTGGCTTAAGGATGAANAAT 5748

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Oy 3043 ACAGATTGAG 3052
Db 5749 ACAGATTGAG 5758

RESULT 15
ACCT0006
ID ACC70006 standard; cDNA; 3408 BP.
XX
AC ACC70006;
XX
DT 29-JUL-2003 (first entry)
XX
DE Nucleotide sequence of the E1a protein of human adenovirus type 5.
XX
KW Cancer; hyperproliferative disorder; viral vector; H19 promoter;
KW carcinoma; sarcoma; adenoma; ganglioblastoma; bladder carcinoma; E1a;
KW gene; ss.
XX
OS Human adenovirus type 5.
XX
Key Location/Qualifiers
FT CDS 44..1029
FT /*tag= a
FT /product= "E1a protein"
FT /note= "contains an intron"
FT exon 44..598
FT /*tag= b
FT /number= 1
FT intron 599..714
FT /*tag= c
FT /number= 1
FT exon 715..1026
FT /*tag= d
FT /number= 2
PN MO2003035883-A2.
XX
PD 01-MAY-2003.
XX
PF 22-OCT-2002; 2002MO-IL000843.
XX
PR 22-OCT-2001; 2001US-00012131.
XX
PA (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
XX
PI Hochberg A, Ayesah S;
XX
DR WP1; 2003-441263/41.
XX
DR P-PSDB; ABR55301.
XX
PT Treating cancer or hyperproliferative disorder comprises administering a
PT conditionally replicative viral vector, where the viral nucleic acid
PT encoding a product essential for its replication is operably linked to
PT H19 regulatory sequence.
XX
PS Example; Fig 7; 122pp; English.
XX
CC The specification describes a method of treating cancer or
CC hyperproliferative disorders. The method comprises administering a
CC conditionally replicative viral vector, where at least one of the viral
CC nucleic acids encoding a product essential for its replication is
CC operably linked to an H19 regulatory sequence. The method is useful for
CC treating cancer or hyperproliferative disorders. The cancer is selected
CC from many different types, for example, carcinoma, sarcoma, adenoma and
CC ganglioblastoma. Preferably, the cancer is bladder carcinoma. The present
CC sequence encodes the E1a protein of human adenovirus type 5. It was
CC linked to a H19 regulatory sequence, and used to produce vectors for use
CC in the method of the invention
XX
SQ Sequence 3408 BP; 767 A; 764 C; 1007 G; 870 T; 0 U; 0 Other;
Query Match 98.1%; Score 2994; DB 9; Length 3408;

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2994; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 GTAGAGTTTCTCTCCGAGCCGCTCCGACACCGGAGTAAATGAGACATATTTATCTG 118
Db 1 GTAGAGTTTCTCTCCGAGCCGCTCCGACACCGGAGTAAATGAGACATATTTATCTG 60
QY 119 CCAGGAGGTATTAATTAATGAGAAATGCGCCGCTCTTTTGACCAAGCTGATGAAAGA 178
Db 61 CCAGGAGGTATTAATTAATGAGAAATGCGCCGCTCTTTTGACCAAGCTGATGAAAGA 120
QY 179 GGTACTGCTGTAATCTTCCACTCTAGACATTTTGAAACCACTTACCAACT 238
Db 121 GGTACTGCTGTAATCTTCCACTCTAGACATTTTGAAACCACTTACCAACT 180
QY 239 GTATGATTTAGACGTGACGCGCCCGGAAAGTCCAAACGAGAGGCGTTTGCGAGATTTT 298
Db 181 GTATGATTTAGACGTGACGCGCCCGGAAAGTCCAAACGAGAGGCGTTTGCGAGATTTT 240
QY 299 TCCGACCTCTGTAATGTTGCGGTGACAGAAAGGATTTGACTTACTCACTTTCCGCGGC 358
Db 241 TCCGACCTCTGTAATGTTGCGGTGACAGAAAGGATTTGACTTACTCACTTTCCGCGGC 300
QY 359 GCCCGCTTCTCCGAGCCGCTCACCTTTCCGCGAGCCCGAGCCGAGACAGAGAGC 418
Db 301 GCCCGCTTCTCCGAGCCGCTCACCTTTCCGCGAGCCCGAGCCGAGACAGAGAGC 360
QY 419 CTGGGCTCCGCTTCTGTAATGCAAACTTGTACCGGAGGTGATGATCTTACCTTCACGA 478
Db 361 CTGGGCTCCGCTTCTGTAATGCAAACTTGTACCGGAGGTGATGATCTTACCTTCACGA 420
QY 479 GGTCTGCTTTTCCACCCAGTGAACGAGAGATGAAGAAGGTGAGAGTTTGTGATTA 538
Db 421 GGTCTGCTTTTCCACCCAGTGAACGAGAGATGAAGAAGGTGAGAGTTTGTGATTA 480
QY 539 TGTGAGACACCCCGGAGCCGTTGACAGGTCTGTGATTAATCAACCGAGAAATACCGGAG 598
Db 481 TGTGAGACACCCCGGAGCCGTTGACAGGTCTGTGATTAATCAACCGAGAAATACCGGAG 540
QY 599 CCCAGATATATATGTTGCTTGTCTATATGAGACCTGTGAGCATGTTGTCTACAGTA 658
Db 541 CCCAGATATATATGTTGCTTGTCTATATGAGACCTGTGAGCATGTTGTCTACAGTA 600
QY 659 GTGAAATTTAATGAGGAGGTGATGAGAGTGTGGTTTGTGTGTAATTTTATTA 718
Db 601 GTGAAATTTAATGAGGAGGTGATGAGAGTGTGGTTTGTGTGTAATTTTATTA 660
QY 719 ATTTTACAGTTTGTGTTTAAAGATTTTGTAATTTTAAAGGTCTGTG 778
Db 661 ATTTTACAGTTTGTGTTTAAAGATTTTGTAATTTTAAAGGTCTGTG 720
QY 779 TCTGAACCTGAGCCGAGCCGAGACAGAACCGAGCCGTCAGAACCTACCGCGCTCT 838
Db 721 TCTGAACCTGAGCCGAGCCGAGACAGAACCGAGCCGTCAGAACCTACCGCGCTCT 780
QY 839 AAAATGGGCTGCTATCTGAGAGCCCGACATCACTGTGTCTAGAGATGCAATGT 898
Db 781 AAAATGGGCTGCTATCTGAGAGCCCGACATCACTGTGTCTAGAGATGCAATGT 840
QY 899 AGTACGATAGCTGATGCTCGGCTCTTCTAACACACCTCTGAGATACACCGGCTGTG 958
Db 841 AGTACGATAGCTGATGCTCGGCTCTTCTAACACACCTCTGAGATACACCGGCTGTG 900
QY 959 CCGCTGTGCCCCATTAAACAGTTGCGGTGAGAGTTGTGGCGCTGCGCAGAGCTGTGAA 1018
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QY 1019 TGTATCGAGACTTGTCTTAAGAGAGCTTGGGCACTTTTGACCTTGAAGTCTGAAACGCCCC 1078
Db 961 TGTATCGAGACTTGTCTTAAGAGAGCTTGGGCACTTTTGACCTTGAAGTCTGAAACGCCCC 1020
QY 1079 AGGCCATTAAGGTGTAACCTGTGATTTGCGTGTGTTTAAAGCCCTTTTGTGTAATGA 1138
Db 1138 AGGCCATTAAGGTGTAACCTGTGATTTGCGTGTGTTTAAAGCCCTTTTGTGTAATGA 1080

Db 1021 AGGCCATTAAGGTGTAACCTGTGATTTGCGTGTGTTTAAAGCCCTTTTGTGTAATGA 1080
QY 1139 GTTATGTAAGTTTAAATTAAGAGGTGAGATTAATTTTAACTTGACATGCGGTGTAATGGG 1198
Db 1081 GTTATGTAAGTTTAAATTAAGAGGTGAGATTAATTTTAACTTGACATGCGGTGTAATGGG 1140
QY 1199 GCGGGCTTAAAGGATATTAATGCGCGGTGGCTAATCTTGTGTAATCTGACTCATG 1258
Db 1141 GCGGGCTTAAAGGATATTAATGCGCGGTGGCTAATCTTGTGTAATCTGACTCATG 1200
QY 1259 GAGGCTTGGAGGTGTTGAGAGATTTTCTGCTGAGTAATCTGCTGGAACAGAGCTCT 1318
Db 1201 GAGGCTTGGAGGTGTTGAGAGATTTTCTGCTGAGTAATCTGCTGGAACAGAGCTCT 1260
QY 1319 AACAGTACCTTGTGTTTGGAGGTTTCTGTGGGCTTCATCCAGGCAAGTTAGTCTGC 1378
Db 1261 AACAGTACCTTGTGTTTGGAGGTTTCTGTGGGCTTCATCCAGGCAAGTTAGTCTGC 1320
QY 1379 AGAATTAAGAGATTAACAGTGGAAATTTGAAAGCTTTGAAATCCTGTGTGAGCTG 1438
Db 1321 AGAATTAAGAGATTAACAGTGGAAATTTGAAAGCTTTGAAATCCTGTGTGAGCTG 1380
QY 1439 TTTGATCTTGAATCTGAGTCAACAGGCGCTTTCCAGAGAAAGTCAAGACTTG 1498
Db 1381 TTTGATCTTGAATCTGAGTCAACAGGCGCTTTCCAGAGAAAGTCAAGACTTG 1440
QY 1499 GATTTTTCACACCGGCGCGCTGCGGCTGCTGTGCTTTTGTGATTTTAAAGAT 1558
Db 1441 GATTTTTCACACCGGCGCGCTGCGGCTGCTGTGCTTTTGTGATTTTAAAGAT 1500
QY 1559 AAATGAGCCGAAGAAACCATCTGAGCGGGGGTACCTGCTGATTTTCTGCGCATGAT 1618
Db 1501 AAATGAGCCGAAGAAACCATCTGAGCGGGGGTACCTGCTGATTTTCTGCGCATGAT 1560
QY 1619 CTGTGAGAGGGGTTGTGAGACAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1678
Db 1561 CTGTGAGAGGGGTTGTGAGACAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
QY 1679 GCGATTAATCCGAGCGAGAGACAGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAG 1738
Db 1621 GCGATTAATCCGAGCGAGAGACAGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
QY 1739 GAGCAGAGCCCATGAGAACCCGAGAGCCGCTGAGACCTCTGGGGAATGAATTTGTAAG 1798
Db 1681 GAGCAGAGCCCATGAGAACCCGAGAGCCGCTGAGACCTCTGGGGAATGAATTTGTAAG 1740
QY 1799 TGGCTGAACCTGATCCAGAACTGAGAGCAATTTGACAAATTAAGAGATGAGAGAGG 1858
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QY 1859 TAAAGGGGTTAAAGAGGAGCGGGGGCTTGTGAGGCTACAGAGAGGCTAGAAATCTAG 1918
Db 1801 TAAAGGGGTTAAAGAGGAGCGGGGGCTTGTGAGGCTACAGAGAGGCTAGAAATCTAG 1860
QY 1919 CTTTACCTTAATGACAGACACCTGCTGAGTATTAATCTTTTCAACAGATCAAGATA 1978
Db 1861 CTTTACCTTAATGACAGACACCTGCTGAGTATTAATCTTTTCAACAGATCAAGATA 1920
QY 1979 ATTGCGCTAATGAGCTTATGCTGTGGGCGAGAGTATTCATAGAGAGCTGACCACTT 2038
Db 1921 ATTGCGCTAATGAGCTTATGCTGTGGGCGAGAGTATTCATAGAGAGCTGACCACTT 1980
QY 2039 ACTGCTGACAGCCAGGAGATGATTTTGAAGAGGCTATTAAGGATATGCAAGGTGAC 2098
Db 1981 ACTGCTGACAGCCAGGAGATGATTTTGAAGAGGCTATTAAGGATATGCAAGGTGAC 2040
QY 2099 TTAGGCCAGATTTGAAATGACATCAAGATCAAGCAATTTGAAATATAGAAATTTGCTACA 2158
Db 2041 TTAGGCCAGATTTGAAATGACATCAAGATCAAGCAATTTGAAATATAGAAATTTGCTACA 2100
QY 2159 TTTCTGAGAAACGGGGCGGAGGTGAGATGATACGAGAGATAGGGTGGCTTTTGAATGTA 2218
Db 2101 TTTCTGAGAAACGGGGCGGAGGTGAGATGATACGAGAGATAGGGTGGCTTTTGAATGTA 2160

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 28, 2005, 02:07:07 ; Search time 8768 Seconds
(without alignments)
13249.561 Million cell updates/sec

Title: US-10-790-562-33

Sequence: 1 cgtgtagtgcattctatacc.....cgtagaagatcacagatcgag 3052

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:
1: gb_eest1.*
2: gb_eest2.*
3: gb_hlc.*
4: gb_eest3.*
5: gb_eest4.*
6: gb_eest5.*
7: gb_eest6.*
8: gb_gsest1.*
9: gb_gsest2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	615.8	20.2	648	4	BM655780	BM655780 170006873
2	615.6	20.2	766	6	CD742927	CD742927 UI-H-FTL1
3	607	19.9	750	6	CD370352	CD370352 UI-H-FTL1
4	592.8	19.4	625	7	CK624194	CK624194 ml18c08.Y
5	587.4	19.2	743	6	CA306882	CA306882 UI-H-FTL1
6	573	18.8	726	6	CA307899	CA307899 UI-H-FTL1
7	460	15.1	602	6	CD370856	CD370856 UI-H-FTL1
8	335.4	11.0	337	4	BM591710	BM591710 170006873
9	249.8	8.2	347	2	BF915148	BF915148 IL3-UT011
10	224.2	7.3	323	2	BF914577	BF914577 IL3-UT011
11	223.4	7.3	321	2	BF915126	BF915126 IL3-UT011
12	222.4	7.3	741	6	CD366021	CD366021 UI-H-FTL1
13	173.6	5.7	667	6	CD742922	CD742922 UI-H-FTL1
14	167	5.5	661	6	CD365243	CD365243 UI-H-FTL2
15	162	5.3	173	4	BM600614	BM600614 170006870
16	131.8	4.3	229	2	BF915892	BF915892 IL3-UT011
17	100.8	3.3	198	2	BF914321	BF914321 IL3-UT011
18	50.2	1.6	884	9	CNS00600	AL065922 Drosophila
19	48.6	1.6	942	9	CNS00601	AL065607 Drosophila
20	48.2	1.6	940	9	CNS03004	AL255325 Tetradon
21	47.6	1.6	1101	9	CNS00100	AL255307 Drosophila
22	47.2	1.5	732	7	CK305430	CK305430 SB02029B1
23	46.8	1.5	1220	6	CD504965	CD504965 CDA71-A08
24	46.6	1.5	1032	9	CU505993	CU505993 SAIL_759_

25	46.4	1.5	519	4	BM439574	pgtic.pk0
26	46.2	1.5	1101	9	CNS017M2	AL108245 Drosophila
27	46	1.5	670	9	CNS04K72	AL1294455 Tetradon
28	46	1.5	807	9	CNS0128R	AL101253 Drosophila
29	46	1.5	1511	9	CG753350	CG753350 P048-2-F0
30	45.8	1.5	662	5	BU303489	BU303489 603609609
31	45.8	1.5	891	5	BU842949	AGENCOURT
32	45.6	1.5	556	9	CR335545	Medicag9
33	45.6	1.5	1003	9	CNS017UQ	AL108524 Drosophila
34	45.6	1.5	1042	9	CNS0039B	AL063916 Drosophila
35	45.4	1.5	922	9	CNS0073M	AL066784 Drosophila
36	45.4	1.5	1101	9	CNS00LT2	AL078714 Drosophila
37	45	1.5	861	9	CNS0075A	AL066834 Drosophila
38	45	1.5	1098	9	CNS015EM	AL103552 Drosophila
39	45	1.5	1101	9	CNS000D1	AL065414 Drosophila
40	44.8	1.5	564	9	CNS01711	AL108067 Drosophila
41	44.8	1.5	768	7	CK306519	CK306519 SB02034A2
42	44.6	1.5	455	2	BE208710	BE208710 b66f08.Y
43	44.6	1.5	713	9	AG506778	AG506778 Mus muscu
44	44.6	1.5	939	9	CNS00CNG	AL059400 Drosophila
45	44.6	1.5	1101	9	CNS0100X	AL098379 Drosophila

ALIGNMENTS

RESULT 1
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LOCUS 17000687386917 A.Gam.ad.cdNAL Anopheles gambiae cDNA clone
DEFINITION 19600449669374 5', mRNA sequence.
ACCESSION BM655780
VERSION BM655780.1 GI:18955291
KEYWORDS EST.

SOURCE
ORGANISM Anopheles gambiae (African malaria mosquito)
Anopheles gambiae

REFERENCE
1 (bases 1 to 648)
Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L.,
Charlab,R., Collins,F.H., Venter,J.C. and Hoffman,S.L.,
Celera Anopheles gambiae EST project
Unpublished (2002)
CONTACT: Holt R.A.
Celera Genomics
45 W. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
Fax: 2404534580
Email: HoltR@celera.com
Plate: N001004A9S row: M column: 20
Seq primer: M13 Reverse.

TITLE
JOURNAL
COMMENT

FEATURES
source
location/Qualifiers
1..648
/organism="Anopheles gambiae"
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/strat_type="RSP-ST (Reduced busc. to Permethrin - std. chromosome)"
/db_xref="taxon:7165"
/clone="19600449669374"
/dev_strage="Adulc"
/lab_host="DHI0b"
/clone_id="A.Gam.ad.cdNAL1"
/note="Vector: pSport1; Site 1: SalI; site 2: NotI; whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."

ORIGIN

Query Match 20.2%; Score 615.8; DB 4; Length 648;
Best Local Similarity 97.7%; Pred. No. 5.4e-157;

Matches	636;	Conservative	0;	Mismatches	12;	Indels	3;	Gaps	1;
Qy	1126	GTTTGCTGAATGAGTTGATGTAAGTTAAATAAGGGTGAATATGTTTAACTTGATCG							1185
Db	1	GTTTGCTGAATGAGTTGATGTAAGTTAAATAAGGGTGAATATGTTTAACTTGATCG							60
Qy	1186	CGTGTAAATGAGGGCGGGCTTAAAGAGGTATATATAAGCGCGTGGCTTAATCTTGTTAC							1245
Db	61	CGTGTAAATGAGGGCGGGCTTAAAGAGGTATATATAAGCGCGTGGCTTAATCTTGTTAC							120
Qy	1246	ATTCGACCTCATGAGGCTTGAGAGTGTGTTGGAAGATTTTCTGCTGTCGCTTAATCTGCT							1305
Db	121	ATTCGACCTCATGAGGCTTGAGAGTGTGTTGGAAGATTTTCTGCTGTCGCTTAATCTGCT							180
Qy	1306	GGAACAGAGCTCTTAACACTACTCTTGTTGAGAGTTTCTGTCGCGCTCATCCAGGC							1365
Db	181	GGAACAGAGCTCTTAACACTACTCTTGTTGAGAGTTTCTGTCGCGCTCATCCAGGC							240
Qy	1366	AAAGTTAGTCGAGAAATTAAGAGGATTACAGTGGGAATTTGGAAGCTTTGGAATC							1425
Db	241	AAAGTTAGTCGAGAAATTAAGAGGATTACAGTGGGAATTTGGAAGCTTTGGAATC							300
Qy	1426	CTGTGTGAGCTGTGTTGATCTTTGAATCTGGATCACCAGCGCTTTTCAAGAGAAAGT							1485
Db	301	CTGTGTGAGCTGTGTTGATCTTTGAATCTGGATCACCAGCGCTTTTCAAGAGAAAGT							360
Qy	1486	CATCAAGCTTTGGATTTTTCACACCGGGCGCGCTGCGCTGTGCTTTTGGAG							1545
Db	361	CATCAAGCTTTGGATTTTTCACACCGGGCGCGCTGCGCTGTGCTTTTGGAG							420
Qy	1546	TTTATATAAGGATTAATGAGGAGAAACCATCTGAGCGGGGGGTACTGCTGATTT							1605
Db	421	TTTATATAAGGATTAATGAGGAGAAACCATCTGAGCGGGGGGTACTGCTGATTT							480
Qy	1606	TCTGSCCATGCTGTGTGAGAGCGGTTGTGAGACACAGAATCGCTTACTGTTGTC							1665
Db	481	TCTGSCCATGCTGTGTGAGAGCGGTTGTGAGACACAGAATCGCTTACTGTTGTC							540
Qy	1666	TTCCTGTCGCGCGCGGATTAATACCGAGCGAGAGACAGACAGACAGAGAAAGCCAG							1725
Db	541	TTCCTGTCGCGCGCGGATTAATACCGAGCGAGAGACAGACAGACAGAGAAAGCCAG							597
Qy	1726	GCGGCGGCGGAGAGAGAGCCCATGGAACCCGAGAGCCGCGCTGAGCC							1776
Db	598	GCGGCGGCGGAGAGAGAGCCCATGGAACCCGAGAGCCGCGCTGAGCC							648

FEATURES

SOURCE

Clone Distribution: Distribution information can be found at <http://genome.utoronto.edu/distribution/cgap.html>

Seq primer: M13 FORWARD

POLYA=Yes.

Location/Qualifiers

1..766

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="UI-H-FT1-Bka-m-09-0-UI"

/tissue_type="Alveolar Macrophage"

/dev_stage="Adult"

/lab_host="DH10B (Life Technologies)"

/clone_lib="NCI_CGAP_Ft1"

/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: Bcl I; Site 2: Not I; NCI CGAP Ft1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/mL, 3 hours; LPS 100 ng/mL, 24 hours; PMA 10 ng/mL, 3 hours; PMA 10 ng/mL, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lemon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into the pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dfr)18 tail. The sequence tag for this library is GGCATGCGG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG_TISSUE=Human Lung Alveolar Macrophage

TAG_LIB=UI-H-FT1

TAG_SEQ=GGCCATGCGG"

ORIGIN

Query Match

Best Local Similarity

Matches

744;

Conservative

0;

Mismatches

6;

Indels

116;

Gaps

1;

20.24;

Score

615.6;

DB

6;

Length

766;

85.9%;

Pred. No.

6,4e-157;

311

AATGTGGCGGTGAGAGAGGATTTGACTTACTCTTTCCGCGGCGCCGTTCTCC

370

766

AATGTGGCGGTGAGAGAGGATTTGACTTACTCTTTCCGCGGCGCCGTTCTCC

707

371

GGAACCGCTTCACTTTTCCGCGAGCCGAGACGCGAGACAGAGACCTTGGTCCGGT

430

706

GGAACCGCTTCACTTTTCCGCGAGCCGAGACGCGAGACAGAGACCTTGGTCCGGT

647

431

TTCTATGCCAACTTGTATACCGAGGTGATGATCTTAACCTTGGCCAGAGGTGCTTCC

490

646

TTCTATGCCAACTTGTATACCGAGGTGATGATCTTAACCTTGGCCAGAGGTGCTTCC

587

491

ACCGAGGAGAGATGAAGAGGTGAGAGTGTGTTAGATTATGAGACACC

550

586

ACCGAGGAGAGATGAAGAGGTGAGAGTGTGTTAGATTATGAGACACC

527

551

CGGCGAGGTTCAGAGTCTTGTCTATTACCGGAGGAATACGGGGAGCCAGATATTAT

610

526

CGGCGAGGTTCAGAGTCTTGTCTATTACCGGAGGAATACGGGGAGCCAGATATTAT

467

CD742927/c
LOCUS
DEFINITION
UI-H-FT1-Bka-m-09-0-UI s1 NCI CGAP_Ft1 Homo sapiens cDNA clone
UI-H-FT1-Bka-m-09-0-UI 3', mRNA sequence.
CD742927
VERSION
CD742927.1 GI:32293777
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 766)
NCI_CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
CONTACT
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

JOURNAL
COMMENT

Qy	611	GTGTTGCGCTTTGGCATATATAGAGAACCTGTGGGATGTTTGTCTACACATAGTAAATAATTATG	670
Db	466	GTGTTGCGCTTTGGCATATATAGAGAACCTGTGGGATGTTTGTCTACAC-----	423
Qy	671	GGCAGTGGGTATAGATGATGGGTTTGGTGTGTAATTTTTTTTTTAATTTTACAGTT	730
Db	422	-----	423
Qy	731	TTTGCGTTTAAGAAATTTTGTATTTGTGATTTTTTTTAAAAAGTCCTGTGTCTGAACCTGAG	790
Db	422	-----GTCTGTGTCTGAACCTGAG	403
Qy	791	CCTGAGCCCGAGCCGAGAACCGGAGCCTGCAAGACCTACCGCGCGCTCAAAAATGGCGCT	850
Db	402	CTTGAAGCCCGAGCCGAGAACCGGAGCCTGCAAGACCTACCGCGCGCTCAAAAATGGCGCT	343
Qy	851	GCTATCCTGAGACGGCCGACATCACTGTGTCTAGAGATGCAATAGTAGTACGATAGC	910
Db	342	GCTATCCTGAGACGGCCGACATCACTGTGTCTAGAGATGCAATAGTAGTACGATAGC	283
Qy	911	TGTGACTCCGGTCCTTTTAAACACACCTTCTGAGATCACCGGATGTCCGCTGTGCCCC	970
Db	282	TGTGACTCCGGTCCTTTTAAACACACCTTCTGAGATCACCGGATGTCCGCTGTGCCCC	223
Qy	971	ATTAAACCGATGCGGTGAGAGTTGTGTGGGGGTGSCAGGCTGTGGAATGTATGAGAAC	1030
Db	222	ATTAAACCGATGCGGTGAGAGTTGTGTGGGGGTGSCAGGCTGTGGAATGTATGAGAAC	163
Qy	1031	TTTGCTTAAACGAGCCTGGCAACCTTTGACTTGTAGCTTAAACGCCAGGCCCATTAAGT	1090
Db	162	TTTGCTTAAACGAGCCTGGCAACCTTTGACTTGTAGCTTAAACGCCAGGCCCATTAAGT	103
Qy	1091	GTTAAACCTGTGATTCGCTGTGTGTTAAACGCTTTGTGCTGAATGAGTTGATGTAAGT	1150
Db	102	GTTAAACCTGTGATTCGCTGTGTGTTAAACGCTTTGTGCTGAATGAGTTGATGTAAGT	43
Qy	1151	TTTATTAAGGTGAGATTAATGTTTAA	1176
Db	42	TTTATTAAGGTGAGATTAATGTTTAA	17

FEATURES	source
LOCUS	CD370352/c
DEFINITION	CD370352
ACCESSION	U1-H-FT1-bkb-j-17-0-U1.g1 NCI CGAP_FTI Homo sapiens CDNA clone
VERSION	U1-H-FT1-bkb-j-17-0-U1.3', mRNA sequence.
KEYWORDS	CD370352
SOURCE	CD370352.1 GI:31154442
ORGANISM	EST.
REFERENCE	Homo sapiens (human)
ALPHAS	Homo sapiens
TITLE	Embryoto; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL	1 (bases 1 to 750)
COMMENT	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
	Unpublished (1997)
	Contact: Robert Strausberg, Ph.D.
	Email: cgapbs-remail.nih.gov
	Tissue Procurement: Dr. Gary W. Hummingsake, U of I
	CDNA library preparation: Dr. M. Bento Soares, University of Iowa
	CDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
	DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
	Clone Distribution: Distribution Information can be found at
	http://genome.uiowa.edu/distribution/cgap.html
	Seq primer: M13 FORWARD
	POLYA=yes.
	location/Qualifiers
	1..750
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 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI_CGAP_F11 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV egfp), moi 500, 3 hours; Adenoviral vector (Ad5 CMV egfp), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dC)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
 TAG_TISSUE=Human Lung Alveolar Macrophage
 TAG_LIB=UI-H-F11
 TAG_SEQ=GGCCATGCCG"

Query Match	19.9%	Score 607	Length 750
Best Local Similarity	86.2%	Prod. No. 1, 48-154	
Matches 733	Conservative 0	Mismatches 1	Indels 116
			Gaps 1

QY	327	GAAAGGATTGACTTACTGACTTTTCCGCGCGGCCCGGGTCTCCGAGCGGCTGACTT	386
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QY	387	TCCCGGACGCCGAGCAGCCCGAGCAGAGGCGTTGGGTCCGGTTCTATGCCAAACCTT	446
Db	690	TCCCGGACGCCGAGCAGCCCGAGCAGAGGCGTTGGGTCTATGCCAAACCTT	631
QY	447	GTACCGGAGGTGATGCACTTACCTGCGACGAGGCTGCGCTTCCACCCAGTGAAGAGAG	506
Db	630	GTACCGGAGGTGATGCACTTACCTGCGACGAGGCTGCGCTTCCACCCAGTGAAGAGAG	571
QY	507	GATGAAGAGGCTGAGGAGCTTTGTGTAGATTATGTGAGCACCOCGGGACCGTTGCAGG	566
Db	570	GATGAAGAGGCTGAGGAGCTTTGTGTAGATTATGTGAGCACCOCGGGACCGTTGCAGG	511
QY	567	TCTTGTCAATATGACCGGAGGAATACGGGGGACCCAGATATTATGTGTGGCTTGGCTAT	626
Db	510	TCTTGTCAATATGACCGGAGGAATACGGGGGACCCAGATATTATGTGTGGCTTGGCTAT	451
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Db	450	ATGAGGACCTGTGGCATGTTGTCTACA-----	423
QY	687	GTGCTGGGTTTGGTGTGCTAATTTTTTTTTTAATTTTAACTGTTTGTGGTTTAAAGAT	746
Db	422	-----	423

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Db 422 -----GTCTGTGTCTGAACCTGAGCTGAGCCGAGCCAG 387
OY 807 AACCGAGCCTGCAAGACTTACCCGCGCTCTAAATGGCGCTGTATCTGTAGAGCC 866
Db 386 AACCGAGCCTGCAAGACTTACCCGCGCTCTAAATGGCGCTGTATCTGTAGAGCC 327
OY 867 CGAGATCACTGTGTCTGAGAAATGCAATAGTACCGAATGCTGTGACTCCGCTCTT 926
Db 326 CGAGATCACTGTGTCTGAGAAATGCAATAGTACCGAATGCTGTGACTCCGCTCTT 267
OY 927 CTAACACACTCTCTGAGATACACCGGAGTCTCCGCTGTGCCCTAAACAGTTGCCG 986
Db 266 CTAACACACTCTCTGAGATACACCGGAGTCTCCGCTGTGCCCTAAACAGTTGCCG 207
OY 987 TGAGAGTTGTGGCGCTGCGCAGGCTGTGAATGTATGAGAGACTTGTCTAACAGCCTG 1046
Db 206 TGAGAGTTGTGGCGCTGCGCAGGCTGTGAATGTATGAGAGACTTGTCTAACAGCCTG 147
OY 1047 GGCAACTTTTGACTGTAGCTGTAAACGCCAGGCTTAAGGTGTAAACCTGTGATTGC 1106
Db 146 GGCAACTTTTGACTGTAGCTGTAAACGCCAGGCTTAAGGTGTAAACCTGTGATTGC 87
OY 1107 GTGTGTGTAAAGCCTTTGTTGCTGAATGATGTAAAGTTTAAATAAAGGAGTGA 1166
Db 86 GTGTGTGTAAAGCCTTTGTTGCTGAATGATGTAAAGTTTAAATAAAGGAGTGA 27
OY 1167 TAATGTTTAA 1176
Db 26 TAATGTTTAA 17

RESULT 4
CK624194 625 bp mRNA linear EST 26-JAN-2004
DEFINITION m18c08.y1 Mouse RPE/choroid, unamplified: ml/mj Mus musculus cDNA
LOCUS CK624194
ACCESSION CK624194
VERSION CK624194.1 GI:41345080
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 625) Mammalia; Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Ida,H., Boylan,S., Weigel,A., Smit-McBride,Z., Chao,A., Gao,J.,
Buchoff,P., Wislow,G. and Hjelmeland,L.
TITLE Expressed sequence tag analysis of mouse RPE/choroid
JOURNAL Unpublished (2004)
COMMENT Contact: Wislow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: greame@helix.nih.gov
Plate: 18 row: c column: 08
Seq primer: M13Rpl reverse primer (ABI).
Location/Qualifiers
1..625
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57Bl6J"
/db_xref="taxon:10090"
/clone="m18c08"
/sex="Male"
/issue_type="RPE/choroid"
/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_id="Mouse RPE/choroid, unamplified: ml/mj"
/note="Organ: Eye; Vector: pSPORT1; 64ug total RNA was
```

extracted from 200 adult male mouse RPE/choroids. A directionally cloned cDNA library in the pSPORT1 vector (Life Technologies) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the Superscript Plasmid System full details of which are contained in the manufacturer's instruction manual (<http://www.lifetech.com/>). First strand synthesis was carried out using a Not I primer-adaptor [5'-pGACTGTTCTAGATGCGACGCGGCCG(r15-3')]. cDNA was cloned in Not I/Sal I sites. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."

ORIGIN

```
Query Match 19.4%; Score 592.8; DB 7; Length 625;
Best Local Similarity 97.6%; Pred. No. 1,1e-150;
Matches 613; Conservative 0; Mismatches 12; Indels 3; Gaps 1;

OY 1127 TTGCTGAATGAGTTGATGTATTAATTAAGGAGTAAATGTTAACTTGATGAGC 1186
Db 1 TTGCTGAATGAGTTGATGTATTAATTAAGGAGTAAATGTTAACTTGATGAGC 60
OY 1187 GTGTTAAATGCGGCGGCTTAAAGGATATTAATGCGCGTGGCTAATCTTGTTACA 1246
Db 61 GTGTTAAATGCGGCGGCTTAAAGGATATTAATGCGCGTGGCTAATCTTGTTACA 120
OY 1247 TGTGACCTCANTGAGAGCTTGGAGCTGTTTGGAAAGATTTTCTGTGCGCTAATCTTGCTG 1306
Db 121 TGTGACCTCANTGAGAGCTTGGAGCTGTTTGGAAAGATTTTCTGTGCGCTAATCTTGCTG 180
OY 1307 GAACAGAGCTCTAAAGTACCTCTTGTTTGGAGTTTCTGTTGAGGCTCATCCAGGCA 1366
Db 181 GAACAGAGCTCTAAAGTACCTCTTGTTTGGAGTTTCTGTTGAGGCTCATCCAGGCA 240
OY 1367 AAGTTAGTCTGCAATTAAGAAGATTAACAATGGGAATTTGAAGCTTTGAAATTC 1426
Db 241 AAGTTAGTCTGCAATTAAGAAGATTAACAATGGGAATTTGAAGCTTTGAAATTC 300
OY 1427 TGTGTGAGCTGTTTGAATCTGTTTGAATCTGTTTGAATCTGTTTGAATCTGTTTGAATCTG 1486
Db 301 TGTGTGAGCTGTTTGAATCTGTTTGAATCTGTTTGAATCTGTTTGAATCTGTTTGAATCTG 360
OY 1487 ATCAAGACTTTGATTTTTCACACCGGCGCGCTGCTGCTGTTGCTTTTGAAT 1546
Db 361 ATCAAGACTTTGATTTTTCACACCGGCGCGCTGCTGCTGTTTGAAT 420
OY 1547 TTTATTAAGATTAATGAGCGGAAGAAACCATCTGAGCGGCGGATCTGTGATTTT 1606
Db 421 TTTATTAAGATTAATGAGCGGAAGAAACCATCTGAGCGGCGGATCTGTGATTTT 480
OY 1607 CTGGCAGTGCATCTGTGAGAGAGGTTGTGACACAAAGAAATGCTGCTATCTGTGCT 1666
Db 481 CTGGCAGTGCATCTGTGAGAGAGGTTGTGACACAAAGAAATGCTGCTATCTGTGCT 540
OY 1667 TCCGTCCGCCCGCGATATACGACGAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1726
Db 541 TCCGTCCGCCCGCGGAATTAACGACGAGG---AGCAACAGCAGCAGCAGCAGCAGCAG 597
OY 1727 CGGCGCGCGAGAGCAGAGCCCATGGA 1754
Db 598 CGGCGCGCGAGAGCAGAGCCCATGGA 625

RESULT 5
CA306892/c 743 bp mRNA linear EST 05-AUG-2004
LOCUS CA306892
DEFINITION UI-H-FT1-bht-p-24-0-UI.s1 NCI CGAP FT1 Homo sapiens cDNA clone
UI-H-FT1-bht-p-24-0-UI 3', mRNA sequence.
ACCESSION CA306892
VERSION CA306892.1 GI:24469946
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
```


REFERENCE 1 (bases 1 to 743)
AUTHORS Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Tumor Gene Index
Unpublished (1997)
Contact: Robert Straube, Ph.D.
Email: gsb@nci.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLYAses.

FEATURES
SOURCE location/Qualifiers

1. 743
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FTI-bht-p-24-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_id="NCI-CGAP_FTI"
/note="Organ: Lung; Vector: pRT73-Pac (Pharmacia) with a
modified polylinker; Site 1: Ecor I; Site 2: Not I;
NCI CGAP FTI is a normalized cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples
were a mixture of these conditions (times refer to
incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of
the conditions, other donor macrophages in different
conditions). The mRNA samples were pooled for library
construction. Control 0 hours; control 3 hours; control 24
hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
mol 10, 3 hours; Klebsiella mol 10, 24 hours; Staph aureus
mol 10, 3 hours; Staph aureus mol 10, 24 hours; Adenoviral
vector (Ad5 CMV GFP), mol 500, 3 hours; Adenoviral vector
(Ad5 CMV GFP), mol 500, 24 hours; wt adenovirus mol 500,
3 hours; wt adenovirus mol 500, 24 hours; Ad vector + LPS
3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3
hours; wt adenovirus + LPS 24 hours. The library was
normalized according to Bonaldo, Lennon and Soares, Genome
Research, 6:791-806, 1996. First strand cDNA synthesis was
primed with an oligo-dT primer containing a Not I site.
Double stranded cDNA was ligated to an Ecor I adaptor,
digested with Not I, and cloned directionally into
pRT73-Pac vector. The oligonucleotide used to prime the
synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
GGCCATGCGG. The tissue was provided by Dr. Gary W.
Hunninghake of the University of Iowa.
TAG TISSUE=Human Lung Alveolar Macrophage
TAG LIB=UI-H-FTI
TAG_SEQ=GGCCATGCGG"

ORIGIN
Query Match 19.24; Score 587.4; DB 6; Length 743;
Best Local Similarity 86.0%; Pred. No. 3.4e-149;
Matches 725; Conservative 0; Mismatches 1; Indels 117; Gaps 2;

QY 341 ACTACCTTTTCCGCGCGCGCGGTTCTCCGAGCCGCTTACTTTTCCGCGAGCCCGA 400
DB 743 ACTACCTTTTCCGCGCGCGCGGTTCTCCGAGCCGCTTACTTTTCCGCGAGCCCGA 684
QY 401 GCAGCCGAGAGAGAGCTTGGTCCGTTTCTATGCAAACTTTACCGAGAGTGAT 460
|||||

DB 683 GCAGCCGAGAGAGAGCTTGGTCCGTTTCTATGCAAACTTTACCGAGAGTGAT 624
QY 461 CGATCTTACCTGCGCCAGAGGCTGCTTTCCACCCAGTAGAGAGATGAGAGGTGA 520
DB 623 CGATCTTACCTGCGCCAGAGGCTGCTTTCCACCCAGTAGAGAGATGAGAGGTGA 564
QY 521 GGAATTTGTGTATGATATATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 580
DB 563 GGAATTTGTGTATGATATATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 504
QY 581 CCGAGAGAGATACGAG 640
DB 503 CCGAGAGAGATACGAG 444
QY 641 CATGTTGTCTACAGTAAAGTAAATATATGAGAGAGAGAGAGAGAGAGAGAG 700
DB 443 CATGTTGTCTACAGTAAAGTAAATATATGAGAGAGAGAGAGAGAGAGAGAG 430
QY 701 GTGCTAATTTTCTTAAATTTTACAGTTTGTGCTTAAAGATTTGTATTTGATT 760
DB 429 ----- 430
QY 761 TTTTAAAGAGTCTGTGCTGTAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 820
DB 429 -----GTCTGTGTCTGTAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 380
QY 821 AGACCTACCGCGCGCTCTTAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 880
DB 379 AGACCTACCGCGCGCTCTTAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 320
QY 881 TCTGAGAGATGCAATATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 940
DB 319 TCTGAGAGATGCAATATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 260
QY 941 GAGATACACCGAG 1000
DB 259 GAGATACACCGAG 200
QY 1001 CGTGCAGAGCTGTGATGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1060
DB 199 CGTGCAGAGCTGTGATGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 140
QY 1061 TTGAGCTGTAAAGCGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1120
DB 139 TTGAGCTGTAAAGCGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 80
QY 1121 CTTTGTGCTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1179
DB 79 CTTTGTGCTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 20
QY 1180 GCA 1182
DB 19 GAA 17
RESULT 6
CA307899/c 726 bp mRNA linear EST 05-AUG-2004
LOCUS UI-H-FTI-b1b-a-23-0-UI.s1 NCI CGAP FTI Homo sapiens cDNA clone
DEFINITION UI-H-FTI-b1b-a-23-0-UI 3', mRNA sequence.
ACCESSION CA307899 GI:24470953
VERSION CA307899.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
REFERENCE 1 (bases 1 to 726)
AUTHORS Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Unpublished (1997)
Contact: Robert Straube, Ph.D.

Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Gary W. Hunninghake, U of I
 CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@iowa.edu
 The following repetitive elements were found in this cDNA
 Sequence: 1-21, >AT rich#low_complexity (matched complement)
 Seq primer: M13 FORWARD
 POLYA=yes.

FEATURES

Location/Qualifiers
 1..726
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-FT1-b1b-a-23-0-UI"
 /cissue_type="Alveolar Macrophage"
 /dev_stage="Adult"
 /lab_host="MDH10B (Life Technologies)"
 /clone_lib="NCI CGAP FT1"
 /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI CGAP FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ads CMV egfp), moi 500, 3 hours; Adenoviral vector (Ads CMV egfp), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
 TAG_TISSUE=Human Lung Alveolar Macrophage
 TAG_LIB=UI-H-FT1
 TAG_SEQ=GGCCATGCCG"

ORIGIN
 Query Match 18.8%; Score 573; DB 6; Length 726;
 Best Local Similarity 85.9%; Pred. No. 3e-145;
 Matches 710; Conservative 0; Mismatches 0; Indels 117; Gaps 2;

350 TCCGCGGCGCGCGGTTCTCCGAGACCGCTCACTTCCGGCAGCCGAGACCGGGA 409
 Db TCCGCGGCGCGCC-GTTCTCCGAGACCGCTCACTTCCGGCAGCCGAGACCGGGA 668
 410 GCAGAGACCTTGGGTCCGATTCTATGCCAAACCTTGTACCGAGAGTGAATCTTAC 469
 Db GCAGAGACCTTGGGTCCGATTCTATGCCAAACCTTGTACCGAGAGTGAATCTTAC 608
 470 CTGCCACAGAGCTGGCTTTCCACCAAGAGAGAGATGAAGAGGTGAGAGTTTGT 529
 Db CTGCCACAGAGCTGGCTTTCCACCAAGAGAGAGATGAAGAGGTGAGAGTTTGT 548

QY 530 GTTAGATTATGTGAGAGACCCCGGAGACGGTGCAGGCTTGTCAATTATCAGCGAGAA 589
 Db 547 GTTAGATTATGTGAGAGACCCCGGAGACGGTGCAGGCTTGTCAATTATCAGCGAGAA 488
 QY 590 TACGGGAGACCAATATTAATGTGCTTGTGCTTAATAGAGACCTGTGGCATGTTGT 649
 Db 487 TACGGGAGACCAATATTAATGTGCTTGTGCTTAATAGAGACCTGTGGCATGTTGT 428
 QY 650 CTACAGTAAGTGAATAATTAAGGACAGGAGTGAAGTGTGGGTTTGTGTGAATT 709
 Db 427 CTACA----- 423
 QY 710 TTTTATTAATTTTACAGTTTGTGTGTTAAAGATTTGTATGTGATTTTAA 769
 Db 422 ----- 423
 QY 770 GGTCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGACCGAGCCTGCAAGCCTACC 829
 Db 422 -GTCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGACCGAGCCTGCAAGCCTACC 364
 QY 830 CGCGGTCTAAATGGGCGCTGCTATCTGTGAGACGCCGACATACCTGTGTCTAGAGAA 889
 Db 363 CGCGGTCTAAATGGGCGCTGCTATCTGTGAGACGCCGACATACCTGTGTCTAGAGAA 304
 QY 890 TGCATATGATGATCGATAGCTGATCTGACCTCGGTCCTTCTAACAACACTCTGAGATACAC 949
 Db 303 TGCATATGATGATCGATAGCTGATCTGACCTCGGTCCTTCTAACAACACTCTGAGATACAC 244
 QY 950 CCGGTGTCCCGCTGTGCCCCCATTTAAACAGTTGCGGTGAGAGTTGTGGGCGTCCGAC 1009
 Db 243 CCGGTGTCCCGCTGTGCCCCCATTTAAACAGTTGCGGTGAGAGTTGTGGGCGTCCGAC 184
 QY 1010 GCTGTGAATGATATCGAGAGCTTGCTTAAGAGCCTGGGGAACCTTGGACCTGAGCGT 1069
 Db 183 GCTGTGAATGATATCGAGAGCTTGCTTAAGAGCCTGGGGAACCTTGGACCTGAGCGT 124
 QY 1070 AAACGCCCGCAGCATAGAGTGTAAACCTGTGATGCGTGTGTGTAAAGCCCTTGTGT 1129
 Db 123 AAACGCCCGCAGCATAGAGTGTAAACCTGTGATGCGTGTGTGTAAAGCCCTTGTGT 64
 QY 1130 GCTGAATGATGATGATGATGATTTAATTAAGAGGTGAGATTAATGTTAA 1176
 Db 63 GCTGAATGATGATGATGATGATTTAATTAAGAGGTGAGATTAATGTTAA 17

RESULT 7
 CD370856/c 602 bp mRNA linear EST 05-AUG-2004
 LOCUS
 DEFINITION
 UI-H-FT1-b1b-a-23-0-UI.s1 NCI CGAP FT1 Homo sapiens cDNA clone
 UI-H-FT1-b1b-a-23-0-UI 3', mRNA sequence.
 CD370856
 CD370856.1 GI:31154946
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE
 1 (bases 1 to 602)
 NCI CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 CONTACT
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Gary W. Hunninghake, U of I
 CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.uiova.edu/distribution/cgap.html>
 Seq primer: M13 FORWARD
 POLYA=yes.
 Location/Qualifiers

FEATURES

Source

1. 602
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FPI-bjz-n-11-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_id="NCI_CGAP_FPI"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: Ecor I; Site 2: Not I; NCI CGAP FPI is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ads CMV egfp), moi 500, 24 hours; Adenoviral vector (Ads CMV egfp), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag (dtt18 tail). The sequence tag for this library is GGCATGCGG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG TISSUE=human Lung Alveolar Macrophage
TAG LIB=UI-H-FPI
TAG_SEQ=GGCATGCGG"

Query Match 15.1%; Score 460; DB 6; Length 602;
Best Local Similarity 83.5%; Pred. No. 2,8e-114;
Matches 586; Conservative 0; Mismatches 0; Indels 116; Gaps 1;

ORIGIN

475 ACGAGGCTGGCTTTCACCCAGTGCAGCAGAGATGAAGAGGCTGAGAGTTGTGTAG 534
602 ACGAGGCTGGCTTTCACCCAGTGCAGCAGAGATGAAGAGGCTGAGAGTTGTGTAG 543
535 ATTATGTGACACACCCGGGACCGTTGAGTCTTTCATTAATACCGGAGGATACG 594
542 ATTATGTGACACACCCGGGACCGTTGAGTCTTTCATTAATACCGGAGGATACG 483
595 GGGACCCAGATATTATGTTGCTTCTATATAGACCTGTGGCATGTTGTCTACA 654
482 GGGACCCAGATATTATGTTGCTTCTATATAGACCTGTGGCATGTTGTCTACA 423
655 GTAAAGTAAATATATGCGCATGTGGTGAATAGAGTGTGGTGTGTAATTTTTT 714
422 ----- 423
715 TTAAATTTTACAGTTTGTGTTTAAAGAAATTTGTATGTGATTTTTTAAAGTTC 774
422 -----GTC 419

775 TGTGCTGAACCTGAGCTGAGCCGAGCCAGAACCGAGCCTGCAAGACCTACCCGCG 834
418 TGTGCTGAACCTGAGCTGAGCCGAGCCAGAACCGAGCCTGCAAGACCTACCCGCG 359

ORIGIN

Query Match 11.0%; Score 335.4; DB 4; Length 337;
Best Local Similarity 99.7%; Pred. No. 3.4e-80;
Matches 336; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

FEATURES

Source

1. 337
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"
/db_xref="taxon:7165"
/clone="19600449695952"
/dev_stage="Adult"
/lab_host="DH10B"
/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; whole adult mosquitoes (mixed sex) frozen on liquid nitrogen 24 hours after human blood feeding. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mrz.org)"

835 TCCTAAATGCGCGCTGTATCTGAGACGCCGACATACCTGTGTCTAGAGATGCA 894
358 TCCTAAATGCGCGCTGTATCTGAGACGCCGACATACCTGTGTCTAGAGATGCA 299
895 TAGTAGTACGAGTATGCTGTACTCCGGCTCTTCTTAACACACCTCGTAGATACACCCGGT 954
298 TAGTAGTACGAGTATGCTGTACTCCGGCTCTTCTTAACACACCTCGTAGATACACCCGGT 239
955 GGTCCCGCTGTGCCCATTAACAGATTGCCGTGAGAGTGTGGCGCTGCCAGGCTGT 1014
238 GGTCCCGCTGTGCCCATTAACAGATTGCCGTGAGAGTGTGGCGCTGCCAGGCTGT 179
1015 GGAATGTATCGAGACTTGTCTTAACAGACCTGGGCAACCTTTGACCTGTGAACG 1074
178 GGAATGTATCGAGACTTGTCTTAACAGACCTGGGCAACCTTTGACCTGTGAACG 119
1075 CCCGAGCCATTAAGTGTAAACCTGTGATTCGTTGTGTTAAGCCTTTGTTGCTGA 1134
118 CCCGAGCCATTAAGTGTAAACCTGTGATTCGTTGTGTTAAGCCTTTGTTGCTGA 59
1135 ATGAGTTGATGATTAATTAAGGCTGAGATATGTTAA 1176
58 ATGAGTTGATGATTAATTAAGGCTGAGATATGTTAA 17

RESULT 8
BM591710 337 bp mRNA linear EST 25-FEB-2002
LOCUS 17000687388831 A.Gam.ad.cDNA.blood1 Anopheles gambiae cDNA clone
DEFINITION 19600449695952 5', mRNA sequence.
ACCESSION BM591710
VERSION BM591710.1 GI:18887571
KEYWORDS EST.
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anophelinae.
REFERENCE 1 (bases 1 to 337)
Holt,R.A., Lin,D.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Chertab,R., Collins,F.H., Venter,J.C. and Hoffman,S.L., Celera Anopheles gambiae EST project
TITLE Unpublished (2002)
JOURNAL
COMMENT Contact: Holt R.A.
Celera Genomics
45 W. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
Fax: 2404534580
Email: HoltRA@celera.com
Plate: N001004AB8 row: P column: 18
Seq primer: M13 Reverse.
Location/Qualifiers

Oy 1126 GTTGTGAATGAGTGTATGTTAATTAATAAGGGTGAATTAATGTTACTTGCAATGG 1185
Db 1 GTTGTGCAATGAGTGTATGTTAATTAATAAGGGTGAATTAATGTTACTTGCAATGG 60
Oy 1186 CGTGTAAATGAGGGCGGGGCTTAAAGGGTATATAAGCCGCTGAGCTAATCTTGTTAC 1245
Db 61 CGTGTAAATGAGGGCGGGGCTTAAAGGGTATATAAGCCGCTGAGCTAATCTTGTTAC 120
Oy 1246 ATCGAAGCTCAATGAGGCTTGGAGCTGTTTGGAGATTTTCTGCTGCGTAATCTTGCT 1305
Db 121 ATCGAAGCTCAATGAGGCTTGGAGCTGTTTGGAGATTTTCTGCTGCGTAATCTTGCT 180
Oy 1306 GAACAGAGCTCTAACAAGTACCTCTTGCTTTGGAGCTTCTGAGGCTCATCCAGGC 1365
Db 181 GGAACAGAGCTCTAACAAGTACCTCTTGCTTTGGAGCTTCTGAGGCTCATCCAGGC 240
Oy 1366 AAGTGTAGCTGCAGAAATTAAGAAGATTACAGTGGGAATTTGAAAGCTTTGAAATC 1425
Db 241 AAGTGTAGCTGCAGAAATTAAGAAGATTACAGTGGGAATTTGAAAGCTTTGAAATC 300
Oy 1426 CTGTGTAGCTGTTTGTATCTTTGAATCTGGCTAC 1462
Db 301 CTGTGTAGCTGTTTGTATCTTTGAATCTGGCTAC 337

RESULT 9
LOCUS BF915148 347 bp mRNA linear EST 18-JAN-2001
DEFINITION IL3-UT0114-041200-328-H03_1 UT0114 Homo sapiens cDNA, mRNA
sequence.
ACCESSION BF915148
VERSION BF915148
KEYWORDS EST. GI:12306606
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Brites, M.R.,
Negal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL MEDLINE 20202663
PUBMED 10737800
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&ct=IL3-UT0114-
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Seq primer: puc 18 forward
High quality sequence stop: 329.

FEATURES
Source Location/Qualifiers
1..347

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Site_2: SmaI; A minilibrary was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN
Query Match 8.2%; Score 249.8; DB 2; Length 347;
Best Local Similarity 95.5%; Pred. No. 1e-56;
Matches 257; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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Db 347 CCGACATCACCTGTGTCTAAGAAATGCAATAGTACGATAGCTGTGACTCCGGTCT 288
Oy 926 TCTAACACACTCTCTGAGATACACCCGGTGTCCCGCTGTGCCCATTTAAACGAGTCC 985
Db 287 TCTAACACACTCTCTGAGATACACCCGGTGTCCCGCTGTGCCCATTTAAACGAGTCC 228
Oy 986 GTGAGATGGTGGGGCGTCCGACGCTGTGGATATATGAGACTTGCTTAACAGCCT 1045
Db 227 GTGAGATGGTGGGGCGTCCGACGCTGTGGATATATGAGACTTGCTTAACAGCCT 168
Oy 1046 GGGCACTTTGGACTTGAAGCTGTAAACGCCCGCATTAAGGTGTAAACCTGTGATTG 1105
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Oy 1106 CGTGTGTGTTAAGCGCTTGTGTTGCTGA 1134
Db 107 CGTGTGTGTTTCTTGTATTGACGCTTA 79

RESULT 10
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DEFINITION IL3-UT0114-011200-362-G09_1 UT0114 Homo sapiens cDNA, mRNA
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ACCESSION BF914577
VERSION BF914577
KEYWORDS EST. GI:12306035
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Brites, M.R.,
Negal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&ct=IL3-UT0114-
011200-362-G09_1&ct3=2000-12-01&ct4=1)
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High quality sequence stop: 322.

FEATURES
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Site_2: Sma1; A mini-library was made by cloning products

No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
the following conditions:

7.3%; Score 223.8; DB 2; Length 321;

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231; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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12 TGTGGAATGTATCGAGGACTTGTCTTAACGAGCCTGGGCAACCTTTGACTTGAGCTGTAA 1071

1 TGTGGAATGATCGAGGACTTCTTAACGAGTCTGGCCACCTTGGACTTGAGCTCTAA 142

[illegible]

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CD366021	741 bp	mRNA	linear	EST 05-AUG-2004
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UI-H-FT1-bjs-k-22-0-UI 3', mRNA sequence.

CD366021.1 GI:31150111

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

1 (pages 1 to 741)

National Cancer Institute. Cancer Genome Anatomy Project (CGAP).
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

Number Gene Index
[Inverted] (1997)

Contact: Robert Strausberg, Ph.D.
Email: ccranba-r@mail.nih.gov

CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at <http://consortia.wisc.edu/distribution/consort.htm>

Seq primer: M13 FORWARD

Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-b3-k-22-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FTL"
/note="Organ: Lung; Vector: pRT3-Pac (Pharmacia) with a modified polylinker; Site_1: Ecor I; Site_2: Not I; NCI CGAP FTL is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions), other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/mL, 3 hours; LPS 100 ng/mL, 24 hours; PMA 10 ng/mL, 3 hours; PMA 10 ng/mL, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV EGFP), moi 500, 24 hours; Adenoviral vector (Ad5 CMV EGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pRT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dfr)18 tail. The sequence tag for this library is GGCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCATGCCG"

ORIGIN
Query Match 7.3%; Score 222.4; DB 6; Length 741;
Best Local Similarity 98.7%; Pred. No. 4.1e-49;
Matches 234; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 2816 AGCCGAGAGCATGTCCAGGTGAACCTGAACGGGGTGTTCATGATGACATGAAGATCT 2875
Db 730 AGCCGAGAGCATGTCCAGGT - AACCTGAACGGGGTGTTCATGATGACATGAAGATCT 672
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Db 671 GGAAGGTCTGAGGTAGATGAGACCCGACACAGGTGACAGCCTCGCAGTGTGGCGGTA 612
QY 2936 AACATATTAGAACACAGCCTGTGATGCTGATGATGACCGAGAGCTGAGGCCCATCT 2995
Db 611 AACATATTAGAACACAGCCTGTGATGCTGATGATGACCGAGAGCTGAGGCCCATCT 552
QY 2996 TGGTGTCTGGCTGACACCGCGCTGAGTTGGCTCTAGCGATGAAGATACAGATTGAG 3052
Db 551 TGGTGTCTGGCTGACACCGCGCTGAGTTGGCTCTAGCGATGAAGATACAGATTGAG 495
RESULT 13
CD742922/CD 667 bp mRNA linear EST 05-AUG-2004
LOCUS
DEFINITION UI-H-FT1-b3-k-23-0-UI.s1 NCI CGAP FTL Homo sapiens cDNA clone
ACCESSION CD742922
VERSION CD742922.1 GI:322937772
KEYWORDS EST.

SOURCE
ORGANISM Homo sapiens (human)
REFERENCE Bukacynska, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eulalia; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 667)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgaps-remail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library Preparation: Dr. W. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. W. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at <http://genome.uiowa.edu/distribution/cgap.html>
The following repetitive elements were found in this cDNA sequence: 546-595, >(CAG)n\$imple_repeat (matched complement)
Seq primer: M13 FORWARD
POLYA=yes.
FEATURES
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Location/Qualifiers
1..667
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="UI-H-FT1-b3-k-23-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FTL"
/note="Organ: Lung; Vector: pRT3-Pac (Pharmacia) with a modified polylinker; Site_1: Ecor I; Site_2: Not I; NCI CGAP FTL is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions), other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/mL, 3 hours; LPS 100 ng/mL, 24 hours; PMA 10 ng/mL, 3 hours; PMA 10 ng/mL, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV EGFP), moi 500, 24 hours; Adenoviral vector (Ad5 CMV EGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pRT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dfr)18 tail. The sequence tag for this library is GGCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCATGCCG"

ORIGIN
Query Match 5.7%; Score 173.6; DB 6; Length 667;
Best Local Similarity 97.8%; Pred. No. 9.7e-36;
Matches 176; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1623 GGAGAGGGGTTGTAGACACAAGAAATGCGCTGCTACTGTGTCTTCCGCTCCGCGCGGA 1682
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 Db 667 GGAGAGCGGTTGTGTGACACAAGAAATGCGCTGCTACTGTGTCTTCCGCTCCGCGCGGA 608
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 Oy 1683 TAAATACGACGAGAGACAGACAGACAGACAGAGAAAGCCAGCGCGCGGACAGAGC 1742
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 Db 607 TAAATACGACGAGAGACAGACAGACAGACAGAGAAAGCCAGCGCGCGGACAGAGC 548
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 Oy 1743 AGAGCCCATGGAACCCGAGACCCGCGCTGGAACCTCGGGAATGATGTTGTACAGTGGC 1802
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 Db 547 AGAGCCCATGGAACCCGAGACCCGCGCTGGAACCTCGGGAATGATGTTGTACAGCGCC 488
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 LOCUS UI-H-FT2-bj1-c-23-0-UI.s1 NCI CGAP FT2 Homo sapiens cDNA clone
 DEFINITION UI-H-FT2-bj1-c-23-0-UI 3', mRNA sequence.
 CD365243
 ACCESSION CD365243
 VERSION CD365243.1 GI:31149333
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 661)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-rcmail.nih.gov
 Tissue Procurement: Dr. Gary W. Hunninghake, U of I
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
 http://genome.uiowa.edu/distribution/cgap.html
 Seq Primer: M13 FORWARD
 POLYAyes.

FEATURES

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 /db_xref="taxon:9606"
 /clone="UI-H-FT2-bj1-c-23-0-UI"
 /tissue_type="Alveolar Macrophage"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_id="NCI CGAP FT2"
 /note="Organ: Lung; Vector: pRTT3-Pac (Pharmacia) with a
 modified polylinker; Site 1: Ecor I; Site 2: Not I;
 NCI CGAP FT2 is a subtracted cDNA library constructed from
 a pool of 81 RNA samples from Alveolar Macrophages.
 challenged with different treatments. The mRNA samples
 were a mixture of these conditions (times refer to
 incubations following isolation by bronchoalveolar lavage)
 (some normal donor macrophages were cultured in some of
 the conditions, other donor macrophages in different
 conditions). The mRNA samples were pooled for library
 construction. Control 0 hours; control 3 hours; control 24
 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
 PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
 mol 10, 3 hours; Klebsiella mol 10, 24 hours; Staph
 aureus mol 10, 3 hours; Staph aureus mol 10, 24 hours;
 Adenoviral vector (Ad5 CMV egfp), mol 500, 3 hours;
 Adenoviral vector (Ad5 CMV egfp), mol 500, 24 hours;
 Adenovirus mol 500, 3 hours; wt adenovirus mol 500, 24
 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours;
 wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours.
 The library was subtracted according to Bonaldo, Lennon
 and Soares, Genome Research, 6:791-806, 1996. The tissue

ORIGIN

was provided by Dr. Gary W. Hunninghake of the University
 of Iowa.
 TAG_TISSUE=Human Lung Alveolar Macrophage
 TAG_LIB=UI-H-FT2
 TAG_SEQ=GGCCATGCGC"

Query Match 5.5%; Score 167; DB 6; Length 661;
 Best Local Similarity 100.0%; Pred. No. 6.2e-34;
 Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 661 GAGGTACGATGAGACCCGACACAGAGACAGACCTGCGAGTGTGCGGTAACATATTAG 602
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 Oy 2946 GAACACAGCTGTGATGTGTGATGTGATGACGAGAGCTGAGGCGCGATCACTTGCTGCGC 3005
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 Db 601 GAACACAGCTGTGATGTGTGATGTGATGACGAGAGCTGAGGCGCGATCACTTGCTGCGC 542
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 Oy 3006 CTGCAACCGCGCTGATGTTGCTCTTACCGATGAAGATACAGATTGAG 3052
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 Db 541 CTGCAACCGCGCTGATGTTGCTCTTACCGATGAAGATACAGATTGAG 495
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RESULT 15

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 LOCUS 1700687054399 A.Gam.ad.cDNA.blood1 Anopheles gambiae cDNA clone
 DEFINITION 19600449720751 5', mRNA sequence.
 CD360614
 ACCESSION BM600614
 VERSION BM600614.1 GI:18898718
 KEYWORDS EST.
 SOURCE Anopheles gambiae (African malaria mosquito)
 ORGANISM Anopheles gambiae
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
 Anopheles.

REFERENCE 1 (bases 1 to 173)
 AUTHORS Holt,R.A., Lin,J.-D., Murphy,S.D., Evans,C.A., Kraft,C.L.,
 Charlab,R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
 TITLE Celera Anopheles gambiae EST project
 JOURNAL Unpublished (2002)
 COMMENT Contact: Holt R.A.
 Celera Genomics
 45 W. Gude Dr., Rockville, MD 20850, USA
 Tel: 2404533151
 Fax: 2404534580
 Email: HoltRA@celera.com
 Plate: NU01004AHI row: J column: 01
 Seq Primer: M13 Reverse.

FEATURES

source
 1. 173
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 /mol_type="mRNA"
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 /clone="19600449720751"
 /dev_stage="Adult"
 /lab_host="DH10B"
 /clone_id="A.Gam.ad.cDNA.blood1"
 /note="Vector: pSport1; Site 1: SalI; Site 2: NotI; whole
 adult mosquitoes (mixed sex) frozen on liquid nitrogen 24
 hours after human blood feeding. cDNA inserts >500 bp
 cloned directionally into pSport 1. Not 1 site is 3'.
 Clones available through the Malaria Research and
 Reference Reagent Resource Center (www.malaria.mrg.org)"

ORIGIN

Query Match 5.3%; Score 162; DB 4; Length 173;
 Best Local Similarity 99.4%; Pred. No. 1e-32;
 Matches 173; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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OY 1186 CGTGTAAATGGGCGGGCTTAAAGGTTAATAATGCGCCGTGGCTAATCTTGTTAC 1245
Db 61 CGTGTAAATGGGCGGGCTTAAAGGTTAATAATGCGCCGTGGCTAATCTTGTTAC 120
OY 1246 ATCTGACCTCATGAGGCTTGGGAGTGTGGAAGATTTTCTGCTGCGCTAA 1299
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Search completed: October 28, 2005, 08:56:38
Job time : 8779 secs

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3	3052	100.0	35935	2	US-08-735-609-1	Sequence 1, Appl1
4	3052	100.0	35935	3	US-08-379-452-43	Sequence 43, Appl1
5	3052	100.0	35935	3	US-09-155-172-1	Sequence 1, Appl1
6	3052	100.0	35935	3	US-09-244-752-1	Sequence 1, Appl1
7	3052	100.0	35935	3	US-09-245-97-1	Sequence 1, Appl1
8	3052	100.0	35935	3	US-09-409-670-43	Sequence 43, Appl1
9	3052	100.0	35935	3	US-09-562-119-1	Sequence 1, Appl1
10	3052	100.0	35978	4	US-09-566-135-1	Sequence 1, Appl1
11	3065.8	98.5	7090	4	US-09-714-550-18	Sequence 18, Appl1
12	2822	92.5	35871	4	US-09-566-635-4	Sequence 2, Appl1
13	2161	70.8	34303	2	US-08-735-609-1	Sequence 4, Appl1
14	2161	70.8	34303	2	US-08-735-609-1	Sequence 4, Appl1
15	2161	70.8	34303	3	US-09-115-702-4	Sequence 4, Appl1
16	2161	70.8	34303	3	US-09-244-752-4	Sequence 4, Appl1
17	2161	70.8	34303	3	US-09-545-97-4	Sequence 4, Appl1
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22	1066.8	35.0	1356	1	US-08-463-184-1	Sequence 1, Appl1
23	1066.8	35.0	1356	1	US-08-463-184-1	Sequence 1, Appl1
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ALIGNMENTS

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RESULT 1
US-08-735-609-1
; Sequence 1, Application US/08735609
; Patent No. 595360
; GENERAL INFORMATION:
; APPLICANT: Chamberlain, Jeffrey S.
; APPLICANT: Amalfitano, Andrea
; APPLICANT: Hauser, Michael A.
; APPLICANT: Kumar-Singh, Rajendra
; APPLICANT: Hartigan-O'Connor, Dennis J.
; TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/735,609
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: UM-02484
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35935 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
US-08-735-609-1

Query Match 100.0%; Score 3052; DB 2; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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Db	579	ACGAGGTGTTATTTACCGAAGAAAATGGCCGCGAGTCTTTTGAGCACGCTGATCGAAGAG	638
Qy	181	TACTGCGCTGAATATCTTCCAGCTCTAGACCATTTTGAACCATACCTTTACGAACTGT	240
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Qy	241	ATGATTTTGAAGCTGACGGCCCCCGAAGATCCCAACGAGAGAGCGGTTCCGAGATTTTTC	300
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Db	1539	GCCATTAAGGTGTAAACCTGTGATTCGCTGTGTGGTTAAACCCCTTTGTTGCTGATGACT	1598
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Db	2139	GATTAATACCGACCGAGAGACAGACAGACAGAGAGAAACCAAGCGCGCGCGCGACAGA	2198
Qy	1741	GCAGAGCCCATGGAACCCGAGAGCGGCGCTGGAACCTCGGGAAATGAATGTTGTACAGGTG	1800
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Qy	1801	GCTGAATCTGTATCCAGAACTGGAAGCGATTTTGAACAATTACAGAGATGGGACAGGGCTA	1860
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Qy	1861	AAGGGGCTTAAAGAGAGCGGGGGGCTTGTGAGGCTTCAAGAGAGGCTTAGAAATCTAGCT	1920
Db	2319	AAGGGGCTTAAAGAGAGCGGGGGGCTTGTGAGGCTTCAAGAGAGGCTTAGAAATCTAGCT	2378
Qy	1921	TTTAGCTTAATGAACACAGACACCGTCTGAGTGTATTACTTTTCAACAGATCAAGATTAAT	1980
Db	2379	TTTAGCTTAATGAACACAGACACCGTCTGAGTGTATTACTTTTCAACAGATCAAGATTAAT	2438
Qy	1981	TGCGCTTAATGAGCTGTACTGTGTGGCGCAAGATTTCCATAGAGAGCTGACCACTTAC	2040
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Qy	2041	TGCGTGCAGCGAGGGAGTGAATTTTGAAGAGAGCTATTAGGGGTAATGCAAAAGGTGGCACTT	2100
Db	2499	TGCGTGCAGCGAGGGAGTGAATTTTGAAGAGAGCTATTAGGGGTAATGCAAAAGGTGGCACTT	2558
Qy	2101	AGGCGAATTTGCAAGTCAAGATCAGCAAACTTGTAAATATCAGGAATTTGTGTCACTAT	2160
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Qy	2161	TCTGGGAACGGGGCCGAGGTGTGAGATATGATACGAGAGATAGGGTGGCTTTAATGTATAGC	2220
Db	2619	TCTGGGAACGGGGCCGAGGTGTGAGATATGATACGAGAGATAGGGTGGCTTTAATGTATAGC	2678

QY 2221 ATGTAATAATGTCGGCGGGGTCCTTGCCATGACCGGGGTGTTATTATGAAATGAAG 2280
 DB 2679 ATGATTAATATGTGGCGGGGGTGCTTGCCATGACCGGGGTGTTATTATGAAATGAAG 2738
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 QY 2341 GGTGTAAGCTTCTATGAGGTTTAAATATACCTGTGTGGAAGGCTGACCGATGTAAGGTT 2400
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 QY 2401 CGGGGCTGTCTTTTAACTGTGTGGAAGGCGGTGTGTGTGCGCCCAAAAGAGGGCT 2460
 DB 2859 CGGGGCTGTCTTTTAACTGTGTGGAAGGCGGTGTGTGTGCGCCCAAAAGAGGGCT 2918
 QY 2461 TCAATTAAGAAATGCTTTTAAAGGTGTAACCTGTGTGTAAGGCTGTAAGGTTACTCC 2520
 DB 2919 TCAATTAAGAAATGCTTTTAAAGGTGTAACCTGTGTGTAAGGCTGTAAGGTTACTCC 2978
 QY 2521 AGGGTGGCCCAATGTCGCTCCGACTGTGTGTTCTTCAATGCTAGTAAAGAGGTCCT 2580
 DB 2979 AGGGTGGCCCAATGTCGCTCCGACTGTGTGTTCTTCAATGCTAGTAAAGAGGTCCT 3038
 QY 2581 GTGATTAAGCAATACATGTAATGTGGCAATGCGAGGAGAGGCGCTTCAAGATCTGACC 2640
 DB 3039 GTGATTAAGCAATACATGTAATGTGGCAATGCGAGGAGAGGCGCTTCAAGATCTGACC 3098
 QY 2641 TGTCTCGAAGCGCAATCTGTACCTGTGTAAGACCAATTCAGTACGACCACTCTCGCAAG 2700
 DB 3099 TGTCTCGAAGCGCAATCTGTACCTGTGTAAGACCAATTCAGTACGACCACTCTCGCAAG 3158
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 DB 3159 GCGTGGCCAGTGTGTGACATACATGCTGACCGGCTGTCTTCAATGCTAGTAAAGAGG 3218
 QY 2761 AGGGGGGTGTCTTCACTTACCAATGCAATTTAGTACCACTTAAGATATTTGCTGAGCCC 2820
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 QY 2821 GAGAGCATGTCGAAGGTGAACCTGAACGGGGTGTGTGACATGACCAATGAAGATCTGGAAG 2880
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 QY 2881 GTGCTGAGTACGATGAGACCCGACCAAGGTGAGACCTTGCAGTGTGCGGTAAACAT 2940
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 QY 2941 ATTAGAACCAAGCTGTGATGCTGATGTGACCGAGAGCTGAGGCGCGATCACTGTGTG 3000
 DB 3399 ATTAGAACCAAGCTGTGATGCTGATGTGACCGAGAGCTGAGGCGCGATCACTGTGTG 3458
 QY 3001 CTGGCCCTGACCCGCGCTGAGTTGGCTTACGATGAAATACGATTTGAG 3052
 DB 3459 CTGGCCCTGACCCGCGCTGAGTTGGCTTACGATGAAATACGATTTGAG 3510

RESULT 2
 US-08-735-609-1
 Sequence 1, Application US/08735609
 Patent No. 5994132

GENERAL INFORMATION:

APPLICANT: Chamberlain, Jeffrey S.
 Amalfitano, Andrea
 Hauser, Michael A.
 Kumar-Singh, Rajendra
 Hartigan-O'Connor, Dennis J.
 TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Medlen & Carroll, LLP
 STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco
 STATE: California
 COUNTRY: United States Of America
 ZIP: 94104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/735,609
 FILING DATE: 23-Oct-1996
 CLASSIFICATION: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Ingolia, Diane E.
 REGISTRATION NUMBER: 40,027
 REFERENCE/DOCKET NUMBER: UM-02484
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 705-8410
 TELEFAX: (415) 397-8338
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 35935 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "DNA"
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-08-735-609-1

Query Match 100.0%; Score 3052; DB 2; Length 35935;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTGTAGTATTATATACCCGGTGTGTCCTCAAGAGCCACTTGTAGTCCGACGAGT 60
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 QY 61 AGATTTTCTCTCCGACCGCTCCGACCGGAGCTGAAATGAGATATTATCTGCC 120
 DB 519 AGATTTTCTCTCCGACCGCTCCGACCGGAGCTGAAATGAGATATTATCTGCC 578
 QY 121 ACGGAGGTGTATTATCCGAAGAAATGCGCCGACGTCTTTTGACACAGTGTATCGAAGG 180
 DB 579 ACGGAGGTGTATTATCCGAAGAAATGCGCCGACGTCTTTTGACACAGTGTATCGAAGG 638
 QY 181 TACTGGCTGATAATCTTCCACTCTCTAGCAATTTTGAACCACTTACAGAACTGT 240
 DB 639 TACTGGCTGATAATCTTCCACTCTCTAGCAATTTTGAACCACTTACAGAACTGT 698
 QY 241 ATGATTTAGAGTACGAGCGCCCGGAGATCCCAAGAGGCGGTTTCGAGATTTTTC 300
 DB 699 ATGATTTAGAGTACGAGCGCCCGGAGATCCCAAGAGGCGGTTTCGAGATTTTTC 758
 QY 301 CCGACTCTGTAATGTGTGCGGTGACAGAAAGGATTTGACTTACTCATTTTCCGCGGCGC 360
 DB 759 CCGACTCTGTAATGTGTGCGGTGACAGAAAGGATTTGACTTACTCATTTTCCGCGGCGC 818
 QY 361 CCGGTTCTCCGAGACCGCTCACCTTTCCCGGACCGCCGAGCCGAGAGAGAGGCT 420
 DB 819 CCGGTTCTCCGAGACCGCTCACCTTTCCCGGACCGCCGAGAGAGAGGCT 878
 QY 421 TGGGTCCGGTTTCTATGCAAACTTGTATCCGAGAGTATGATCTTACTCTGCCAGAGG 480
 DB 879 TGGGTCCGGTTTCTATGCAAACTTGTATCCGAGAGTATGATCTTACTCTGCCAGAGG 938
 QY 481 CTGGCTTTCCACCAGTGAAGAGATGAAAGGAGTGAAGATTTGTATTATATG 540
 DB 939 CTGGCTTTCCACCAGTGAAGAGATGAAAGGAGTGAAGATTTGTATTATATG 998
 QY 541 TGAGACACCCGGGACGAGGTGACAGTCTTGTCAATTATCACCGAGGAATACGGGGGACC 600

Db 999 TGAGACACCCGGGCGAGGTTGCAAGTCTGTGCATATACCGAGAAATACGGGGAGACC 1058
Qy 601 CAGATATATATGTTCCTTTCCTATATAGAGACCTGTGGCATGTTCATACGTAAGT 660
Db 1059 CAGATATATGTTCCTTTCCTATATAGAGACCTGTGGCATGTTCATACGTAAGT 1118
Qy 661 GAAATTTATGGGCGAGTGGGTATAGAGTGTGGGTTTGGTGGTAATTTTTTTTTTAT 720
Db 1119 GAAATTTATGGGCGAGTGGGTATAGAGTGTGGGTTTGGTGGTAATTTTTTTTTTAT 1178
Qy 721 TTTTACAGTTTGTGTTTAAAGAAATTTGTATGTGTATTTTTTTTAAAGGTCGTGTGC 780
Db 1179 TTTTACAGTTTGTGTTTAAAGAAATTTGTATGTGTATTTTTTTTAAAGGTCGTGTGC 1238
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Db 1239 TGAACCTGAGCTGAGCCCGGACCGAGACCGAGCTTGCAACCTTACCCCGCTCTTAA 1298
Qy 841 AATGGCGCTGCTATTCCTGAGACGCGCCGACATCACCTGTCTAGAGAAATGCAATAGTAG 900
Db 1299 AATGGCGCTGCTATTCCTGAGACGCGCCGACATCACCTGTCTAGAGAAATGCAATAGTAG 1358
Qy 901 TACGATATGCTGTGATCTCCGCTCTTCTTAAACAACCTTCAGATATACCCGGTGTCCC 960
Db 1359 TACGATATGCTGTGATCTCCGCTCTTCTTAAACAACCTTCAGATATACCCGGTGTCCC 1418
Qy 961 GCTGCGCCCATTTAAACAGATGCGCTGAGAGTGTGGGGGTGGCCAGGCTGTGGAAATG 1020
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Db 1479 TATCGAGACTTGTCTTAAACGAGCCTGGGCAACCTTTGACCTTGAAGCTGTAAACGCCAG 1538
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Db 1539 GCCATTAAGTGTAAACCTGTGATTCGCTGTGTGTAAACGCTTTGTTTGTGTGAATGAGT 1598
Qy 1141 TGAATTAAGTTTAAAGGGGTGAGATTAATGTTTAACTTGATGGCGGTAAATGTGGGCG 1200
Db 1599 TGAATTAAGTTTAAAGGGGTGAGATTAATGTTTAACTTGATGGCGGTAAATGTGGGCG 1658
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Db 1659 GGGGCTTAAAGGGGTATTAATATGCGCGGTGGCTAATCTTGTATCAATCTGACTATGTA 1718
Qy 1261 GCGTTGGAGTGTTTGGAAGATTTTTTCTGCTGTGCTAATCTTGCTGAAACAGAGCTCTAA 1320
Db 1719 GCGTTGGAGTGTTTGGAAGATTTTTTCTGCTGTGCTAATCTTGCTGAAACAGAGCTCTAA 1778
Qy 1321 CAGTACCTCTTGTTTGGAGGTTTCTGTGGGGCTCATCCGAGCAAGTTAAGTCTGAG 1380
Db 1779 CAGTACCTCTTGTTTGGAGGTTTCTGTGGGGCTCATCCGAGCAAGTTAAGTCTGAG 1838
Qy 1381 AATTAAAGAGATTACAAGTGGGAATTTGAAGCTTTGAAATCTGTGGTGAAGTGT 1440
Db 1839 AATTAAAGAGATTACAAGTGGGAATTTGAAGCTTTGAAATCTGTGGTGAAGTGT 1898
Qy 1441 TGAATTTTGAATCTGGGTCAACAGGCGCTTTTCCAGAGAAAGTCAATCAAGACTTTGGA 1500
Db 1899 TGAATTTTGAATCTGGGTCAACAGGCGCTTTTCCAGAGAAAGTCAATCAAGACTTTGGA 1958
Qy 1501 TTTTTCACACCGGGGGCGGCTGGGGGCTGCTGTTGCTTTTGAAGTTTATTAAGGATTA 1560
Db 1959 TTTTTCACACCGGGGGCGGCTGGGGGCTGCTGTTGCTTTTGAAGTTTATTAAGGATTA 2018
Qy 1561 ATGAGCGAAGAAAACCACTGAGCGGGGGGTACCTGTGATTTTCTGSCCATGCAATCT 1620
Db 2019 ATGAGCGAAGAAAACCACTGAGCGGGGGGTATCTGTGTGAATTTTCTGSCCATGCAATCT 2078
Qy 1621 GTGAGAGCGGTTGTGAGACACAAAGATCGCTGTCTACTGTTGTCTCCGTCCCGCGGC 1680
Db 2079 GTGAGAGCGGTTGTGAGACACAAAGATCGCTGTCTACTGTTGTCTCCGTCCCGCGGC 2138

Qy 1681 GATAATACCCAGGAGAGACGACGACGACGAGGAAAGCCAGCGCGCGGACAGA 1740
Db 2139 GATAATACCCAGGAGAGACGACGACGACGAGGAAAGCCAGCGCGCGGACAGA 2198
Qy 1741 GCAGAGCCATGGAACCCGAGAGCGGCTGGAACCTTCGGGAATGAATGTTGTACAGGTG 1800
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Db 2259 GCTGAATCTGATCCAGAACTGAGACGCAATTTGACAAATTACAGAGATGGCAGGGGCTA 2318
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Db 2319 AAGGGGGTAAAGAGAGGAGCGGGGGCTTTGAGGCTACAGAGAGGCTAGGAATCTACT 2378
Qy 1921 TTTAGCTTAAATGACAGACACCGTCTGAGTGTATTAATTTTCAACAGATCAAGATTAAT 1980
Db 2379 TTTAGCTTAAATGACAGACACCGTCTGAGTGTATTAATTTTCAACAGATCAAGATTAAT 2438
Qy 1981 TGCCCTAATGAGCTTGAATCTGTGGCGGAGAAATTCATATGACAGCTGACCACTTAC 2040
Db 2439 TGCCCTAATGAGCTTGAATCTGTGGCGGAGAAATTCATATGAGAGCTGACCACTTAC 2498
Qy 2041 TGCGTGAGCCAGGGGATGAATTTTGAAGAGCTATTAAGGATATGCAAAAGGTGGCACTT 2100
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Db 2559 AGGCGAATGTCAGATACAGATCAGAAACCTTGTAATATCAGAAATGTGTCTACATTT 2618
Qy 2161 TCTGGAAACGGGCGCGAGGCTGAGATATGATACGAGATAGGGTGGCTTTAGATGTAGC 2220
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Qy 2401 CGGGGCTGTGCTTTTAACTGCTGTGGAAGGGGGTGGGTGTGCGCCCAAAAGAGGAGCT 2460
Db 2859 CGGGGCTGTGCTTTTAACTGCTGTGGAAGGGGGTGGGTGTGCGCCCAAAAGAGGAGCT 2918
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Qy 2521 AGGGTGGCCACAATGTGGGCTCGGACTGTGTGCTTCAATGCTATGTAAGAAAGGTGGCT 2580
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Qy 2581 GTGATTAAGCATTAACATGATGTGGAACCTGCGAGAGACAGGGGCTCTCAGATCTGAGC 2640
Db 3039 GTGATTAAGCATTAACATGATGTGGAACCTGCGAGAGACAGGGGCTCTCAGATCTGAGC 3098
Qy 2641 TGCTCGAGCGCAACTGTCACTGTCTGAAGCAATTCACGATAGCAGCACTTCGCAAG 2700
Db 3099 TGCTCGAGCGCAACTGTCACTGTCTGAAGCAATTCACGATAGCAGCACTTCGCAAG 3158
Qy 2701 GCTGTGCAAGTGTTTAGCATTAACATCTGACCGGCTGTCTTGTGCAATTTGGGTAAACAGG 2760
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Qy 2941 ATTAGGAACCAAGCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3000
Db 3399 ATTAGGAACCAAGCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3458
Qy 3001 CTGGCCCTGACCCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3052
Db 3459 CTGGCCCTGACCCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3510

RESULT 3

US-08-379-452-43
Sequence 43, Application US/08379452
Patent No. 6040174
GENERAL INFORMATION:
APPLICANT: IMER, Jean-Luc
APPLICANT: MEHTALI, Majid
APPLICANT: PAVRANI, Andrea
TITLE OF INVENTION: DEFECTIVE ADENOVIRUSES AND CORRESPONDING
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESSES:
ADDRESSES: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: 1737 King Street, Suite 500
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22314-2756
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,452
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR94/00624
FILING DATE: 27-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93 06482
FILING DATE: 28-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Dadio, Susan M.
REGISTRATION NUMBER: 40,373
REFERENCE/DOCKET NUMBER: 029395-002
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 35935 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-379-452-43

Query Match 100.0%; Score 3052; DB 3; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGTAGTATTTATACCGGTGAGTTCCTCAAGAGCCACTCTTGATGCCAGCGAGT 60
|||||

Db 459 CGGTAGTATTTATACCGGTGAGTTCCTCAAGAGCCACTCTTGATGCCAGCGAGT 518
Qy 61 AGAGTTTCTCTCGAGCCGCTCCGACACCGGAGCTGAAATGAGACATATATCTTGCC 120
Db 519 AGAGTTTCTCTCGAGCCGCTCCGACACCGGAGCTGAAATGAGACATATATCTTGCC 578
Qy 121 ACGAGGTGTTATACCGAAGAAATGGCCGCACTCTTTTGACACCACTGATCGAAGAG 180
Db 579 ACGAGGTGTTATACCGAAGAAATGGCCGCACTCTTTTGACACCACTGATCGAAGAG 638
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Qy 301 CCGACTCTGATATGTCGAGGATGAGAGGATGATGATGATGATGATGATGATGATGATGAT 360
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Db 819 CCGGTTCTCCGAGCCGCTCACCTTCCGAGACCCGAGACCGGAGAGAGGCT 878
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Qy 541 TGGAGACCCCGGAGCGGTTGAGGCTTGTCTATTAACCGAGAGATACCGGAGAGC 600
Db 999 TGGAGACCCCGGAGCGGTTGAGGCTTGTCTATTAACCGAGAGATACCGGAGAGC 1058
Qy 601 CAGATATATGTTGCTGCTTGTCTATTAAGAGACCTGAGCATGTTGTCTACAGTAA 660
Db 1059 CAGATATATGTTGCTGCTTGTCTATTAAGAGACCTGAGCATGTTGTCTACAGTAA 1118
Qy 661 GAAATTTATGCGAGTGGGTGATGAGTGGGTGTTGGTGGTAAATTTTTTTTAA 720
Db 1119 GAAATTTATGCGAGTGGGTGATGAGTGGGTGTTGGTGGTAAATTTTTTTTAA 1178
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Db 1179 TTTTACGTTTGGTAAAGAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1238
Qy 781 TGAACCTGAGCTGAGCCGAGCCAGAACCGAGACCTGCAAGACCTACCCGCTCTAA 840
Db 1239 TGAACCTGAGCTGAGCCGAGCCAGAACCGAGACCTGCAAGACCTACCCGCTCTAA 1298
Qy 841 AATGGCGCTGCTATCTGAGAGCCCGGACATCACTGTGCTGAGAAATGATAG 900
Db 1299 AATGGCGCTGCTATCTGAGAGCCCGGACATCACTGTGCTGAGAAATGATAG 1358
Qy 901 TAGGATAGCTGATCTCGGCTCTTCTAACAACCTCTGAGATCAACCCGGTGTCC 960
Db 1359 TAGGATAGCTGATCTCGGCTCTTCTAACAACCTCTGAGATCAACCCGGTGTCC 1418
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Db 1419 GCTGTGCCCATTTAAACAGTTGCGTGAAGTGTGGGCTGCGCAAGCTGTGAATG 1478
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Db 1479 TATGAGAGCTTGCTTAAACAGCTGAGCACTTTGAGCTTGAAGCTTAAACGCCCTAG 1538
Qy 1081 GCCATTAAGTAAACCTGATGCGTGTGGTAAACGCTTGTGTTGCTGATGAGT 1140
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1719 GGGCTTGGGAGTGTGGAGATTTTTCGTGCTGTGCTGATCTTGGAACAGAGCTCTAA 1778
1321 CAGTACCTCTGTTTGGAGGTTCTGTGGGGCTCATCCAGGCAAGTTAGTCTGAG 1380
1779 CAGTACCTCTGTTTGGAGGTTCTGTGGGGCTCATCCAGGCAAGTTAGTCTGAG 1838
1381 AATTAAAGAGGATTAACAAGTGGGAATTTGAAAGCTTTTGAATCTGTGTGAGCTGTT 1440
1839 AATTAAAGAGGATTAACAAGTGGGAATTTGAAAGCTTTTGAATCTGTGTGAGCTGTT 1898
1441 TGATTTCTTTGAATCTGGGTCAACAGCGCTTTTCCAGAGAAAGTCAATCAAGACTTTGA 1500
1899 TGATTTCTTTGAATCTGGGTCAACAGCGCTTTTCCAGAGAAAGTCAATCAAGACTTTGA 1958
1501 TTTTTCACACCGGGGGCGCGCTGCGGCTGTGTGCTTTTGAAGTTTAAAGGATTA 1560
1959 TTTTTCACACCGGGGGCGCGCTGCGGCTGTGTGCTTTTGAAGTTTAAAGGATTA 2018
1561 ATGAGAGGAAAGAAACCAATCTGAGCGGGGGGTACCTGTGATTTTCTGGCCATGCACT 1620
2019 ATGAGAGGAAAGAAACCAATCTGAGCGGGGGGTACCTGTGATTTTCTGGCCATGCACT 2078
1621 GTGAGAGCGGTTGTGAGACAAAGAAATCGCTGTCTACTGTGTCTTCCGTCCCGCGGC 1680
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2139 GATTAATCCGACGAG 2198
1741 GCAGAGCCCATGGAACCCGAGAGCGCGCTGTGAGCTCTGTGGAAATGAATGTGTACAGGTG 1800
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2319 AAGGGGGTAAAG 2378
1921 TTTAGCTTAATGACACAGACCGTCTGTAGTGTATTAATTTTCAACAGATCAAGATTAAT 1980
2379 TTTAGCTTAATGACACAGACCGTCTGTAGTGTATTAATTTTCAACAGATCAAGATTAAT 2438
1981 TGCGCTAATGAGCTTGAATCTGTCTGGCCGAGAAATTTCCATAGAGAGAGCTGACCACTTAC 2040
2439 TGCGCTAATGAGCTTGAATCTGTCTGGCCGAGAAATTTCCATAGAGAGAGCTGACCACTTAC 2498
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2101 AGGCGAGATTTGCAAGTACAGAGATCAGCAAACTTGTAAATATCAGGAAATGTGTCTACAT 2160
2559 AGGCGAGATTTGCAAGTACAGAGATCAGCAAACTTGTAAATATCAGGAAATGTGTCTACAT 2618
2161 TCTGGGAAACGGGGCGAGAGTGGAGATTAATCCGAGAGATAGGGTGGCTTTAGATGATGAC 2220
2619 TCTGGGAAACGGGGCGAGAGTGGAGATTAATCCGAGAGATAGGGTGGCTTTAGATGATGAC 2678

2221 ATGATAAATATGTGGCCGGGGGTGCTTGCCATGGAACGGGGGTGTTATTAATGATGTAAG 2280
2679 ATGATAAATATGTGGCCGGGGGTGCTTGCCATGGAACGGGGGTGTTATTAATGATGTAAG 2738
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2521 AGGTGGGCCCAATGTGGCTCCGACTGTGTGCTTCAATGTAGTGAAGAAAGGTGGCT 2580
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RESULT 4
US-09-315-372-1
Sequence 1, Application US/09315372
Patent No. 6057158
GENERAL INFORMATION:
APPLICANT: Chamberlain, Jeffrey S.
APPLICANT: Amalfitano, Andrea
APPLICANT: Hauser, Michael A.
APPLICANT: Kumar-Singh, Rajendra
APPLICANT: Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Medien & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco

STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,372
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/735,609
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-02484
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 35935 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-09-315-372-1

Query Match 100.0%; Score 3052; DB 3; Length 35935;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGTAGTATTTATACCGGTGATTCCTCAAGAGCGCACTTTAGTCCGAGCT 60
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QY 61 AGAGTTTCTCCTCGAGCGCTCCGACACCGGAGCTGAATGACATTTATCTGCC 120
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QY 519 AGAGTTTCTCCTCGAGCGCTCCGACACCGGAGCTGAATGACATTTATCTGCC 578
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 121 ACGAGGATTTATACCGAAGAAATGCGCGCACTTTTGGACCACTGATCGAAGG 180
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QY 579 ACGAGGATTTATACCGAAGAAATGCGCGCACTTTTGGACCACTGATCGAAGG 638
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QY 181 TACTGGCTGATTAATCTTCCACTCTCTAGCCATTTTGAACCACTTACCACTGT 240
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QY 639 TACTGGCTGATTAATCTTCCACTCTCTAGCCATTTTGAACCACTTACCACTGT 698
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QY 361 CCGGTTCTCCGAGACCGCTTCACTTTCGCGGACGCCGAGACCGGAGAGAGGCTT 420
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QY 819 CCGGTTCTCCGAGACCGCTTCACTTTCGCGGACGCCGAGACCGGAGAGAGGCTT 878
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QY 1059 CAGATATTATGTGTTCCGCTTGTATATGAGACCTGCGCATGTTGTCTACAGTAAGT 1118
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QY 1119 GAAATTTATGGGCGGTGGATATGAGTGGGTTGGTGTATATTTTTTTTAAAT 1178
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QY 721 TTTTACAGTTTGTGTTTAAAGATTTGTATGTGATTTTTTTTAAAGGCTGTGTC 780
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QY 1179 TTTTACAGTTTGTGTTTAAAGATTTGTATGTGATTTTTTTTAAAGGCTGTGTC 1238
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QY 781 TGAACCTGAGGCTGAGCCGAGCCAGAACCGAGCTGCAAGACCTACCCGCGCTCTAA 840
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QY 1239 TGAACCTGAGGCTGAGCCGAGCCAGAACCGAGCTGCAAGACCTACCCGCGCTCTAA 1298
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 841 AATGGCGCTGCTATCTTGAGACGCGCCGACATCACTGTGTCTTGAAGATGCAATAGTAG 900
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QY 1299 AATGGCGCTGCTATCTTGAGACGCGCCGACATCACTGTGTCTTGAAGATGCAATAGTAG 1358
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QY 901 TACGGATAGCTGTAATCCGCTCTCTTAAACACACTCTGAGATACACCGCGGTGCC 960
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1359 TACGGATAGCTGTAATCCGCTCTCTTAAACACACTCTGAGATACACCGGTGCC 1418
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 961 GCTGTGCCCATTTAAACCACTTGCCTGAGAGTGTGGGCTGCGCAGCTGTGATG 1020
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QY 1479 TATGAGAGACTTGTCTTACGAGCTGCGCAACTTTTGAATTGAGCTGTAAACGCCCTCAG 1538
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QY 1599 TGATGTAAGTTTAAATAAAGGCTGAGATATGTTTAACTTGATGCGCTGTTAAATGGGGCC 1658
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
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DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
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QY 121 ACCGAGGTGTTATTAACGGAAGAAATGGCCGCGCAGTCTTTTGAACAGCTGATCGAAGAG 180
Db 579 ACCGAGGTGTTATTAACGGAAGAAATGGCCGCGCAGTCTTTTGAACAGCTGATCGAAGAG 638
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QY 1981 TGGGCTAATGAGCTTATCTGTGCGGCGAGAGATTTCAATAGAGACCTGACCACTTAC 2040
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Qy 2281 TTTACTGGCCCCCAATTTTAAAGCGGTCTTGAGCATGACGGGGGTGTATTAATGAATGAAG 2340
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Qy 2641 TGCTCGGACGGCAATCTGACCTGTGAAAGCAATTCAGTAGGACGACCTCTCGCAAG 2700
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RESULT 6
US-09-245-497-1

Sequence 1, Application US/09245497
Patent No. 6083750
GENERAL INFORMATION:
APPLICANT: Chamberlain, Jeffrey S.
APPLICANT: Amalfitano, Andrea
APPLICANT: Hauser, Michael A.
APPLICANT: Kumar-Singh, Rajendra
APPLICANT: Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:

ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/245,497
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/735,609
APPLICATION NUMBER: FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-02484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 35935 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-09-245-497-1

Query Match 100.0%; Score 3052; DB 3; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 819 CCGGTTTCTCCGAGCGCCCTCACTTTTCCGCGAGCCCGAGACCCGAGAGAGAGCT 878
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Qy 481 CTGGCTTTCACCGAGTGAAGAGAGATGAAGAGGTGAGAGTTGTGTTAGATTATG 540
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TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medien & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/562,919
FILING DATE: 02-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/735,609
FILING DATE: 23-Oct-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-02484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8538
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 35935 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-562-919-1
Query Match 100.0%; Score 3052; DB 3; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2881 GTGCTGAGTACGATGAGACCCGACCAAGGTGACAGCCCTGAGTGTGGGGTAAACAT 2940
DB 3339 GTGCTGAGTACGATGAGACCCGACCAAGGTGACAGCCCTGAGTGTGGGGTAAACAT 3398
QY 2941 ATTAGAAACAGCCTGTGATGCTGATGTGAACGAGAGCTGAGGCGCCGATCACTGGTG 3000
DB 3399 ATTAGAAACAGCCTGTGATGCTGATGTGAACGAGAGCTGAGGCGCCGATCACTGGTG 3458
QY 3001 CTGGCTGACCCGCGCTGAGTGTGCTCTAGCGATGAAGATTAAGATTGAG 3052
DB 3459 CTGGCTGACCCGCGCTGAGTGTGCTCTAGCGATGAAGATTAAGATTGAG 3510

RESULT 9
US-09-956-335-1
; Sequence 1, Application US/09956335
; Patent No. 6627190
; GENERAL INFORMATION:
; APPLICANT: WOLD, William
; APPLICANT: TOTH, Karoly
; APPLICANT: KUPPASHAMI, Mohan
; APPLICANT: DORONIN, Konstantin
; TITLE OF INVENTION: RECOMBINANT ADENOVIRUS VECTORS THAT ARE
; FILE REFERENCE: 16153-8394
; CURRENT APPLICATION NUMBER: US/09/956,335
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 35978
; TYPE: DNA
; ORGANISM: Adenovirus
US-09-956-335-1

Query Match 100.0%; Score 3052; DB 4; Length 35978;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTGTAGTATTTTAAACCGGAGTCTCTCAAGAGCCACTTTGAGTCCAGCGAGT 60
DB 459 CGTGTAGTATTTTAAACCGGAGTCTCTCAAGAGCCACTTTGAGTCCAGCGAGT 518
QY 61 AGATTTTCTCTCCGAGCGGCTCCGACACCGGGACTGAAATAGACATTAATCTGGCC 120
DB 519 AGATTTTCTCTCCGAGCGGCTCCGACACCGGGACTGAAATAGACATTAATCTGGCC 578
QY 121 ACGAGGTGTTATTAACGAAAGAAATGCGCGCACTTTTGAACAGGTGATGCAAGAG 180
DB 579 ACGAGGTGTTATTAACGAAAGAAATGCGCGCACTTTTGAACAGGTGATGCAAGAG 638
QY 181 TACTGGCTGATATCTTCACTCTTACGCAATTTTGAACCACTTACCTTCAAGACTGT 240
DB 639 TACTGGCTGATATCTTCACTCTTACGCAATTTTGAACCACTTACCTTCAAGACTGT 698
QY 241 ATGATTTAGAGTGAACGCGCCCGAAGATCCCAACGAGAGGCGGTTTGCAGATTTTTC 300

Db 699 ATGATTTAGAGTGCAGCGCCCGGAGATCCCAACGAGAGCGGTTTCGCAATTTTTC 758
Qy 301 CCGACTCTGTAAATGTGGCGGTGCAGAGAGATTGACTTAATCTACTTTTCCCGCGCGC 360
Db 759 CCGACTCTGTAAATGTGGCGGTGCAGAGAGATTGACTTAATCTACTTTTCCCGCGCGC 818
Qy 361 CCGGTTCTCGGAGCGGCTCACCTTCCCGGAGCCCGAGCAGCGGAGAGAGAGCT 420
Db 819 CCGGTTCTCGGAGCGGCTCACCTTCCCGGAGCCCGAGCAGCGGAGAGAGCT 878
Qy 421 TGGTCCGGTTTCTATGCAAACTTGTACCGAGGTGATCGATCTTAACCTGCCAGAG 480
Db 879 TGGTCCGGTTTCTATGCAAACTTGTACCGAGGTGATCGATCTTAACCTGCCAGAG 938
Qy 481 CTGGCTTTCCACCAGAGAGAGAGAGATGAAAGGGGTGAGAGATTGTGTAAATTAATG 540
Db 939 CTGGCTTTCCACCAGAGAGAGAGAGATGAAAGGGGTGAGAGATTGTGTAAATTAATG 998
Qy 541 TGGAGCACCCCGGAGCAGGTTGCAGGCTTGTCTATTAACCGGAGGAAATACGGGGAGC 600
Db 999 TGGAGCACCCCGGAGCAGGTTGCAGGCTTGTCTATTAACCGGAGGAAATACGGGGAGC 1058
Qy 601 CAGATTAATATGTGTCTTGTCTATAAGAGACCTGTGCATGTTGTCTACAGTAAGT 660
Db 1059 CAGATTAATATGTGTCTTGTCTATAAGAGACCTGTGCATGTTGTCTACAGTAAGT 1118
Qy 661 GAAATTAATGGGCGATGGGTGATAGATGTGGGTTGGTGTGTATTTTTTTTTTAAAT 720
Db 1119 GAAATTAATGGGCGATGGGTGATAGATGTGGGTTGGTGTGTATTTTTTTTTTAAAT 1178
Qy 721 TTTTACAGTTTGTGTTTAAAGAAATTTGTATGTGATTTTTTTTAAAGGCTCTGTGC 780
Db 1179 TTTTACAGTTTGTGTTTAAAGAAATTTGTATGTGATTTTTTTTAAAGGCTCTGTGC 1238
Qy 781 TGAACCTGAGCTGAGCCCGAGCCAGAACCGGAGCTTGCAGAGCTACCCGCGCTCTAA 840
Db 1239 TGAACCTGAGCTGAGCCCGAGCCAGAACCGGAGCTTGCAGAGCTACCCGCGCTCTAA 1298
Qy 841 AATGGCCGCTGCTATCTTGAGACGCGCGACATCACTGTGCTAGAGAAATGCAATTAATG 900
Db 1299 AATGGCCGCTGCTATCTTGAGACGCGCGACATCACTGTGCTAGAGAAATGCAATTAATG 1358
Qy 901 TACGATAGCTGTACTCCGGCTCTTCTAACACACACTCTGAGATACACCGGAGTCCC 960
Db 1359 TACGATAGCTGTACTCCGGCTCTTCTAACACACTCTGAGATACACCGGAGTCCC 1418
Qy 961 GCTGTGCCCAATTAACCAAGTTCGCTGAGAGTTGTGGGCGTCCGACGCTGTGAATG 1020
Db 1419 GCTGTGCCCAATTAACCAAGTTCGCTGAGAGTTGTGGGCGTCCGACGCTGTGAATG 1478
Qy 1021 TATCGAGAGACTTGTCTTAACGAGCCTGGGCAACTTTGGACTTGAAGCTGTAAACGCCCAG 1080
Db 1479 TATCGAGAGACTTGTCTTAACGAGCCTGGGCAACTTTGGACTTGAAGCTGTAAACGCCCAG 1538
Qy 1081 GCCATTAAGTGTAAACCTGTATGCGTGTGTGTTAACGCTTGTGTGTGATGATG 1140
Db 1539 GCCATTAAGTGTAAACCTGTATGCGTGTGTGTTAACGCTTGTGTGTGATGATG 1598
Qy 1141 TGATGTAAATTAATTAAGGAGTGAATGTTTAACCTGATGAGCGCTTTAAATGGGCGC 1200
Db 1599 TGATGTAAATTAATTAAGGAGTGAATGTTTAACCTGATGAGCGCTTTAAATGGGCGC 1658
Qy 1201 GGGGCTTAAGGAGTATTAATGCGCGGCGCTAATCTTGGTTAATCTGACCTCAATGGA 1260
Db 1659 GGGGCTTAAGGAGTATTAATGCGCGGCGCTAATCTTGGTTAATCTGACCTCAATGGA 1718
Qy 1261 GGCTTGGAGAGTGTGGAAGATTTTCTGTGTGCTTAATCTTGTGGAACAGACTCTAA 1320
Db 1719 GGCTTGGAGAGTGTGGAAGATTTTCTGTGTGCTTAATCTTGTGGAACAGACTCTAA 1778
Qy 1321 CAGTACCTTTGTGTTTGGAGGTTTCTGTGGGCTCATCCAGGCAAGTTAATGTCTGAG 1380
Db 1779 CAGTACCTTTGTGTTTGGAGGTTTCTGTGGGCTCATCCAGGCAAGTTAATGTCTGAG 1838

Qy 1381 AATTAAGAGAGATTACAGATGGGAAATTTGAAGCTTTTGAATTCCTGTGTGAGCTGTT 1440
Db 1839 AATTAAGAGAGATTACAGATGGGAAATTTGAAGCTTTTGAATTCCTGTGTGAGCTGTT 1898
Qy 1441 TGATTTCTTGAATCTGGGTACCAAGCGCTTTTCAAGAGAGGTCAATCAACTTTTGA 1500
Db 1899 TGATTTCTTGAATCTGGGTACCAAGCGCTTTTCAAGAGAGGTCAATCAACTTTTGA 1958
Qy 1501 TTTTTCACACCCGGGCGCGCTGCGTGTGCTTTTGTAGTTTATTAAGATTA 1560
Db 1959 TTTTTCACACCCGGGCGCGCTGCGTGTGCTTTTGTAGTTTATTAAGATTA 2018
Qy 1561 ATGAGCGAAGAAACCCATCTGAGCGGGGGTACTGCTGGAATTTTTCGCGCATGACT 1620
Db 2019 ATGAGCGAAGAAACCCATCTGAGCGGGGGTACTGCTGGAATTTTTCGCGCATGACT 2078
Qy 1621 GTGAGAGCGGTTGTGAGACAAAGATTCGCTGTGCTTCCGTCCGCGCGC 1680
Db 2079 GTGAGAGCGGTTGTGAGACAAAGATTCGCTGTGCTTCCGTCCGCGCGC 2138
Qy 1681 GATTAATCCGACGAGAGAGACAGACAGCAGCAGAGAGAAACCGGCGCGCGCAGGA 1740
Db 2139 GATTAATCCGACGAGAGAGAGACAGACAGCAGAGAGAAACCGGCGCGCGCAGGA 2198
Qy 1741 GCAGAGCCCATGGAAACCGAGAGCGGCGCTGGAAACCTCGGGAAATGAATGTTTACAGGTG 1800
Db 2199 GCAGAGCCCATGGAAACCGAGAGCGGCGCTGGAAACCTCGGGAAATGAATGTTTACAGGTG 2258
Qy 1801 GCTGAACCTGTATCCAGAACTGAGACGCAATTTTGCATTAACAGAGATGGGCAAGGCTA 1860
Db 2259 GCTGAACCTGTATCCAGAACTGAGACGCAATTTTGCATTAACAGAGATGGGCAAGGCTA 2318
Qy 1861 AAGGGGTAAAGAGAGAGCGGGGCGTTGTGAGCTTACAGAGAGCTTAGGAATCTAGCT 1920
Db 2319 AAGGGGTAAAGAGAGAGCGGGGCGTTGTGAGCTTACAGAGAGCGCTAGGAATCTAGCT 2378
Qy 1921 TTTTACCTTAATGACCAAGACCCGCTGAGGTATTCTTTTCAACAGATCAAGATTAAT 1980
Db 2379 TTTTACCTTAATGACCAAGACCCGCTGAGGTATTCTTTTCAACAGATCAAGATTAAT 2438
Qy 1981 TGGCCTAATGAGCTTGAATCTGTGCGCGCAGAAATTTCAATAGACGCTGACCACTTAC 2040
Db 2439 TGGCCTAATGAGCTTGAATCTGTGCGCGCAGAAATTTCAATAGACGCTGACCACTTAC 2498
Qy 2041 TGGCTGAGCCAGGGGATGATTTTGAAGAGCTTATGAGGTATATGCAAGGTGGCACTT 2100
Db 2499 TGGCTGAGCCAGGGGATGATTTTGAAGAGCTTATGAGGTATATGCAAGGTGGCACTT 2558
Qy 2101 AGGCGAATTTGCAAGTACAAATCAGCAAACTTGTAAATATCAGGAATGTTGCTACATT 2160
Db 2559 AGGCGAATTTGCAAGTACAAATCAGCAAACTTGTAAATATCAGGAATGTTGCTACATT 2618
Qy 2161 TCTGGGAACCGGGCCGAGGTGAGATGATACGAGAGATAGGGTGCCTTTAGATGATG 2220
Db 2619 TCTGGGAACCGGGCCGAGGTGAGATGATACGAGAGATAGGGTGCCTTTAGATGATG 2678
Qy 2221 ATGATTAATATGTGCGCGGGGCTTGTGCAATGACCGGGTGTATTAATGAATGTAAG 2280
Db 2679 ATGATTAATATGTGCGCGGGGCTTGTGCAATGACCGGGTGTATTAATGAATGTAAG 2738
Qy 2281 TTTTACGGCCCAATTTTACGGGTACGGTTCCTGTGCAATACCAACTTATCTTACAC 2340
Db 2739 TTTTACGGCCCAATTTTACGGGTACGGTTCCTGTGCAATACCAACTTATCTTACAC 2798
Qy 2341 GGTGTAAAGCTTCTATATGGGTTTAAACAATACCTGTGTGGAAGCTGTGAAGGTT 2400
Db 2799 GGTGTAAAGCTTCTATATGGGTTTAAACAATACCTGTGTGGAAGCTGTGAAGGTT 2858
Qy 2401 CCGGCGCTGTGCTTTTATCTGCTGTGGAAGGGGTGTGTGTGCTCCCAAAAGCAGGCT 2460
Db 2859 CCGGCGCTGTGCTTTTATCTGCTGTGGAAGGGGTGTGTGTGCTCCCAAAAGCAGGCT 2918

QY 2461 TCAATTAAGAAATGCTTTGAAAGGTGTAACCTTGGGTATCTGTCTGAGGTTAACTCC 2520
 DB 2519 TCAATTAAGAAATGCTTTGAAAGGTGTAACCTTGGGTATCTGTCTGAGGTTAACTCC 2978
 QY 2521 AGGGTGGCCCAATGATGAGCTTCCGACTGATGATGCTTCACTAGTAAAGAGGCT 2580
 DB 2979 AGGGTGGCCCAATGATGAGCTTCCGACTGATGATGCTTCACTAGTAAAGAGGCT 3038
 QY 2581 GTGATTAAGCATTAATGATGATGAGCACTGCGAGACAGAGGCTCTCAGATCTGACC 2640
 DB 3039 GTGATTAAGCATTAATGATGATGAGCACTGCGAGACAGAGGCTCTCAGATCTGACC 3098
 QY 2641 TGCCTCGAAGCGCAATGCTGCACTGCTGAAAGACATGACGTAAGCAGCAGCATCTCGCAG 2700
 DB 3099 TGCCTCGAAGCGCAATGCTGCACTGCTGAAAGACATGACGTAAGCAGCAGCATCTCGCAG 3158
 QY 2701 GCCCTGCGCAAGTGTGAGCATTAACATACTGACCCGCTGTCTTGGATTTGGATTAACAG 2760
 DB 3159 GCCCTGCGCAAGTGTGAGCATTAACATACTGACCCGCTGTCTTGGATTTGGATTAACAG 3218
 QY 2761 AGGGGGGTGTTCTTACCTTACCAATGCAATTTGAGTCACTAAGATATTGCTTGAAGCCC 2820
 DB 3219 AGGGGGGTGTTCTTACCTTACCAATGCAATTTGAGTCACTAAGATATTGCTTGAAGCCC 3278
 QY 2821 GAGGAGCATGTCGCAAGTGAACCTGAACGGGGTGTGATGATGACATTAAGATATTGCTTGAAG 2880
 DB 3279 GAGGAGCATGTCGCAAGTGAACCTGAACGGGGTGTGATGATGACATTAAGATATTGCTTGAAG 3338
 QY 2881 GTGCTGAGTGAATGAGTGAACCCGACACGAGTGAACCTGCGAGTGTGGGGTAAACAT 2940
 DB 3339 GTGCTGAGTGAATGAGTGAACCCGACACGAGTGAACCTGCGAGTGTGGGGTAAACAT 3398
 QY 2941 ATTAGAACAACGCTGTGATGCTGATGATGAACGAGAGTGAAGCCGATCACTTGGTGTG 3000
 DB 3399 ATTAGAACAACGCTGTGATGCTGATGATGAACGAGAGTGAAGCCGATCACTTGGTGTG 3458
 QY 3001 CTGGCCCTGCAACCCGCGCTGAGTGTGCTCTAGCGATGAAGTAAAGATTGAG 3052
 DB 3459 CTGGCCCTGCAACCCGCGCTGAGTGTGCTCTAGCGATGAAGTAAAGATTGAG 3510

RESULT 10
 US-09-714-550-18
 ; Sequence 18, Application US/09714550
 ; Patent No. 6558948
 ; GENERAL INFORMATION:
 ; APPLICANT: Kochanek, Stefan
 ; APPLICANT: Schliedner, Gudrun
 ; TITLE OF INVENTION: Permanent amniocytic cell line, its
 ; TITLE OF INVENTION: production and use for the production of gene transfer
 ; FILE REFERENCE: 50125/007002
 ; CURRENT APPLICATION NUMBER: US/09/714,550
 ; CURRENT FILING DATE: 2000-11-16
 ; PRIOR APPLICATION NUMBER: US 60/167,439
 ; PRIOR FILING DATE: 1999-11-23
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 18
 ; LENGTH: 7090
 ; TYPE: DNA
 ; ORGANISM: P1asmid STR146
 ; US-09-714-550-18

Query Match 98.5%; Score 3006.8; DB 4; Length 7090;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 3008; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 43 TCTTGAATGCGCAGGAGTGAAGTTTCTCTCGAGCGCTCCGACACCGGAGTGAATA 102
 DB 2749 TATGAGATGCGCAGGAGTGAAGTTTCTCTCGAGCGCTCCGACACCGGAGTGAATA 2808
 QY 103 TGAGACATATTATCTGCGCAGGAGTGTATTACCGAAGAAATGGCCGCAAGTCTTTGG 162

DB 2809 TGAGACATATTATCTGCGCAGGAGTGTATTACCGAAGAAATGGCCGCAAGTCTTTGG 2868
 QY 163 ACCAGCTGATGAGAGGATCTGCTGATTAATCTTCAACCTCTAGCCATTGTAACAC 222
 DB 2869 ACCAGCTGATGAGAGGATCTGCTGATTAATCTTCAACCTCTCTAGCCATTGTAACAC 2928
 QY 223 CTACCTTTCACGAACTGATGATTTAAGACGTGACGGCCCCCGAAGATCCACAGAGAGG 282
 DB 2929 CTACCTTTCACGAACTGATGATTTAAGACGTGACGGCCCCCGAAGATCCACAGAGAGG 2988
 QY 283 CGGTTTGGCAGATTTTCCGACCTCTGTAATGTTGGGGGTGACAGAGAGGTTGACTTAC 342
 DB 2989 CGGTTTGGCAGATTTTCCGACCTCTGTAATGTTGGGGGTGACAGAGAGGTTGACTTAC 3048
 QY 343 TCACCTTTCGCGCCGCGCCCGGTTCTCGAGAGCCGCTCACTTCCCGAGCCGAGC 402
 DB 3049 TCACCTTTCGCGCCGCGCCCGGTTCTCGAGAGCCGCTCACTTCCCGAGCCGAGC 3108
 QY 403 AGCCGAGCAGAGAGCCTTGGGTCCGATTTCTATGCAAACTTGTACCGAGGTGATCG 462
 DB 3109 AGCCGAGCAGAGAGCCTTGGGTCCGATTTCTATGCAAACTTGTACCGAGGTGATCG 3168
 QY 463 ATCTTACCTGCGCAGAGGCTGCTTCCACCACTGACGACGAGATGAAGAGGTGAGG 522
 DB 3169 ATCTTACCTGCGCAGAGGCTGCTTCCACCACTGACGACGAGATGAAGAGGTGAGG 3228
 QY 523 AGTTGTGTTAGATTATGTTGAGACACCCCGGCGACGAGTGAAGGCTTGTGATATCAC 582
 DB 3229 AGTTGTGTTAGATTATGTTGAGACACCCCGGCGACGAGTGAAGGCTTGTGATATCAC 3288
 QY 583 GAGAGAAATACGGGGGACCCAGATTTATGTTGCTTGTGCTTGTATGAGACCTGTGCA 642
 DB 3289 GAGAGAAATACGGGGGACCCAGATTTATGTTGCTTGTGCTTGTATGAGACCTGTGCA 3348
 QY 643 TGTTTGCTACAGTAATGAAATTAAGCGAGTGTGATGAGTGTGCTTGTGCT 702
 DB 3349 TGTTTGCTACAGTAATGAAATTAAGCGAGTGTGATGAGTGTGCTTGTGCT 3408
 QY 703 GGTAAATTTTATTTTATTTTAACTGTTTGTGTTAAAGATTTTGTATGATTTT 762
 DB 3409 GGTAAATTTTATTTTATTTTAACTGTTTGTGTTAAAGATTTTGTATGATTTT 3468
 QY 763 TTTAAAGTCTGTTGTTGTAACCTGAGCCTGAGCCGAGCAGAACCGAGCCTGCAAG 822
 DB 3469 TTTAAAGTCTGTTGTTGTAACCTGAGCCTGAGCCGAGCAGAACCGAGCCTGCAAG 3528
 QY 823 ACCTACCCGCGCTCTAAATATGAGGCTGCTGATCTCTGAGACGCCGACATCACTGTGTC 882
 DB 3529 ACCTACCCGCGCTCTAAATATGAGGCTGCTGATCTCTGAGACGCCGACATCACTGTGTC 3588
 QY 883 TAGAGATGCAATGATGATGAGTACGATGATGATGATGATGATGATGATGATGATGATGAT 942
 DB 3589 TAGAGATGCAATGATGATGAGTACGATGATGATGATGATGATGATGATGATGATGATGAT 3648
 QY 943 GATACACCGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1002
 DB 3649 GATACACCGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3708
 QY 1003 TCGCAGAGCTGTGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1062
 DB 3709 TCGCAGAGCTGTGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3768
 QY 1063 GAGCTGTAAACGCCCGCAGGCAATGAGTGAACCTGTGATGATGATGATGATGATGATGATGAT 1122
 DB 3769 GAGCTGTAAACGCCCGCAGGCAATGAGTGAACCTGTGATGATGATGATGATGATGATGATGAT 3828
 QY 1123 TTTGTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1182
 DB 3829 TTTGTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3888
 QY 1183 TGGGCTGTTAAATGAGGCGGAGGCTTAAAGGATATTAATGCGCGGTGAGTATCTTGGT 1242

Db 3889 TGGCGTGTAAATGGGGCGGGGCTTAAAGGGTATATATATGCGCCGTGGGCTAATCTTGCT 3948
Qy 1243 TACATCTGACCTCATGGAAGGCTTGGAGTGTCTTTGGAGATTTTTCGTGCTGCGTAATCTT 1302
Db 3949 TACATCTGACCTCATGGAAGGCTTGGAGTGTCTTTGGAGATTTTTCGTGCTGCGTAATCTT 4008
Qy 1303 GCTGGAACAGAGCTCTAACAGTACCTCTTGCTTTTGGAGTTCGTGCGGCTCATCCCA 1362
Db 4009 GCTGGAACAGAGCTCTAACAGTACCTCTTGCTTTTGGAGTTCGTGCGGCTCATCCCA 4068
Qy 1363 GCGAAAGTTAGTCTGCGAATTTAAGAGATTACAGTGGGAATTTGAAAGCTTTTGA 1422
Db 4069 GCGAAAGTTAGTCTGCGAATTTAAGAGATTACAGTGGGAATTTGAAAGCTTTTGA 4128
Qy 1423 ATCTGTGTGTAAGCTGTGTGATTTCTTTGAATCTGGGTCAACAGGCGCTTTTCCAAAGAA 1482
Db 4129 ATCTGTGTGTAAGCTGTGTGATTTCTTTGAATCTGGGTCAACAGGCGCTTTTCCAAAGAA 4188
Qy 1483 GGTGATCAAGACTTTGGAATTTTCCACACCGGGGCGCTGCGGCTGCTGTGCTTTT 1542
Db 4189 GGTGATCAAGACTTTGGAATTTTCCACACCGGGGCGCTGCGGCTGCTGTGCTTTT 4248
Qy 1543 GAGTTTATAAAGATTAATGAGCGAAGAAACCCATCTGAGCGGGGGTACCTGTGGA 1602
Db 4249 GAGTTTATAAAGATTAATGAGCGAAGAAACCCATCTGAGCGGGGGTACCTGTGGA 4308
Qy 1603 TTTTCTGGCCATGATCTGTGTGAGAGCGGTGTGTGACACAAAGATCCCTGTGCTA 1662
Db 4309 TTTTCTGGCCATGATCTGTGTGAGAGCGGTGTGTGACACAAAGATCCCTGTGCTA 4368
Qy 1663 GTCTTCGCTCCGCGCGGATATATCCGACGAGAGACAGAGACAGAGAGAGAAAGC 1722
Db 4369 GTCTTCGCTCCGCGCGGATATATCCGACGAGAGAGACAGAGACAGAGAGAGAAAGC 4428
Qy 1723 CAGCGCGCGCGGAG 1782
Db 4429 CAGCGCGCGCGGAG 4488
Qy 1783 ATGAAATGTGTAACAGTGTGCTGAACTGTATCCAGAACTGAAACCATTTTGAACA 1842
Db 4489 ATGAAATGTGTAACAGTGTGCTGAACTGTATCCAGAACTGAAACCATTTTGAACA 4548
Qy 1843 GAGGATGGGACAGGGGCTTAAAGGGGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAG 1902
Db 4549 GAGGATGGGACAGGGGCTTAAAGGGGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAG 4608
Qy 1903 GAGGCTAGGAATCTAGCTTTTAGCTTAAATGACACAGACACCGTCTGAGTGTATTA 1962
Db 4609 GAGGCTAGGAATCTAGCTTTTAGCTTAAATGACACAGACACCGTCTGAGTGTATTA 4668
Qy 1963 CAACAGATCAAGGATTAATTTGGGCTAATGAGCTTGAATCTGCTGGGCGAAGATTTCCA 2022
Db 4669 CAACAGATCAAGGATTAATTTGGGCTAATGAGCTTGAATCTGCTGGGCGAAGATTTCCA 4728
Qy 2023 GAGGAGCTGACCACTTACTGCTGCGAGCCAGGGGATGATTTTGGAGAGGCTATTAGGGTA 2082
Db 4729 GAGGAGCTGACCACTTACTGCTGCGAGCCAGGGGATGATTTTGGAGAGGCTATTAGGGTA 4788
Qy 2083 TATGCAAAAGGTGGCACTTAGGCGCAGATTTGCAAGTACAGCAAACTTTGAATATC 2142
Db 4789 TATGCAAAAGGTGGCACTTAGGCGCAGATTTGCAAGTACAGCAAACTTTGAATATC 4848
Qy 2143 AGGAATTTGCTCTAATTTCTGGGAAAGGGGCGAGGTGTGAGATGATGATGATGATGATG 2202
Db 4849 AGGAATTTGCTCTAATTTCTGGGAAAGGGGCGAGGTGTGAGATGATGATGATGATGATG 4908
Qy 2203 GTGGCCCTTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2262
Db 4909 GTGGCCCTTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4968
Qy 2263 GTTATTTATGAATGTAAAGTTTATCTGGCCCAATTTTACGGGTACGGTTCCTGGCCAT 2322
Db 4969 GTTATTTATGAATGTAAAGTTTATCTGGCCCAATTTTACGGGTACGGTTCCTGGCCAT 5028

Qy 2323 ACCAACCTTATCCACAGCGGTGTAGCTTCTATGSGTTTAAACAATACCTGTGTGAAGCC 2382
Db 5029 ACCAACCTTATCCACAGCGGTGTAGCTTCTATGSGTTTAAACAATACCTGTGTGAAGCC 5088
Qy 2383 TGGACCGATGTAAAGGGTTCGGGGCTGTGCTTTTATCTGCTGTGGAAGGGGGTGTGT 2442
Db 5089 TGGACCGATGTAAAGGGTTCGGGGCTGTGCTTTTATCTGCTGTGGAAGGGGGTGTGTGT 5148
Qy 2443 CGCCCCAAAAGCAGGGCTTCAATTAAGAAATGCTCTTTTGAAGGTGTACCTTGGGTATC 2502
Db 5149 CGCCCCAAAAGCAGGGCTTCAATTAAGAAATGCTCTTTTGAAGGTGTACCTTGGGTATC 5208
Qy 2503 CTGTCTAGGGGTAACTCCAGGGTGGCCACAAATGTGACTCCGACTGTGTTGCTTCATG 2562
Db 5209 CTGTCTAGGGGTAACTCCAGGGTGGCCACAAATGTGACTCCGACTGTGTTGCTTCATG 5268
Qy 2563 CTAGTAAAGCGGTGTGTGATTTAAGCATTAACATGATGTGTGCAACTGCGAGAACAG 2622
Db 5269 CTAGTAAAGCGGTGTGTGATTTAAGCATTAACATGATGTGTGCAACTGCGAGAACAG 5328
Qy 2623 GCTCTCAATGCTGACCTGTGAGAGGCACTGTCACTGCTGAAGACATTCAGTA 2682
Db 5329 GCTCTCAATGCTGACCTGTGAGAGGCACTGTCACTGCTGAAGACATTCAGTA 5388
Qy 2683 GCCAGCAGCTCTGCAAGAGGCTGGCAGTGTGAGCATTAACATGACTGACCCGCTGTTCC 2742
Db 5389 GCCAGCAGCTCTGCAAGAGGCTGGCAGTGTGAGCATTAACATGACTGACCCGCTGTTCC 5448
Qy 2743 TTGCATTTGGGTAAACAGAGGGGGGTGTTCTTACTTAACAAATGCAATTTGATGACACT 2802
Db 5449 TTGCATTTGGGTAAACAGAGGGGGGTGTTCTTACTTAACAAATGCAATTTGATGACACT 5508
Qy 2803 AAGATATTGCTTGAAGCCCGAAGATGTCCAAGTTGAACCTGAAACGGGGTCTTGAATG 2862
Db 5509 AAGATATTGCTTGAAGCCCGAAGATGTCCAAGTTGAACCTGAAACGGGGTCTTGAATG 5568
Qy 2863 ACCATGAAGATCTGGAAGGTGTGAGGTAGATGAGACCCGACCAAGGTGAGAGACCTGC 2922
Db 5569 ACCATGAAGATCTGGAAGGTGTGAGGTAGATGAGACCCGACCAAGGTGAGAGACCTGC 5628
Qy 2923 GAGTGTGGCGGTAAACATTAATTAGGAACCAAGCTGTGTGATGTGACCGAGAGCTG 2982
Db 5629 GAGTGTGGCGGTAAACATTAATTAGGAACCAAGCTGTGTGATGTGACCGAGAGACCTG 5688
Qy 2983 AGGCGCGATCACTTGTGTGTGCTGTGACCCGCGCTGAATTTGGCTTACGAGTAAGAT 3042
Db 5689 AGGCGCGATCACTTGTGTGTGCTGTGACCCGCGCTGAATTTGGCTTACGAGTAAGAT 5748
Qy 3043 ACAGATTGAG 3052
Db 5749 ACAGATTGAG 5758

RESULT 11
US-09-956-335-2
; Sequence 2, Application US/09956335
; Patent No. 6627190
; GENERAL INFORMATION:
; APPLICANT: WOLD, William
; APPLICANT: TOTH, Karoly
; APPLICANT: KUPPASMAMI, Mohan
; APPLICANT: DORONIN, Konstantin
; TITLE OF INVENTION: RECOMBINANT ADENOVIRUS VECTORS THAT ARE
; FILE REFERENCE: 16153-8394
; CURRENT APPLICATION NUMBER: US/09/956,335
; CURRENT FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 35871
; TYPE: DNA

ORGANISM: Adenovirus
US-09-956-335-2

Query Match 92.5%; Score 2822; DB 4; Length 35871;
Best Local Similarity 96.6%; Pred. No. 0;
Matches 2947; Conservative 0; Mismatches 0; Indels 105; Gaps 2;

QY 1 CGGTAGTATTTATATACCGCGTGAAGTTCCTCAAGAGGCCACTCTTGAGTCCAGCGAGT 60
DB 459 CGGTAGTATTTATATACCGCGTGAAGTTCCTCAAGAGGCCACTCTTGAGTCCAGCGAGT 518
QY 61 AGAGTTTCTCTCCGAGCGGCTCGACACCGGGGCTGAATATGACATATATCTGCC 120
DB 519 AGAGTTTCTCTCCGAGCGGCTCGACACCGGGGCTGAATATGACATATATCTGCC 568
QY 121 ACGAGGTGTTATTAACGAGAAATGGCCGCGCAGTCTTTTGACCAAGCTGATCGAAGNG 180
DB 569 -----GAGG 572
QY 181 TACTGCGTATATATCTTCCACTCTCTAGCCATTTTGAAACCACTTACCTTACGAACTGT 240
DB 573 TACTGCGTATATATCTTCCACTCTCTAGCCATTTTGAAACCACTTACCTTACGAACTGT 632
QY 241 ATGATTTAGACGTACCGCCCCCGAAGATCCCAACGAGAGCGGTTTGGAGATTTTTC 300
DB 633 ATGATTTAGACGTACCGCCCCCGAAGATCCCAACGAGAGCGGTTTGGAGATTTTTC 692
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QY 481 CTGCGCTTCCACCGACGTACGACGAGATGAAGAGGTGAGAGATTTGTATGATTAATG 540
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DB 894 TGGAGCACCCCGGGGCGAGGTGCAAGTCTTGTCAATATCACCGAGAAATACGGGGGACC 953
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DB 1314 GCTGTGCCCATTAACCAAGTTGCGGTGAGAGTTGTGGGCGTGCAGAGCTGTGAATG 1373
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QY 1141 TGATGATTAATTAAGGGTGAATATATTTTAACTTGATGGCGTGAATATGAGGC 1200
DB 1494 TGATGATTAATTAAGGGTGAATATATTTTAACTTGATGGCGTGAATATGAGGC 1553
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DB 2334 TGGGCTATATGAGCTTGTATGCTGTGGCGAGAAATTCATATGAGAGCTGACCACTTAC 2393
QY 2041 TGGCTGACCGCAGGAGATGATTTTGAAGAGCTTAAAGGATATATGCAAGGTGGCACTT 2100
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2514 TCTGGGAAACGGGGCCGAGAGTGAAGATAGATA CGAGAGATAGAGGTGCGCTTTAGA TGTAGC 2573
2221 ATGATTAATATAGTGGCCGGGGGGTGTGGCATGGA CGGGGGTGTATTATTAATGAATGTAAAG 2280
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3001 CTGGCCCTGACCCCGCGCTGAGTTTGGCTCTAGCGATGGAATGAGATTGAG 3052
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RESULT 12
US-08-735-609-4

; Sequence 4, Application US/08735609

; Patent No. 5955360

; GENERAL INFORMATION:

; APPLICANT: Chamberlain, Jeffrey S.

; APPLICANT: Amalfitano, Andrea

APPLICANT: Hauser, Michael A.
APPLICANT: Kumar-Singh, Rajendra
APPLICANT: Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/735,609
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
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REFERENCE/DOCKET NUMBER: UM-02484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 34303 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-08-735-609-4

Query Match 70.8%; Score 2161; DB 2; Length 34303;

Best Local Similarity 100.0%; Pred. No. 0; Matches 2161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 952 GGTGTCCTCCGTCGTCCTTAAACCAAGTTCCTGTGAGAGTGTGTGGCGTCCGACAGGC 1011
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DB 2973 TGTGGAATGTATGAGAGACTTGTGCTTAACGAGCCGTGGGCAACCTTGGACTTGAAGCTGTAA 3072
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 Db ACCACTTACTGCTGAGCGCAGGGGATGATTTTGAAGAGCTATTAGGGTATATGCAAG 4052
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 QY 3052 G 3052
 Db 5013 G 5013

RESULT 13
 US-08-735-609-4
 ; Sequence 4, Application US/08735609
 ; Patent No. 5994132
 ; GENERAL INFORMATION:
 ; APPLICANT: Chamberlain, Jeffrey S.
 ; Amalfitano, Andrea
 ; Hauser, Michael A.
 ; Kumar-Singh, Rajendra
 ; Hartigan-O'Connor, Dennis J.
 ; TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Medlen & Carroll, LLP
 ; STREET: 220 Montgomery Street, Suite 2200
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: United States Of America
 ; ZIP: 94104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/735,609
 ; FILING DATE: 23-Oct-1996
 ; CLASSIFICATION: <Unknown>

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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 34303 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-08-735-609-4

Query Match 70.8%; Score 2161; DB 2; Length 34303;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 892 CAATAGTATGATCGATAGCTGTGACTCCGGTCTTTCTAACAACACCTCTCTGAGATACACC 951
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QY 2332 ATCTTAACAGGTGTAACCTTCTATAGGTTTAAACAATCTGTGTGGAAGCCTGGAACGAT 2391
DB 4293 ATCTTAACAGGTGTAACCTTCTATAGGTTTAAACAATCTGTGTGGAAGCCTGGAACGAT 4352
QY 2392 GTAAGGTTGCGGGCTGTGCTTTTACTGCTGTGGAAGGGGGTGTGTGCGCCCAA 2451
DB 4353 GTAAGGTTGCGGGCTGTGCTTTTACTGCTGTGGAAGGGGGTGTGTGCGCCCAA 4412
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QY 2512 GGTAACTCCAGGGTCCCAATGTGCGCTTCCGACATGTGTGCTTCAATGCTAGTAA 2571
DB 4473 GGTAACTCCAGGGTCCCAATGTGCGCTTCCGACATGTGTGCTTCAATGCTAGTAA 4532
QY 2572 AGCGTGTGATTAAGCATTAATCATGTATGTGGCAACTGCGAGACAGAGGCTCTGAG 2631
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DB 4593 ATGCTGACTGTGCTGAGCGCAACTGTACCTGTGAAGCAATTAACAGACCCAC 4652
QY 2692 TCTGCAAGGCTGCGCAAGTCTTGAACATTAACAATGACCCGCTTCTTGCATTTG 2751
DB 4653 TCTGCAAGGCTGCGCAAGTCTTGAACATTAACAATGACCCGCTTCTTGCATTTG 4712

QY	2752	GGTAACAGAGAGGGGGTTCCTCACTTACCAATGCAATTGAGTCACACTTAAGATTATG	2811
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QY	2812	CTTAAGCCCGAGAGCAATGTCCTCAAGTGAACTGTAAACGGGGGTGTTGACATGACATGAAG	2871
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QY	2872	ATCTGAAGAGTGCTGAGGTACGATGAGAGACCCGCACACAGGTGCAGACCCTGCGAGTGTGGC	2931
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QY	2932	GGTAACACTATTAGAAACCAAGCCTGTGATGCTTGATGTGACACCGAGAGACTTAAGCCCCGAT	2991
Db	4893	GGTAACACTATTAGAAACCAAGCCTGTGATGCTTGATGTGACACCGAGAGACTTAAGCCCCGAT	4952
QY	2992	CACCTGTGTCTGGCCTGCGACCCGGCGTGAATTTGGCTCTTAACGATGAAAGATACAGATTGA	3051
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QY	3052	G 3052	
Db	5013	G 5013	

RESULT 14
US-09-315-372-4 :

1 APPLICANT: Chamberlain, Jeffrey S.
2 APPLICANT: Amalfitano, Andrea
3 APPLICANT: Heuser, Michael A.
4 APPLICANT: Kumar-Singh, Rajendra
5 APPLICANT: Hartigan-O'Connor, Dennis J.
6 TITLE OF INVENTION: IMPROVED ADENOVIIRUS VECTORS
7 NUMBER OF SEQUENCES: 15
8 CORRESPONDENCE ADDRESS:

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; COMPUTER READABLE FORM:
;
;   MEDIUM TYPE: Floppy disk
;
;   COMPUTER: IBM PC compatible
;
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;
;   SOFTWARE: Patent In Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:

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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/735,609

ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane B.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-0248
TELECOMMUNICATION INFORMATION:
MARSHALL, LESTER A

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; INFORMATION FOR SEQ ID NO: 4
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; SEQUENCE CHARACTERISTICS:
;     LENGTH: 34303 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: double

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;      MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:    /desc = "DNA"
US-09-315-372-4

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US-09-315-372-4

Query Match Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;									
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;									
Query	Similarity	Score	2161	DB	3	Length	34303		
Dp	892	CAATAGTAGTACGGATAGCTGTGACTCCGGCTCTTCAACACACTCTCGAGATACACC	951						
Dp	2853	CAATAGTAGTACGGATAGCTGTGACTCCGGCTCTTCAACACACTCTCGAGATACACC	2912						
Qy	952	GGTGGTCCCGCTGGCCCATTTAAACCAAGTTGCCGTGAGAGTTGGTGGGCTCCGACGGC	10111						
Dp	2913	GGTGGTCCCGCTGGCCCATTTAAACCAAGTTGCCGTGAGAGTTGGTGGGCTCCGACGGC	2972						
Qy	1012	TGTGGAAATGTATCGAGGACTTGTCTTAAACGAGCTGGGCAACCTTTGGACTGAGCTGPA	1072						
Dp	2973	TGTGGAAATGTATCGAGGACTTGTCTTAAACGAGCTGGGCAACCTTTGGACTGAGCTGPA	3032						
Qy	1072	ACGCCCAAGGCGCATTAAGGTGTAAACCTGTGATTCGTTGGTGTAAACGCTTTGTTTTC	1133						
Dp	3033	ACGCCCAAGGCGCATTAAGGTGTAAACCTGTGATTCGTTGGTGTAAACGCTTTGTTTTC	3092						
Qy	1132	TGAATGAGTTGATGTAAAGTTAATTAAGGCTGAGATTAAGTTAACTTGACATGGCGTGT	1192						
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Qy	1192	AAATGGGGCGGGGCTTAAAGGCTAATAACCGCGGGGCTAATCTTGATTAATCTGA	1252						
Dp	3153	AAATGGGGCGGGGCTTAAAGGCTAATAACCGCGGGGCTAATCTTGATTAATCTGA	3212						
Qy	1252	CCTCATGAGGCTTGGGAGTGTGTGAAGATTTTTCGTCTGTGCTAATCTGTGAACA	1312						
Dp	3213	CCTCATGAGGCTTGGGAGTGTGTGAAGATTTTTCGTCTGTGCTAATCTGTGAACA	3272						
Qy	1312	GAGCTCTAACAGTACCTCTTGGTTTTGAGGTTTTCTGTGGGCTCATCCAGCAAAATT	1372						
Dp	3273	GAGCTCTAACAGTACCTCTTGGTTTTGAGGTTTTCTGTGGGCTCATCCAGCAAAATT	3332						
Qy	1372	AGTCTGCAGATTTAAGAGGATTTCAAGTGGGAATTTGAAAGCTTTTGAATCCTGTGG	1432						
Dp	3333	AGTCTGCAGATTTAAGAGGATTTCAAGTGGGAATTTGAAAGCTTTTGAATCCTGTGG	3392						
Qy	1432	TGAGCTGTTTTGATCTTTTGAATCTGGGCTCACACAGGCTTTTCCAAAGAGATCATCA	1492						
Dp	3393	TGAGCTGTTTTGATCTTTTGAATCTGGGCTCACACAGGCTTTTCCAAAGAGATCATCA	3452						
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Dp	3453	GACTTTGGATTTTTTCCACACCGGGGCGCGCTGCGGCTGCTGTTTCTTTTGAATTTAT	3512						
Qy	1552	AAAGAGATTAATGAGCGCAAGAAACCATCTGAGCGGGGGGTACCTGCTGATTTTCTGGC	1612						
Dp	3513	AAAGAGATTAATGAGCGCAAGAAACCATCTGAGCGGGGGGTACCTGCTGATTTTCTGGC	3572						
Qy	1612	CATGCACTGTGTGAGAGCGGTTGTGAGACACAAATTCGCTGTACTGTTGTCTTCCGT	1672						
Dp	3573	CATGCACTGTGTGAGAGCGGTTGTGAGACACAAATTCGCTGTACTGTTGTCTTCCGT	3632						
Qy	1672	CCGCGCCGCGATTAATACCGACGAGAGACAGACAGCAGCAGAGAGGAAACGACGCGG	1732						
Dp	3633	CCGCGCCGCGATTAATACCGAGAGAGACAGACAGCAGCAGAGAGGAAACGACGCGG	3692						
Qy	1732	GCGGCAGAGACAGAGCCCATGGAACCCGAGAGCGGCTTGACCTTGGGATGATGTT	1792						
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Qy	1792	GTAAGAGTGGCTGAACGTGTATCCGAACCTGAGACGCAATTTTGAACAATTAACAAGAGTGG	1852						
Dp	3753	GTAAGAGTGGCTGAACGTGTATCCGAACCTGAGACGCAATTTTGAACAATTAACAAGAGTGG	3812						
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Qy	1912	AATCTAGCTTTTACCTTAATGACACAGACCGCTCTGAGTGTATTACTTTCAACAGATC	1972						

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Qy 1972 AAGGATTAATTCGGCTTAATAGACTTGATCTGCTGGCGCAAGATATTCATAGACAGCTG 2031
Db 3933 AAGGATTAATTCGGCTTAATAGACTTGATCTGCTGGCGCAAGATATTCATAGACAGCTG 3992
Qy 2032 ACCACTTACTGCTGACGACGAGGGATGATTTTGAGAGGCTAATAGGGTATATGCAAG 2091
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Qy 2092 GTGGCACTTAGGCGCAGATTCGACAGATCAGCAAACTTGTAATATCAGGAATTTGT 2151
Db 4053 GTGGCACTTAGGCGCAGATTCGACAGATCAGCAAACTTGTAATATCAGGAATTTGT 4112
Qy 2152 TGCTAACATTTCTGGGAAACGGGGCCGAGGTGAGATAGATAGGAGATAGGGTGCCCTTT 2211
Db 4113 TGCTAACATTTCTGGGAAACGGGGCCGAGGTGAGATAGGAGATAGGGTGCCCTTT 4172
Qy 2212 AGATGTAGCATGATTAATATATGTCGGGGGTGCTTGACATGACGGGGGTGATTATATG 2271
Db 4173 AGATGTAGCATGATTAATATATGTCGGGGGTGCTTGACATGACGGGGGTGATTATATG 4232
Qy 2272 AATGTAAAGTTTACTGGCCCAATTTTAGCGGTACGGTTTCTTGCCCAATACCAACTT 2331
Db 4233 AATGTAAAGTTTACTGGCCCAATTTTAGCGGTACGGTTTCTTGCCCAATACCAACTT 4292
Qy 2332 ATCTTACACCGGTAAAGCTTCTAATGAGTTTAAACAATACCTGTGGAAGCCTGACCGAT 2391
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Qy 2392 GTAAAGGTTCCGGGGCTGCTTTTAACTGCTGCTGGAAGGGGGTGTGTGCGCCCAAA 2451
Db 4353 GTAAAGGTTCCGGGGCTGCTTTTAACTGCTGCTGGAAGGGGGTGTGTGCGCCCAAA 4412
Qy 2452 AGCAGGGCTTCAATTAAGAAAATGCTCTTTGAAAAGGTACCTTGAGTATCTGTAG 2511
Db 4413 AGCAGGGCTTCAATTAAGAAAATGCTCTTTGAAAAGGTACCTTGAGTATCTGTAG 4472
Qy 2512 GGTAACCTCCAGGGGCGCCCAATGTCGCCCTCCGATGCTGTTTCTTCAATCTAGTAAA 2571
Db 4473 GGTAACCTCCAGGGGCGCCCAATGTCGCCCTCCGATGCTGTTTCTTCAATCTAGTAAA 4532
Qy 2572 AGCGTGGCTGTATTAAGCATATGATGATGAGCACTCGAGAGACAGGGCTCTAG 2631
Db 4533 AGCGTGGCTGTATTAAGCATATGATGATGAGCACTCGAGAGACAGGGCTCTCTAG 4592
Qy 2632 ATGCTGACCTGCTCGACGCGCACTGTCACTGTGTAAGACCAATTCAGTACCAAGCCAC 2691
Db 4593 ATGCTGACCTGCTCGACGCGCACTGTCACTGTGTAAGACCAATTCAGTACCAAGCCAC 4652
Qy 2692 TCTGCGAAGGCTGCGCCAGTGTGAGAGATTAACAATCACTGACCCCTGTTCTTTCATTTG 2751
Db 4653 TCTGCGAAGGCTGCGCCAGTGTGAGAGATTAACAATCACTGACCCCTGTTCTTTCATTTG 4712
Qy 2752 GGTAACAGAGAGGGGGGTCTCTACCTTAACAATGCAATTTGAGTCAACAATAATATG 2811
Db 4713 GGTAACAGAGAGGGGGGTCTCTACCTTAACAATGCAATTTGAGTCAACAATAATATG 4772
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Qy 2872 ATCTGGAAGGCTGAGGTAAGATGAGACCGGCAACGAGGTGCAACCTGTGAGATGTGGC 2931
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Qy 2932 GGTAACATATTTAGAGAACCAAGCTGTGATGCTGATGATGACCGAGAGCTGAGGCCGAT 2991
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Qy 3052 G 3052
Db 5013 G 5013

RESULT 15
US-09-244-752-4
; Sequence 4, Application US/09244752
; Patent No. 6063622
; GENERAL INFORMATION:
; APPLICANT: Chamberlain, Jeffrey S.
; APPLICANT: Amalfitano, Andrea
; APPLICANT: Hauser, Michael A.
; APPLICANT: Kumar-Singh, Rajendra
; APPLICANT: Hartigan-O'Connor, Dennis J.
; TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/244,752
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/735,609
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: UM-02484
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34303 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
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; US-09-244-752-4

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Best Local Similarity 100.0%; Pred. No. 0;
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Db 2973 TGTCGAATGATGAGAGACTTGCTTAACGAGCCTGGCAACCTTTGGACTTGA 3032
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Db 4293 ATCTTACACGGGTATGAGCTTATAGGTTTAAACATACCTGTGTGAGACCTGACGAT 4352
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Db 4353 GTAAGGTTCCGGGCTGTGCTTTTACCTGCTGCTGAGAAAGGGGGTGTGTGCCCAA 4412
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Db 4413 AGCAGGGCTTCAATTAAGAAATGCTCTTGAAGAGGTACCTTGGGATCTGTGAG 4472
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Qy 2632 ATGCTGACCTGTGAGAGAGGCACTGTGACCTGTGAGAGACATTAACGTAGCCAGC 2691
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Qy 2692 TCTGCAAGGCTGCGCAGTGTGTTGAGCATTAACATGATGACCCGCTGTTCTTGATTTG 2751
Db 4653 TCTGCAAGGCTGCGCAGTGTGTTGAGCATTAACATGATGACCCGCTGTTCTTGATTTG 4712
Qy 2752 GGTAAACAGAGAGGGGGTGTCTTACCTTAACATGCAATTTGAGTCACTAATATATG 2811
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Db 4833 ATCTGAAGGTGCTGAGATGATGAGACCCGCAACAGTGCAGACCTGCGAGGTGGC 4892
Qy 2932 GGTAAACATTAATAGAAACAGGCTGTGATGCTGATGATGACCGAGAGAGCTGAGCCGAT 2991
Db 4893 GGTAAACATTAATAGAAACAGGCTGTGATGCTGATGATGACCGAGAGAGCTGAGCCGAT 4952
Qy 2992 CACTTGTGTGCTGCTGACCCGCGCTGAGTGTGCTCTGCGATGGAAGATACAGATTGA 3051
Db 4953 CACTTGTGTGCTGCTGACCCGCGCTGAGTGTGCTCTGCGATGGAAGATACAGATTGA 5012
Qy 3052 G 3052
Db 5013 G 5013

Search completed: October 28, 2005, 09:05:32
Job time : 528 secs

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Query Match	100.0%;	Score 3052;	DB 26;	Length 3052
Best Local Similarity	100.0%;	Pred. No. 0;		

Matches 3052: Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	1	CGGTAGTGTATTTTATACCCGGTGAATTCTCAAGAGCCACTTTGATGCCAGAGT	60	
Db	1	CGGTAGTGTATTTATACCCGGTGAATTCTCAAGAGCCACTTTGATGCCAGAGT	60	
Qy	61	AGAGTTTTCTCTCCGAGCGGCTCCGACACGGGAGCTGAAATGACATTTATCTGCC	120	
Db	61	AGAGTTTTCTCTCCGAGCGGCTCCGACACGGGAGCTGAAATGACATTTATCTGCC	120	
Qy	121	ACGAGGTGTTATTAACGAAATAATGCGCGCAGTCTTTTGACAGCTGATCGAAGAG	180	
Db	121	ACGAGAGGTATTATACGAAATAATGCGCGCAGTCTTTTGACAGCTGATCGAAGAG	180	
Qy	181	TACTGGCTGATTAATCTTCACACTCTAGCCATTTTGAACCACTAACCTTACCAACTGT	240	
Db	181	TACTGGCTGATTAATCTTCACACTCTAGCCATTTTGAACCACTAACCTTACCAACTGT	240	
Qy	241	ATGATTTTAGAGTACGAGCGGCCCCGGAAGATCCCAAGAGGAGCGGTTTCGAGATTTTTC	300	
Db	241	ATGATTTTAGAGTACGAGCGGCCCCGGAAGATCCCAAGAGGAGCGGTTTCGAGATTTTTC	300	
Qy	301	CCGACTCTGTAATGTGGCGGTGACGAAAGGATTTGACTTCACTTTTCGCGCGCGC	360	
Db	301	CCGACTCTGTAATGTGGCGGTGACGAAAGGATTTGACTTCACTTTTCGCGCGCGC	360	
Qy	361	CCGGTTCTCCGAGCGGCTCACTTTTCGCGCAGCCGAGCAGCCGAGCAGAGGCT	420	
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Qy	721	TTTTACAGTTTGTGTTTAAAGAAATTTTGTATGTGATTTTTTTTAAAGGTCTGTGTC	780	
Db	721	TTTTACAGTTTGTGTTTAAAGAAATTTTGTATGTGATTTTTTTTAAAGGTCTGTGTC	780	
Qy	781	TGAACCTGAGCTGAGCCCGAGCAGAAACCGAGCTGCAAGACTACCCGCTCTTAA	840	
Db	781	TGAACCTGAGCTGAGCCCGAGCAGAAACCGAGCTGCAAGACTACCCGCTCTTAA	840	
Qy	841	AATGCGCGCTGCTATCTGAGACGCGCCGACATCACTGTGTCTAGAGATGCAATAGTAG	900	
Db	841	AATGCGCGCTGCTATCTGAGACGCGCCGACATCACTGTGTCTAGAGATGCAATAGTAG	900	
Qy	901	TACGAGTACCTGATCTCCGCTCTTTTAAACACCTTCTAGATACACCCGGTGTGCC	960	
Db	901	TACGAGTACCTGATCTCCGCTCTTTTAAACACCTTCTAGATACACCCGGTGTGCC	960	
Qy	961	GCTGTGCCCCATTAAACGATGTCGCTGAGATGTGTGGCGTGCAGGCTGTGGAATG	1020	
Db	961	GCTGTGCCCCATTAAACGATGTCGCTGAGATGTGTGGCGTGCAGGCTGTGGAATG	1020	
Qy	1021	TATGAGGACTTGTCTTAAAGAGCTGGGCAACTTTTGACTTGAAGCTGTAAAGCCCCAG	1080	
Db	1021	TATGAGGACTTGTCTTAAAGAGCTGGGCAACTTTTGACTTGAAGCTGTAAAGCCCCAG	1080	

Qy	1081	GCCATTAAGGTGTAAACCTGTGATTTGCTGTGTGTTAACCCCTTTGTTGCTGATGAGT	1140	
Db	1081	GCCATTAAGGTGTAAACCTGTGATTTGCTGTGTGTTAACCCCTTTGTTGCTGATGAGT	1140	
Qy	1141	TGATGTAAAGTTTAAATAAGGTGAGATTAATGTTTAACTTGCAATGGCTGTAAATGGGGC	1200	
Db	1141	TGATGTAAAGTTTAAATAAGGTGAGATTAATGTTTAACTTGCAATGGCTGTAAATGGGGC	1200	
Qy	1201	GAGGCTTAAAGGTATTAATGCGCGGTGAGCTTAATCTTGTTACATCTGACTATGGA	1260	
Db	1201	GAGGCTTAAAGGTATTAATGCGCGGTGAGCTTAATCTTGTTACATCTGACTATGGA	1260	
Qy	1261	GCTTGGGAGATGTTTGAATAATTTTCTGCTGCGGATCACTGTGTGAAACAGAGCTCTAA	1320	
Db	1261	GCTTGGGAGATGTTTGAATAATTTTCTGCTGCGGATCACTGTGTGAAACAGAGCTCTAA	1320	
Qy	1321	CAGTACCTCTTGGTTTGGAGGTTTCTGTGGGGCTCATCCAGGCAAGTTAGCTGACG	1380	
Db	1321	CAGTACCTCTTGGTTTGGAGGTTTCTGTGGGGCTCATCCAGGCAAGTTAGCTGACG	1380	
Qy	1381	AATTAAGAGGATTTACAAGTGGGAATTTGAAGCTTTGAATCTGTGTGAGCTGTT	1440	
Db	1381	AATTAAGAGGATTTACAAGTGGGAATTTGAAGCTTTGAATCTGTGTGAGCTGTT	1440	
Qy	1441	TGATTTCTTGAATCTGGGTACACAGGGCTTTTCCAGAGAGGTCATCAAGACTTTTGA	1500	
Db	1441	TGATTTCTTGAATCTGGGTACACAGGGCTTTTCCAGAGAGGTCATCAAGACTTTTGA	1500	
Qy	1501	TTTTTCCACACCGGGGCGGCTGCGGCTGTGTGCTTTTGTGAGTTTAAAGATTA	1560	
Db	1501	TTTTTCCACACCGGGGCGGCTGCGGCTGTGTGCTTTTGTGAGTTTAAAGATTA	1560	
Qy	1561	ATGAGCGGAAGAAACCATCTGAGCGGGGGTACCTGTGGATTTTCTGGCCTATGCACT	1620	
Db	1561	ATGAGCGGAAGAAACCATCTGAGCGGGGGTACCTGTGGATTTTCTGGCCTATGCACT	1620	
Qy	1621	GTTGAGAGCGGTTGTGAGACAAAGAAATCGCTGTCTGTGTGCTTCCGTCGCGCGGCG	1680	
Db	1621	GTTGAGAGCGGTTGTGAGACAAAGAAATCGCTGTCTGTGTGCTTCCGTCGCGCGGCG	1680	
Qy	1681	GATTAATCCGACCGGAGGAGCAGCAGCAGCAGAGAGAAACAGCGCGCGGCGAGGA	1740	
Db	1681	GATTAATCCGACCGGAGGAGCAGCAGCAGCAGAGAGAAACAGCGCGCGGCGAGGA	1740	
Qy	1741	GCAAGCCCATGGAACCCGAGAGCCGGCTGTGACCTTCGGGAATGAATGTTGTACAGGTG	1800	
Db	1741	GCAAGCCCATGGAACCCGAGAGCCGGCTGTGACCTTCGGGAATGAATGTTGTACAGGTG	1800	
Qy	1801	GCTGAACGTATCCAGAACGAGACGATTTTGAACAATTAACAGAGATGGCAGGGGCTA	1860	
Db	1801	GCTGAACGTATCCAGAACGAGACGATTTTGAACAATTAACAGAGATGGCAGGGGCTA	1860	
Qy	1861	AAGGGGTAAAGAGGAGCGGGGGCTTGTAGAGCTACAGAGAGGCTAGGAATCTAGCT	1920	
Db	1861	AAGGGGTAAAGAGGAGCGGGGGCTTGTAGAGCTACAGAGAGGCTAGGAATCTAGCT	1920	
Qy	1921	TTTAGCTTAATGACCAAGACCGTCTGAGTGTATCTTTTCAACAGATCAAGATTAAT	1980	
Db	1921	TTTAGCTTAATGACCAAGACCGTCTGAGTGTATCTTTTCAACAGATCAAGATTAAT	1980	
Qy	1981	TGGGCTAATGAGCTGATCTGTGGCGCAGAAAGTATTCATAGAGCAGCTGACCACTTAC	2040	
Db	1981	TGGGCTAATGAGCTGATCTGTGGCGCAGAAAGTATTCATAGAGCAGCTGACCACTTAC	2040	
Qy	2041	TGGCTGACGACGAGGAGTGAATTTTGAAGAGCTTAATGAGGTATATGCAAAAGTGGCACTT	2100	
Db	2041	TGGCTGACGACGAGGAGTGAATTTTGAAGAGCTTAATGAGGTATATGCAAAAGTGGCACTT	2100	
Qy	2101	AGGCCAGATTGCAAGTACAAAGATCAGCAAACTGTATAATCAGGAATTTGTGCTACATT	2160	
Db	2101	AGGCCAGATTGCAAGTACAAAGATCAGCAAACTGTATAATCAGGAATTTGTGCTACATT	2160	

2161 TCTGGAAACGGGGCCGAGGTGAGATAGATACGAGATAGAGGTGCTTTAGATGAC 2220
 2161 TCTGGAAACGGGGCCGAGGTGAGATAGATACGAGATAGAGGTGCTTTAGATGAC 2220
 2221 ATGATTAATATGTGCGCCGGGGGTGCTTGGCATGACGAGGTGCTTATATGATGAG 2280
 2221 ATGATTAATATGTGCGCCGGGGGTGCTTGGCATGACGAGGTGCTTATATGATGAG 2280
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 2281 TTTTACTGCGCCCAATTTTACGGGTACGGTTTCTGCGCAATACCACTTATCTACAC 2340
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 2341 GGTGAAGCTCTTATAGGTTTAAACAATCTGTGTGGAAGCGGTGACGATGAGGTT 2400
 2401 CGGGGCTGTGCTTTTACTGTGCTGAGAAAGGGGTGTGTGCGCCCAAAAGAGGCT 2460
 2401 CGGGGCTGTGCTTTTACTGTGCTGAGAAAGGGGTGTGTGCGCCCAAAAGAGGCT 2460
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 2461 TCAATTAAGAAATGCTCTTTGAAAAGGTGATCTGTGATCTGTGAGGGTAACTCC 2520
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 2521 AGGGGCGCCCAATGTGCGCTCCGACGTGCTTCAATGCTGATGAAAAGGTGCT 2580
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 2581 GTGATTAAGCAATCATGTATGTGCAACTGCGAGACAGAGGCTCTCAGATCTGACC 2640
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 2701 GCGTGGCCAGTGTGAGCAATCACTGACCGCGTCTTCTGCAATTTGGGTAACAG 2760
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 2881 GTGCTGAGTACGATGAGACCGGACCAAGGTGAGACCGTGTGAGTGTGGGTAACAT 2940
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 3001 CTGCGCTGACACCGCGCTGAGTGTGCTTACGATGAGTAAATACAGATTGAG 3052
 3001 CTGCGCTGACACCGCGCTGAGTGTGCTTACGATGAGTAAATACAGATTGAG 3052

US-10-731-961-3
 ; Sequence 3, Application US/10731961
 ; Publication No. US20050130306A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Voelkm, Richard W.
 ; TITLE OF INVENTION: VIRAL VECTORS WHOSE REPLICATION AND, OPTIONALLY, PASSENGER GENE
 ; TITLE OF INVENTION: ARE CONTROLLED BY A GENE SWITCH ACTIVATED BY HEAT IN THE PRESENCE
 ; FILE REFERENCE: Replicating virus
 ; CURRENT APPLICATION NUMBER: US/10/731,961
 ; CURRENT FILING DATE: 2003-12-10

Query Match 100.0%; Score 3052; DB 24; Length 9905;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGTATGATATTTATATACCGGTGATGCTTCAAGAGGCCCTTTAGATGACGAGT 60
 458 CGTGTAGTATTTATATACCGGTGATGCTTCAAGAGGCCCTTTAGATGACGAGT 517
 61 AGATTTTCTCTCCGAGCGCTCCGACACCGGAGTGAATAAGATATATATCTGCC 120
 518 AGATTTTCTCTCCGAGCGCTCCGACACCGGAGTGAATAAGATATATATCTGCC 577
 121 ACGAGGTGTTATATACGAAAGAAATGCGCGCACTTTTGGACAGCTGATCGAAG 180
 578 ACGAGGTGTTATATACGAAAGAAATGCGCGCACTTTTGGACAGCTGATCGAAG 637
 181 TACTGCTGATATCTTCCACTCTTACCTTATGAAACCACTTCAAGAACTGT 240
 638 TACTGCTGATATCTTCCACTCTTACCTTATGAAACCACTTCAAGAACTGT 697
 241 ATGATTTAGAGTACCGCGCCCGGAGATCCCAAGAGAGCGGTTTGGAGATTTTTC 300
 698 ATGATTTAGAGTACCGCGCCCGGAGATCCCAAGAGAGCGGTTTGGAGATTTTTC 757
 301 CCGACTCTGTAATGTTGGCGGTGAGAGAGGATTTGAATCACTTTTCCGCGCGC 360
 758 CCGACTCTGTAATGTTGGCGGTGAGAGAGGATTTGAATCACTTTTCCGCGCGC 817
 361 CCGGTTTCTCCGAGCGGCTTCACTTTCCCGGAGCGCCGAGAGCGGAGAGGACT 420
 818 CCGGTTTCTCCGAGCGGCTTCACTTTCCCGGAGCGCCGAGAGCGGAGAGGACT 877
 421 TGGGTCCGTTTCTATATCCAAACCTTGTACCGAGGTGATGATCTTACCTGCCAG 480
 878 TGGGTCCGTTTCTATATCCAAACCTTGTACCGAGGTGATGATCTTACCTGCCAG 937
 481 CTGCTTTTCAACCGAGTACGAGAGATGAGAGGTGAGAGTGTGTAGATTATG 540
 938 CTGCTTTTCAACCGAGTACGAGAGATGAGAGGTGAGAGTGTGTAGATTATG 997
 541 TGAAGACACCGCGGACGTTTGCAGGCTTGTATATACCGAGAGAAATACGGGGAGC 600
 998 TGAAGACACCGCGGACGTTTGCAGGCTTGTATATACCGAGAGAAATACGGGGAGC 1057
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 1058 CAGATATTATGTGTGCTTGTATATGAGACCTGTGAGATGTTGTCTACAGTAAGT 1117
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 1118 GAAATATTATGAGAGTGTGATGAGTGTGAGTGTGTGTATTTTATTTTAT 1177
 721 TTTTACAGTTTGTGTTTAAAGATTTTGTATGATGATTTTAAAGAGTCTGTGTC 780
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 1238 TGAACCTGAGCCTGAGCGCGAGACGAGAGCTGCAAGAGCTTACCGCGCTCTAA 1297

QY 841 AATGGCGCTGCTATCTGTGAGACGCCCGACATCACTGTGTCTAGAGATTCATATAG 900
Db 1298 AATGGCGCTGCTATCTGTGAGACGCCCGACATCACTGTGTCTAGAGATTCATATAG 1357
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QY 1021 TATCGAGGACTTGCCTTAACGAGCCCTGGGCAACCTTTGGACTTGGAGCTGTAAACCCCCAG 1080
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QY 1081 GCCATAAGTGTAAACCTGTGATTGCGTGTGTGTTAAAGCCTTTGTTTGTCTGATGAGT 1140
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QY 1441 TGATTTCTTGAATCTGGGTCAACAGCGCTTTTCCAAAGAGAGTCAATCAAGACTTTGA 1500
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QY 1681 GATTAATACCGACGAGAGACGACGACAGCAGAGAGAAACCCAGCGCGCGCGCAGGA 1740
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QY 1741 GCAGAGCCCATGTAACCGGAGCGCGGCTGGAACCTCTGGGAAATGAATGTTGACAGTG 1800
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QY 1921 TTTAGCTTAATGACCCAGACACCGGCTGAGTATTAATCTTTCAACAGATCAAGATAT 1980
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QY 1981 TGCGCTAATGAGCTTGTATCTGTGGCCAGAGATTTCCATAGACAGCTGACCACTTAC 2040
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QY 2041 TGGCTGACGCCAGGGGATGATTTTGAAGAGGCTATTAGGATATATGCAAGGTGCACTT 2100
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QY 2101 AGGCCAATTGCAAGTACAAGATCAGCAACTTGTAAATATACAGAAATGTGTCAACT 2160
Db 2558 AGGCCAATTGCAAGTACAAGATCAGCAACTTGTAAATATCAGAAATGTGTCAACT 2617
QY 2161 TCTGGGAACGGGGCGAGAGTGTAGATAGATACGAGAGATAGGCTGACCTTATGATGAG 2220
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QY 2221 ATGATTAATATGTGGCCGGGGGTGCTTGGCATGGAACGGGTGCTTATATGAAATGTAAG 2280
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QY 2821 GAGAGCATGTCCAAGGTGAACCTGMAAGGGGTGTTTGAATGACATGAAGATCTGAAAG 2880
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QY 3001 CTGGCTGACCGCGCTGAGTTTGGCTTACGATGAAGATACAGATTGAG 3052

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Db 3458 CTGGCCCTGACCCGGCGCTGAGTTGGCTTACGATGAAATACAGATTGAG 3509:
RESULT 3
US-10-766-307A-3
/ Sequence 3, Application US/10766307A
/ Publication No. US2004020263A1
/ GENERAL INFORMATION:
/ APPLICANT: Shanghai Sunway Biotech Co., LTD.
/ TITLE OF INVENTION: Treatment for Metastatic Cancer
/ FILE REFERENCE: 121300.00003
/ CURRENT APPLICATION NUMBER: US/10/766,307A
/ CURRENT FILING DATE: 2004-01-28
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 3
/ LENGTH: 32802
/ TYPE: DNA
/ ORGANISM: Adenovirus
US-10-766-307A-3

Query Match 100.0%; Score 3052; DB 21; Length 32802;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTGTAGTATTTATATACCCGGTGAAGTTCCTCAAGAGCCACTCTTAGTCCAGAGT 60
Db 459 CGTGTAGTATTTATATACCCGGTGAAGTTCCTCAAGAGCCACTCTTAGTCCAGAGT 518
QY 61 AGAGTTTCTCTCCGAGCCGCTCCGACACCGGGACTGAAATGACATTTATCTGCC 120
Db 519 AGAGTTTCTCTCCGAGCCGCTCCGACACCGGGACTGAAATGACATTTATCTGCC 578
QY 121 ACGAGAGGTATTTATACGGAAGAAATGGCGGCAAGCTTTTGAACAGCTGATCGAAGG 180
Db 579 ACGAGAGGTATTTATACGGAAGAAATGGCGGCAAGCTTTTGAACAGCTGATCGAAGG 638
QY 181 TACGGCTGATTAATCTTCCACTCTAGCCATTTTGAACACCTAACCTTCAGACAGT 240
Db 639 TACGGCTGATTAATCTTCCACTCTAGCCATTTTGAACACCTAACCTTCAGACAGT 698
QY 241 ATGATTTAGACGTACGCGCCCGGAAATCCCAACGAGAGGCGGTTTCGACATTTTC 300
Db 699 ATGATTTAGACGTACGCGCCCGGAAATCCCAACGAGAGGCGGTTTCGACATTTTC 758
QY 301 CCGACTCTGTAATGTGGCGGTGACAGAAAGGATTTGACTTCACTTTCGCGCGGCGC 360
Db 759 CCGACTCTGTAATGTGGCGGTGACAGAAAGGATTTGACTTCACTTTCGCGCGGCGC 818
QY 361 CCGGTTCTCCGAGACCGCTCACTTTCGCGAGCCCGAGCAGCCGAGAGAGAGCCT 420
Db 819 CCGGTTCTCCGAGACCGCTCACTTTCGCGAGCCCGAGCAGCCGAGAGAGAGCCT 878
QY 421 TGGGTCGGGTTTCTATGCAAACTTTGACCGAGGTATGATCTTACCTGCCACGAGG 480
Db 879 TGGGTCGGGTTTCTATGCAAACTTTGACCGAGGTATGATCTTACCTGCCACGAGG 938
QY 481 CTGGCTTTCCACCGAGTACGAGATGAAAGAGGTGAGAGATTGTTAGATTATG 540
Db 939 CTGGCTTTCCACCGAGTACGAGATGAAAGAGGTGAGAGATTGTTAGATTATG 998
QY 541 TGGAGACCCCGGAGACGGTTGACAGTCTTGTCAATTACCGAGAGAAATACGGGAGCC 600
Db 999 TGGAGACCCCGGAGACGGTTGACAGTCTTGTCAATTACCGAGAGAAATACGGGAGCC 1058
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Db 1059 CAGATATTAATGTTCGTTTGTCTATATGAGAGCTGTGGCATGTTTGTCTACAGTAAGT 1118
QY 661 GAAATATTAATGAGAGTGAATAGAGTGTGGTTTGTGTAATTTTTTTTTTAT 720
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QY 781 TGAACCTGAGCTGAGCCGAGCCAGAACCCGAGCCGGAAGCTTACCCGCGCTCTAA 840
Db 1239 TGAACCTGAGCTGAGCCGAGCCAGAACCCGAGCCGGAAGCTTACCCGCGCTCTAA 1298
QY 841 AATGGCCCTGCTATCTGTGAGACGCGGACATCACTGTGCTAGAAATGCAATAGTAG 900
Db 1299 AATGGCCCTGCTATCTGTGAGACGCGGACATCACTGTGCTAGAAATGCAATAGTAG 1358
QY 901 TACGATAGCTGTGACTTCGCGTCTTTAAACACCTCTCTGAGATACACCGGTGTC 960
Db 1359 TACGATAGCTGTGACTTCGCGTCTTTAAACACCTCTCTGAGATACACCGGTGTC 1418
QY 961 GCTGTGCCCATTAACAGATGCGGTGAGAGTGTGGGGGTGCGCAGGCTGGAATG 1020
Db 1419 GCTGTGCCCATTAACAGATGCGGTGAGAGTGTGGGGGTGCGCAGGCTGGAATG 1478
QY 1021 TATGAGAGACTTGTCTTAAACGAGCCTGGGCAACTTTGGAATTGAGCTGTAAACGCCAG 1080
Db 1479 TATGAGAGACTTGTCTTAAACGAGCCTGGGCAACTTTGGAATTGAGCTGTAAACGCCAG 1538
QY 1081 GCCATTAAGTGTAAACCTGTGATTCGTGTGAGTTAACGCTTTGTTGCTGAATGAGT 1140
Db 1539 GCCATTAAGTGTAAACCTGTGATTCGTGTGAGTTAACGCTTTGTTGCTGAATGAGT 1598
QY 1141 TGATGTAAGTTTATTAAGGTTGATTAAGTTTAACTGTGATGCGGTGTAATAGGGGC 1200
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Db 1659 GGGGCTTAAAGGATTAATTAATGCGCGGTGATATCTTGTGTTACATCTGACTATGGA 1718
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Db 1719 GGGTGGAGTGTGGAAGATTTTCTGCTGTGCTGTAATCTGCTGGAACAGAGCTTAA 1778
QY 1321 CAGTACCTCTGTTTGTGAGGTTTCTGTGGGGCTCATCCAGGCAAGTAAATGCTGAG 1380
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RESULT 4
US-09-725-720-43
Sequence 43, Application US/09725720
Patent No. US20010049136A1
GENERAL INFORMATION:
APPLICANT: IMELER, Jean-Luc
APPLICANT: MEHTALI, Majid
APPLICANT: PAVIRANI, Andrea
TITLE OF INVENTION: DEFECTIVE ADENOVIRUSES AND CORRESPONDING
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: 1737 King Street, Suite 500
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22314-2756
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/725,720
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/379,452
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93 06482
FILING DATE: 28-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Dadio, Susan M.
REGISTRATION NUMBER: 40,373
REFERENCE/DOCKET NUMBER: 029395-002
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 35935 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-725-720-43
Query Match 100.0%; Score 3052; DB 9; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 5

US-09-782-378A-4

Sequence 4, Application US/09782378A

Patent No. US20020102731A1

GENERAL INFORMATION:

APPLICANT: Hearing, Patrick

APPLICANT: Bahou, Wadie

APPLICANT: Sandelon, Ziv

APPLICANT: Gnatenko, Dmitri

TITLE OF INVENTION: Adenoviral Vectors

FILE REFERENCE: STONIB-04970

CURRENT APPLICATION NUMBER: US/09/782,378A

PRIOR FILING DATE: 2001-02-12

PRIOR APPLICATION NUMBER: 60/237,747

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PatentIn version 3.0

SEQ ID NO 4

LENGTH: 35935

TYPE: DNA

ORGANISM: Human adenovirus type 5

US-09-782-378A-4

Query Match 100.0%; Score 3052; DB 9; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;

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Qy 1441 TGATTTCTTGAATCTGGGTCAACGAGCGCTTTTCCAGAGAAGGTCATCAAGCTTTGA 1500
Db 1899 TGATTTCTTGAATCTGGGTCAACGAGCGCTTTTCCAGAGAAGGTCATCAAGCTTTGA 1958
Qy 1501 TTTTCCACACCGGGGGCGCTGGGGCTGCTGCTTTTGTAGTTTAAAGGATTA 1560
Db 1959 TTTTCCACACCGGGGGCGCTGGGGCTGCTGCTTTTGTAGTTTAAAGGATTA 2018
Qy 1561 ATGAGAGGAAGAAAACCATCTGAGCGGGGGTACCTGCTGATTTTCTGCGCATGCACT 1620
Db 2019 ATGAGAGGAAGAAAACCATCTGAGCGGGGGTACCTGCTGATTTTCTGCGCATGCACT 2078
Qy 1621 GTGAGAGCGGTTGTGAGACACAAGAAATCGCTGCTAATCTGTTCTTCCGCTCGCCG 1680
Db 2079 GTGAGAGCGGTTGTGAGACACAAGAAATCGCTGCTAATCTGTTCTTCCGCTCGCCG 2138
Qy 1681 GATTAATCCGACGAGAGGACGAGCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
Db 2139 GATTAATCCGACGAGAGGACGAGCAGCAGCAGAGAGAGAGAGAGAGAGAGAGAGAG 2198
Qy 1741 GCAAGAGCCATGGAACCCGAGAGCGGCTGAGCCTTGAGATGAATGTTGTAAGGTTG 1800
Db 2199 GCAAGAGCCATGGAACCCGAGAGCGGCTGAGCCTTGAGATGAATGTTGTAAGGTTG 2258
Qy 1801 GCTGAATCTGTATCCAGAACTGAGACGCAATTTTGAACAATTAAGAGATGGCAGGGCTA 1860
Db 2259 GCTGAATCTGTATCCAGAACTGAGACGCAATTTTGAACAATTAAGAGATGGCAGGGCTA 2318
Qy 1861 AAGGGGTTAAAGAGAGAGCGGGGGCTTTGAGAGCTACAGAGAGAGAGAGAGAGAGAG 1920
Db 2319 AAGGGGTTAAAGAGAGAGCGGGGGCTTTGAGAGCTACAGAGAGAGAGAGAGAGAGAG 2378
Qy 1921 TTTAGCTTAATGACAGACACCGTCTGAGTGTATTAATTTTCAACAGATCAAGATTAAT 1980
Db 2379 TTTAGCTTAATGACAGACACCGTCTGAGTGTATTAATTTTCAACAGATCAAGATTAAT 2438
Qy 1981 TGCGCTAATGAGCTTGAATCTGCTGCGCAGAAATTCATAGAGAGAGCTGAGCACTTAC 2040
Db 2439 TGCGCTAATGAGCTTGAATCTGCTGCGCAGAAATTCATAGAGAGAGCTGAGCACTTAC 2498
Qy 2041 TGCGCTGAGCCAGGGGAGATTTTGAAGAGCTTATGAGGATTAATGAAAGTGGCCTT 2100
Db 2499 TGCGCTGAGCCAGGGGAGATTTTGAAGAGCTTATGAGGATTAATGAAAGTGGCCTT 2558
Qy 2101 AGGCGAGATTCAGAGTACAGAGTACAGAACTTGTAAATATCAAGAAATTTGTTGCTACAT 2160
Db 2559 AGGCGAGATTCAGAGTACAGAGTACAGAACTTGTAAATATCAAGAAATTTGTTGCTACAT 2618

Qy 2161 TCTGGGAACGGGGCCGAGGTGAGATATGATACGAGAGATAGGGTGGCTTTAGATGAC 2220
Db 2619 TCTGGGAACGGGGCCGAGGTGAGATATGATACGAGAGATAGGGTGGCTTTAGATGAC 2678
Qy 2221 ATGATTAATATATGAGCGGGGGTCTTGAGATGAGACGGGGGTGTTATATGAAATGAAG 2280
Db 2679 ATGATTAATATATGAGCGGGGGTCTTGAGATGAGACGGGGGTGTTATATGAAATGAAG 2738
Qy 2281 TTTACTGGCCCAATTTTAAAGGATACGGTTCCTGGCCAAATACCAACTTATCTTACAC 2340
Db 2739 TTTACTGGCCCAATTTTAAAGGATACGGTTCCTGGCCAAATACCAACTTATCTTACAC 2798
Qy 2341 GGTGTAAGCTTTATATGAGTTTAAATATCTGTGTGGAAGCTTGACCGAGATGAAGGTT 2400
Db 2799 GGTGTAAGCTTTATATGAGTTTAAATATCTGTGTGGAAGCTTGACCGAGATGAAGGTT 2858
Qy 2401 CGGGGCTGTGCTTTTACTGCTGCTGGAAGGGGGGTGAGTGTGCGCCCAAAAGAGGCT 2460
Db 2859 CGGGGCTGTGCTTTTACTGCTGCTGGAAGGGGGTGTGAGTGTGCGCCCAAAAGAGGCT 2918
Qy 2461 TCAATTAAGAAATGCTCTTTGAAGGTTAATCTTGGGTATCTGTCTGAGGGTAACTCC 2520
Db 2919 TCAATTAAGAAATGCTCTTTGAAGGTTAATCTTGGGTATCTGTCTGAGGGTAACTCC 2978
Qy 2521 AGGGTGGCCCAATGTGCTCCGACTGTGCTTCTTCAATGTAAGAAAGCTGCT 2580
Db 2979 AGGGTGGCCCAATGTGCTCCGACTGTGCTTCTTCAATGTAAGAAAGCTGCT 3038
Qy 2581 GTGATTAAGCATATCATGTATGTGGAACCTGGAGGACAGGGGCTCTCAATGCTGAGC 2640
Db 3039 GTGATTAAGCATATCATGTATGTGGAACCTGGAGGAGAGAGAGAGAGAGAGAGAGAG 3098
Qy 2641 TGCTGGAGCGCACTGTCACTGCTGAGAGACCAATTCAGTACGAGCACTCTCGAAG 2700
Db 3099 TGCTGGAGCGCACTGTCACTGCTGAGAGACCAATTCAGTACGAGCACTCTCGAAG 3158
Qy 2701 GCTGGCCAGTGTGAGCATATCACTGACCGGCTGTTCTTGCAATTTGGGTAAACAG 2760
Db 3159 GCTGGCCAGTGTGAGCATATCACTGACCGGCTGTTCTTGCAATTTGGGTAAACAG 3218
Qy 2761 AGGGGGGTGTTCCATACCTTACCAATGCAATTTAGTACCTAAGATTAATGCTTGAAGCC 2820
Db 3219 AGGGGGGTGTTCCATACCTTACCAATGCAATTTAGTACCTAAGATTAATGCTTGAAGCC 3278
Qy 2821 GAGAGCATGTCAGAGTGAACCTGAAAGGGGTGTTTGAATGACATGAGATGAGATCTGAG 2880
Db 3279 GAGAGCATGTCAGAGTGAACCTGAAAGGGGTGTTTGAATGACATGAGATGAGATCTGAG 3338
Qy 2881 GTGCTGAGTACGATGAGACCCGACAGAGTGCAGACCTTGCGAGTGTGGCGTAAACAT 2940
Db 3339 GTGCTGAGTACGATGAGACCCGACAGAGTGCAGACCTTGCGAGTGTGGCGTAAACAT 3398
Qy 2941 ATTAGGAACCAAGCTGTGATGCTGATGATGACGAGAGAGCTGAGAGCCGATCACTGGTG 3000
Db 3399 ATTAGGAACCAAGCTGTGATGCTGATGATGACGAGAGAGCTGAGAGCCGATCACTGGTG 3458
Qy 3001 CTGGCTGACACCGCGCTGAGTTTGGCTTACGATGAAGATACAGATTGAG 3052
Db 3459 CTGGCTGACACCGCGCTGAGTTTGGCTTACGATGAAGATACAGATTGAG 3510

RESULT 6
US-09-782-378A-5
; Sequence 5, Application US/09782378A
; Patent No. US20020102731A1
GENERAL INFORMATION:
; APPLICANT: Hearing, Patrick
; APPLICANT: Bahou, Wadie
; APPLICANT: Sandalon, Ziv
; APPLICANT: Gnatenko, Dmitri
; TITLE OF INVENTION: Adenoviral Vectors
; FILE REFERENCE: STONYB-04970
; CURRENT APPLICATION NUMBER: US/09/782.378A

; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/237,747
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 35935
; TYPE: DNA
; ORGANISM: Human adenovirus type 5
US-09-782-378A-5

Query Match 100.0%; Score 3052; DB 9; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CGTGTAGTATTTATATACCCGGTGAATTCCTCAAGAGCCACTCTTAGTCCGACGAGT	60
Db	459	CGTGTAGTATTTATATACCCGGTGAATTCCTCAAGAGCCACTCTTAGTCCGACGAGT	518
Qy	61	AGAGTTTCTCTCCGAGCCGCTCCGACACCGGACTGAATAATGACATATTAATCTGCC	120
Db	519	AGAGTTTCTCTCCGAGCCGCTCCGACACCGGACTGAATAATGACATATTAATCTGCC	578
Qy	121	ACGAGGTGTATTAACCGAAGAAATGCGCGCACTTTTGGACCACTGATCGAAGAG	180
Db	579	ACGAGGTGTATTAACCGAAGAAATGCGCGCACTTTTGGACCACTGATCGAAGAG	638
Qy	181	TACTGGCTGAATATCTTCCACTCTCTAGCCATTTTGAACCACTACCTTACGAACTGT	240
Db	639	TACTGGCTGAATATCTTCCACTCTCTAGCCATTTTGAACCACTACCTTACGAACTGT	698
Qy	241	ATGATTTAGACGTACGAGCCGCCGAAAGATCCCAAGAGAGCGGTTTCGAGATTTTTC	300
Db	699	ATGATTTAGACGTACGAGCCGCCGAAAGATCCCAAGAGAGCGGTTTCGAGATTTTTC	758
Qy	301	CCGACTCTGATATGTGGCGGTGACAGAAAGGATTTGACTTACTCACTTTTCGCGCGGC	360
Db	759	CCGACTCTGATATGTGGCGGTGACAGAAAGGATTTGACTTACTCACTTTTCGCGCGGC	818
Qy	361	CCGCTTCTCCGAGCCGCTCACTTTCCCGGACCCCGACAGCCCGAGACAGAGAGCT	420
Db	819	CCGCTTCTCCGAGCCGCTCACTTTCCCGGACCCCGACAGCCCGAGACAGAGAGCT	878
Qy	421	TGGGTCGCGTTTCTATGCAACCTTGTACCGAGGTGATCGATCTTACCTGCCACGAG	480
Db	879	TGGGTCGCGTTTCTATGCAACCTTGTACCGAGGTGATCGATCTTACCTGCCACGAG	938
Qy	481	CTGGCTTTCACCAAGTACAGAGATGAAGAGGTGAGAGTTTGTAGATTATG	540
Db	939	CTGGCTTTCACCAAGTACAGAGATGAAGAGGTGAGAGTTTGTAGATTATG	998
Qy	541	TGGAGACCCCGGGGACGAGTTCAGATCTTGTCAATACACCGAGAAATCGGGGAC	600
Db	999	TGGAGACCCCGGGGACGAGTTCAGATCTTGTCAATACACCGAGAAATCGGGGAC	1058
Qy	601	CAGATATATGTTGCTTGTCTATATGAGACCTGTGCGATGTTTGTCTACAGTAACT	660
Db	1059	CAGATATATGTTGCTTGTCTATATGAGACCTGTGCGATGTTTGTCTACAGTAACT	1118
Qy	661	GAATAATTAAGGACAGTGGGTATAGAGTGGGTTTGGTGGTAAATTTTTTTTAAAT	720
Db	1119	GAATAATTAAGGACAGTGGGTATAGAGTGGGTTTGGTGGTAAATTTTTTTTAAAT	1178
Qy	721	TTTTTAACAGTTTGTGGTTTAAAGAAATTTTGTATTTGATTTTTTAAAGGTCCTGTC	780
Db	1179	TTTTTAACAGTTTGTGGTTTAAAGAAATTTTGTATTTGATTTTTTAAAGGTCCTGTC	1238
Qy	781	TGAACCTGAGCTGAGCCCGAGCCAGAACCGAGGCTTCAAGACCTTACCGCGCTCTAA	840
Db	1239	TGAACCTGAGCTGAGCCCGAGCCAGAACCGAGGCTTCAAGACCTTACCGCGCTCTAA	1298
Qy	841	AATGGCGCTGCTATCTCTGAGACGCGCCGACATCACTGTGTCTAGAGATCAATAGTAG	900
Db			

Db	1299	AATGCGCCTGCTATCTCTGAGACCCGACATGACCTGTGTCTAGAGATGCAATAGTAG	1358
Qy	901	TAGGATATGCTGTGACTCCGGCTCTTCAACACACCTTGAGTAAACCGGAGTCCC	960
Db	1359	TAGGATATGCTGTGACTCCGGCTCTTCAACACACCTTGAGTAAACCGGAGTCCC	1418
Qy	961	GCTGTGCCCATTAACCAAGTTCCGTGAGAGTTGTGGCGCTGCGCAGGCTGTGAATG	1020
Db	1419	GCTGTGCCCATTAACCAAGTTCCGTGAGAGTTGTGGCGCTGCGCAGGCTGTGAATG	1478
Qy	1021	TATCGAGGACTTGCTTACGAGGCTGGGACCACTTTGACTTGAAGCTGTAAAGCCCCAG	1080
Db	1479	TATCGAGGACTTGCTTACGAGGCTGGGACCACTTTGACTTGAAGCTGTAAAGCCCCAG	1538
Qy	1081	GCCATAGGTGTAAACCTGTGATTTGCGTGTGGTTAACGCTTTGTTGTGATGATAGT	1140
Db	1539	GCCATAGGTGTAAACCTGTGATTTGCGTGTGGTTAACGCTTTGTTGTGATGATAGT	1598
Qy	1141	TGATGTAGTTTAAATAAAGGTGAGATATGTTAACTTGCAATGGCGTTTAAATGGGCG	1200
Db	1599	TGATGTAGTTTAAATAAAGGTGAGATATGTTAACTTGCAATGGCGTTTAAATGGGCG	1658
Qy	1201	GGGGCTTAAAGGATATTAATGCGCGGTGGCTAATCTTGTTACATCTGACTCATGGA	1260
Db	1659	GGGGCTTAAAGGATATTAATGCGCGGTGGCTAATCTTGTTACATCTGACTCATGGA	1718
Qy	1261	GGCTTGGAGATTTTGGAGATTTTCTGCTGCGCTAATCTTGCTGGAACGAGCTCTAA	1320
Db	1719	GGCTTGGAGATTTTGGAGATTTTCTGCTGCGCTAATCTTGCTGGAACGAGCTCTAA	1778
Qy	1321	CAGTACCTTGGTTTGGAGGTTTCTGTGGGCTCATCCAGGCAAAATTAATGCTCAG	1380
Db	1779	CAGTACCTTGGTTTGGAGGTTTCTGTGGGCTCATCCAGGCAAAATTAATGCTCAG	1838
Qy	1381	AATTAAGAGATTTACAAGTGGGAATTTGAAGCTTTGAAATCTGTGTGAGCTGTT	1440
Db	1839	AATTAAGAGATTTACAAGTGGGAATTTGAAGCTTTGAAATCTGTGTGAGCTGTT	1898
Qy	1441	TGATCTTTGAATCTGGGTGACCAAGGCTTTTCCAGAGAGGTGATCAAGACTTTGGA	1500
Db	1899	TGATCTTTGAATCTGGGTGACCAAGGCTTTTCCAGAGAGGTGATCAAGACTTTGGA	1958
Qy	1501	TTTTTCCACACCGGGGCGCTGCGGCTGCTGTTGCTTTTGAAGTTTAAAGATAA	1560
Db	1959	TTTTTCCACACCGGGGCGCTGCGGCTGCTGTTGCTTTTGAAGTTTAAAGATAA	2018
Qy	1561	ATGAGCGAAAGAAACCATCTGAGCGGGGGTACCTGCTGATTTTCTGGCCATGACT	1620
Db	2019	ATGAGCGAAAGAAACCATCTGAGCGGGGGTACCTGCTGATTTTCTGGCCATGACT	2078
Qy	1621	GTGGAGGCGGTTGTGAGACCAAGAAATGCGCTGCTAATCTGTGTCTCCGTCGCGCGG	1680
Db	2079	GTGGAGGCGGTTGTGAGACCAAGAAATGCGCTGCTAATCTGTGTCTCCGTCGCGCGG	2138
Qy	1681	GATTAATCCGACGAGAGAGCAGCAGCAGCAGAGAGAAACCAAGCGCGCGGCGAGGA	1740
Db	2139	GATTAATCCGACGAGAGAGCAGCAGCAGCAGAGAGAAACCAAGCGCGCGGCGAGGA	2198
Qy	1741	GCAGAGCCCATGGAACCCGAGAGCCGCGCTGAGACCTTCGGGAATGAATTTGTACAGTG	1800
Db	2199	GCAGAGCCCATGGAACCCGAGAGCCGCGCTGAGACCTTCGGGAATGAATTTGTACAGTG	2258
Qy	1801	GCTGAACGTATCCAGAACTGAGACGATTTTGAATTAACAGAGGATGGGCAAGGGCTA	1860
Db	2259	GCTGAACGTATCCAGAACTGAGACGATTTTGAATTAACAGAGGATGGGCAAGGGCTA	2318
Qy	1861	AAGGGGTTAAAGAGGAGCGGGGGCTTGTAGAGCTACAGAGAGGCTAGGAATCTAGCT	1920
Db	2319	AAGGGGTTAAAGAGGAGCGGGGGCTTGTAGAGCTACAGAGAGGCTAGGAATCTAGCT	2378
Qy	1921	TTTAGCTTAATGACCAAGACCGTCTGAGGTATTAATTTTCAACAGATCAAGATTAAT	1980
Db	2379	TTTAGCTTAATGACCAAGACCGTCTGAGGTATTAATTTTCAACAGATCAAGATTAAT	2438

Db 759 CCGACTGTAAATGTGGCGGTGACAGAAAGGAATTGACTTACTGACTTTTCCGCGGCGC 818
Qy 361 CCGGTTCTCCGGAGCCGCTCACTTTTCCGGCAGACCCGAGACGCCGAGAGAGCTT 420
Db 819 CCGGTTCTCCGGAGCCGCTCACTTTTCCGGCAGACCCGAGACGCCGAGAGAGCTT 878
Qy 421 TGGTCCGGTTTCTATGCGCAAACTTTGTACCGGAGGTGATGATCTTACCTTGCCACGAG 480
Db 879 TGGTCCGGTTTCTATGCGCAAACTTTGTACCGGAGGTGATGATCTTACCTTGCCACGAG 938
Qy 481 CTGCTTTTCCACCGAGTACGACGAGAGATGAAAGAGGTGAGAGATTGTGTAAATATG 540
Db 939 CTGCTTTTCCACCGAGTACGACGAGATGAAAGAGGTGAGAGATTGTGTAAATATG 998
Qy 541 TGGAGCACCCCGGACAGCTTGGAGTCTTGTCAATATACCGGAGAAATCCGGGGACC 600
Db 999 TGGAGCACCCCGGACAGCTTGTGAGTCTTGTCAATATACCGGAGAAATCCGGGGACC 1058
Qy 601 CAGATATATATGTGTGCTTGTATATAGAGACCTGTGGCATGTTGTCTACAGTAAGT 660
Db 1059 CAGATATATATGTGTGCTTGTATATAGAGACCTGTGGCATGTTGTCTACAGTAAGT 1118
Qy 661 GAAATATATGAGGAGATGAGTATAGATGTGTGGTTGGTGTGTAATTTTTTTTAAAT 720
Db 1119 GAAATATATGAGGAGATGAGTATAGATGTGTGGTTGGTGTGTAATTTTTTTTAAAT 1178
Qy 721 TTTTACGTTTTGTGTTTAAAGAAATTTTGTATGTGATTTTTTTTAAAGTCCGTGTGTC 780
Db 1179 TTTTACGTTTTGTGTTTAAAGAAATTTTGTATGTGATTTTTTTTAAAGTCCGTGTGTC 1238
Qy 781 TGAACCTGAGCCTGAGCCGAGCCGAGAACCCGAGCCTGCAAGACTACCCGCGTCTTAA 840
Db 1239 TGAACCTGAGCCTGAGCCGAGCCGAGAACCCGAGCCTGCAAGACTACCCGCGTCTTAA 1298
Qy 841 AATGGCGCTGTCTATCTGAGAGCCGCGACATCACTGTGTCTTAAAGATGCAATAGTAG 900
Db 1299 AATGGCGCTGTCTATCTGAGAGCCGCGACATCACTGTGTCTTAAAGATGCAATAGTAG 1358
Qy 901 TAGGATAGCTGTGACTCCGCTCTTCTAACACACTCCCTGAGATACACCCGGGTGTCCC 960
Db 1359 TAGGATAGCTGTGACTCCGCTCTTCTAACACACTCCCTGAGATACACCCGGGTGTCCC 1418
Qy 961 GCTGTGCCCCATTAACCAAGTGTGCGTGAAGATTGTGTGGCGGAGCTGTGAATG 1020
Db 1419 GCTGTGCCCCATTAACCAAGTGTGCGTGAAGATTGTGTGGCGGAGCTGTGAATG 1478
Qy 1021 TATGAGAGACTTGTCTTAAACGAGCTTGAGCAACTTTGACTTGAAGTGTAAAGCCCCAG 1080
Db 1479 TATGAGAGACTTGTCTTAAACGAGCTTGAGCAACTTTGACTTGAAGTGTAAAGCCCCAG 1538
Qy 1081 GCCATTAAGTGTAAACCTGTGATGTGCGTGTGTAACGCTTGTGTTGCTGAATGAGT 1140
Db 1539 GCCATTAAGTGTAAACCTGTGATGTGCGTGTGTAACGCTTGTGTTGCTGAATGAGT 1598
Qy 1141 TGAATGAATTTAAATAAGGTGAGATATATGTTTAACTTGCATGGCGTGTAAATGAGGC 1200
Db 1599 TGAATGAATTTAAATAAGGTGAGATATATGTTTAACTTGCATGGCGTGTAAATGAGGC 1658
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Db 1659 GGGGCTTAAAGGATATATATGCGCGCTGGGCTTACTTGGTTACATCTGACTCATGGA 1718
Qy 1261 GGGTGGAGAGTGTGGAAGATTTTCTGCTGAGCGTAACTTGTGGAACGAGACTGTAA 1320
Db 1719 GGGTGGAGAGTGTGGAAGATTTTCTGCTGAGCGTAACTTGTGGAACGAGACTGTAA 1778
Qy 1321 CAGTACCTCTTGTGTTGAGAGTTCGTGTGGGCTCAATCCAGGCAAAATTAAGTCTGAG 1380
Db 1779 CAGTACCTCTTGTGTTGAGAGTTCGTGTGGGCTCAATCCAGGCAAAATTAAGTCTGAG 1838
Qy 1381 AATTAAGAGAGATTAACAAGTGGAAATTTGAAGAGCTTTGAAATCTGTGTGAGCTGT 1440
Db 1839 AATTAAGAGAGATTAACAAGTGGAAATTTGAAGAGCTTTGAAATCTGTGTGAGCTGT 1898

Qy 1441 TGAATTTTGAATCTGGGTCAACGAGCGCTTTTCCAGAGAAAGTCAATCAAGACTTTGGA 1500
Db 1899 TGAATTTTGAATCTGGGTCAACGAGCGCTTTTCCAGAGAAAGTCAATCAAGACTTTGGA 1958
Qy 1501 TTTTTCACACCGGGGGCGCTGTGGCTGTGCTTTTGTAGTTTATTAAGATTA 1560
Db 1959 TTTTTCACACCGGGGGCGCTGTGGCTGTGCTTTTGTAGTTTATTAAGATTA 2018
Qy 1561 ATGAGCGAAGAAACCATCTGAGCGGGGGTACCTGTGATTTTCTGGCATGATCT 1620
Db 2019 ATGAGCGAAGAAACCATCTGAGCGGGGGTACCTGTGATTTTCTGGCATGATCT 2078
Qy 1621 GTGAGAGCGGTTGTGAGACAAAGAAATGCGCTGTACTGTGTCTTCCGTCGCGCCGCGC 1680
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Qy 1681 GATTAATCCGACCGGAGGAGCAGCAGCAGCAGAGAGAAAGCCAGCGCGCGCAGGA 1740
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Qy 1801 GCTGAATGTATCCAGAACTGAGACGATTTTGAATTAACAAGAGATGGGCAAGGGCTA 1860
Db 2259 GCTGAATGTATCCAGAACTGAGACGATTTTGAATTAACAAGAGATGGGCAAGGGCTA 2318
Qy 1861 AAGGGGTTAAAGAGGAGCGGGGGCTTGTGAGGCTTACAGAGAGCTAGGAATCTAGCT 1920
Db 2319 AAGGGGTTAAAGAGGAGCGGGGGCTTGTGAGGCTTACAGAGAGCTAGGAATCTAGCT 2378
Qy 1921 TTTTACTTAATGACACAGACCCGTCTGTAGTATTACTTTTCAACGATCAAGATTAAT 1980
Db 2379 TTTTACTTAATGACACAGACCCGTCTGTAGTATTACTTTTCAACGATCAAGATTAAT 2438
Qy 1981 TGGGCTTAATGAGCTTGAATCTGTGGGAGAAAGATTCATPAGAGAGCTGACCACTTAC 2040
Db 2439 TGGGCTTAATGAGCTTGAATCTGTGGGAGAAAGATTCATPAGAGAGCTGACCACTTAC 2498
Qy 2041 TGGCTGACGACGAGGGGATGATTTTGTAGAGACTTATGAGGATATGCAAAAGTGGCACTT 2100
Db 2499 TGGCTGACGACGAGGGGATGATTTTGTAGAGACTTATGAGGATATGCAAAAGTGGCACTT 2558
Qy 2101 AGGCGAATTTGCAATTAACAAGTCAAGCAAACTTGTAAATATCAGGAATTTGTGCTACATT 2160
Db 2559 AGGCGAATTTGCAATTAACAAGTCAAGCAAACTTGTAAATATCAGGAATTTGTGCTACATT 2618
Qy 2161 TCTGGGAAAGGGGCGAGGTGAGATGATATACGAGAGATGAGGGTGGCTTTAGATGTAGC 2220
Db 2619 TCTGGGAAAGGGGCGAGGTGAGATGATATACGAGAGATGAGGGTGGCTTTAGATGTAGC 2678
Qy 2221 ATGATTAATATGTGCGCGGGGTGCTTGGCATGGAACGGGGTGTATTATGATGATGAAG 2280
Db 2679 ATGATTAATATGTGCGCGGGGTGCTTGGCATGGAACGGGGTGTATTATGATGATGAAG 2738
Qy 2281 TTTTACTGCCCCAATTTTACCGGTGCGGTTTTCTGTGCGCAATACCACTTTATCTTACAC 2340
Db 2739 TTTTACTGCCCCAATTTTACCGGTGCGGTTTTCTGTGCGCAATACCACTTTATCTTACAC 2798
Qy 2341 GGTGTAGCTTCTATGAGGTTTAAACAATACCTGTGTGGAACCTGGAACGATGTAAGGTT 2400
Db 2799 GGTGTAGCTTCTATGAGGTTTAAACAATACCTGTGTGGAACCTGGAACGATGTAAGGTT 2858
Qy 2401 CCGGGCTGTGCTTTTACTGTGCTGTGAAGGGGATGTGTGTCGCCCAAAAGCAGGAGCT 2460
Db 2859 CCGGGCTGTGCTTTTACTGTGCTGTGAAGGGGATGTGTGTCGCCCAAAAGCAGGAGCT 2918
Qy 2461 TCAATTAAGAAATGCTCTTTTGAAGGTGTAACCTTGGGTATCTGTGTGAGGGTAACTCC 2520
Db 2919 TCAATTAAGAAATGCTCTTTTGAAGGTGTAACCTTGGGTATCTGTGTGAGGGTAACTCC 2978

Qy 2521 AGGGTGGCCCAATGAGGCTCCGACGTGGTTCCTTCAATGCTAGTGAAGAGGTGGCT 2580
Db 2579 AGGGTGGCCCAATGAGGCTCCGACGTGGTTCCTTCAATGCTAGTGAAGAGGTGGCT 3038
Qy 2581 GTGATTAAGCAATACATGATATGTCGCACTGCGAGGACAGGGCTCTCAGATCTGACC 2640
Db 3039 GTGATTAAGCAATACATGATATGTCGCACTGCGAGGACAGGGCTCTCAGATCTGACC 3098
Qy 2641 TGTCTGGACGGCAACTGTCACTGCTGTGAAGACATTTCAGTACGCAAGCACTCTCGCAG 2700
Db 3099 TGTCTGGACGGCAACTGTCACTGCTGTGAAGACATTTCAGTACGCAAGCACTCTCGCAG 3158
Qy 2701 GCGTGGCAGGTGTTGAGCATATACATGACCGGCTGCTTGGCACTTGGGTTAAGAG 2760
Db 3159 GCGTGGCAGGTGTTGAGCATATACATGACCGGCTGCTTGGCACTTGGGTTAAGAG 3218
Qy 2761 AGGGGGGTGTTCTCACTTACCAATGCAATTGAGTCACTAAGATATGCTTGAAGCCC 2820
Db 3219 AGGGGGGTGTTCTCACTTACCAATGCAATTGAGTCACTAAGATATGCTTGAAGCCC 3278
Qy 2821 GAGAGCATGTCAGAGTGAACCTGAACGGGGTGTGTCATGACCATGAAGATCTGGAAG 2880
Db 3279 GAGAGCATGTCAGAGTGAACCTGAACGGGGTGTGTCATGACCATGAAGATCTGGAAG 3338
Qy 2881 GTGTGAGTACGATGAGACCCGACAGGTGAGACCTGCGAGTGTGGCGTTAAACAT 2940
Db 3339 GTGTGAGTACGATGAGACCCGACAGGTGAGACCTGCGAGTGTGGCGTTAAACAT 3398
Qy 2941 ATTAGAACAAGCCTGTGATGCTGATGTGACCGAGAGCTGAGAGCCGATCATCTTGGTG 3000
Db 3399 ATTAGAACAAGCCTGTGATGCTGATGTGACCGAGAGCTGAGAGCCGATCATCTTGGTG 3458
Qy 3001 CTGGCCTGACACCGCGCTGAGTTGGCTCTAGCGATGAAGATACAGATTGAG 3052
Db 3459 CTGGCCTGACACCGCGCTGAGTTGGCTCTAGCGATGAAGATACAGATTGAG 3510

RESULT 8
US-10-264-839-12
Sequence 12, Application US/10264839
Publication No. US20040086485A1
GENERAL INFORMATION:
APPLICANT: AGILUAR-CORDOVA, CARLOS ESTUARDO
TITLE OF INVENTION: CHIMERIC VIRAL VECTORS FOR GENE THERAPY
FILE REFERENCE: 13087-105 US
CURRENT APPLICATION NUMBER: US/10/264,839
PRIOR FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: 60/327,179
PRIOR FILING DATE: 2001-10-04
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 12
LENGTH: 35935
TYPE: DNA
ORGANISM: Adenovirus
FEATURE:
OTHER INFORMATION: Adenovirus serotype 5
US-10-264-839-12

Query Match 100.0%; Score 3052; DB 19; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGTAGTGTATTATACCGCGTGAATTCCTCAAGAGGCCACTTGTAGTCCAGCGAGT 60
Db 459 CGGTAGTGTATTATACCGCGTGAATTCCTCAAGAGGCCACTTGTAGTCCAGCGAGT 518
Qy 61 AGATTTTTCCTCCGAGCGGCTCCGACCCGGAGCTGAAGATGACATATTATCTGCC 120
Db 519 AGATTTTTCCTCCGAGCGGCTCCGACCCGGAGCTGAAGATGACATATTATCTGCC 578
Qy 121 ACAGAGGTGTTATTAACGAAGAAATGCGCGCACTCTTTGGACCACTGATCGAAGAG 180

Db 579 ACAGAGGTGTTATTAACGAAGAAATGCGCGCACTCTTTGGACCACTGATCGAAGAG 638
Qy 181 TACTGCTGAATATCTTCCACCTCTACCACTTTTGAACCACTTACCTTACGAACCTGT 240
Db 639 TACTGCTGAATATCTTCCACCTCTCTAGCACTTTTGAACCACTTACCTTACGAACCTGT 698
Qy 241 ATGATTTAGACGTGACGGCCCCCGAAGATCCCAACGAGAGGCGGTTTCCGAGATTTTTC 300
Db 699 ATGATTTAGACGTGACGGCCCCCGAAGATCCCAACGAGAGGCGGTTTCCGAGATTTTTC 758
Qy 301 CCGACTCTGTAATGTTGGCCGTGAGAGGATTTGACTTACTGACTTTTCCGCCGCGC 360
Db 759 CCGACTCTGTAATGTTGGCCGTGAGAGGATTTGACTTACTGACTTTTCCGCCGCGC 818
Qy 361 CCGGTTCTCGGAGCGGCTTCACTTTCCCGGACGCCGAGACCGGAGCAGAGAGCTT 420
Db 819 CCGGTTCTCGGAGCGGCTTCACTTTCCCGGACGCCGAGACCGGAGCAGAGAGCTT 878
Qy 421 TGGGTCCGGTTTCTATGCGCAACCTTGTACCGAGGTGATGATCTTACCTGCGACGAG 938
Db 879 TGGGTCCGGTTTCTATGCGCAACCTTGTACCGAGGTGATGATCTTACCTGCGACGAG 938
Qy 481 CTGGCTTTCACCAAGTGAAGAGAGATGAAGAGGTTGTGTATGATTATG 540
Db 939 CTGGCTTTCACCAAGTGAAGAGAGTGAAGAGGTTGTGTATGATTATG 998
Qy 541 TGAAGACCCCGGACAGGTTGCAAGTCTTGTCTATATCAACCGAGGAATACGGGGAGC 600
Db 999 TGAAGACCCCGGACAGGTTGCAAGTCTTGTCTATATCAACCGAGGAATACGGGGAGC 1058
Qy 601 CAGATATTATGTTGCTGCTTGTATATGAGACCTGTGGCATTTGTCTACAGTAACT 660
Db 1059 CAGATATTATGTTGCTGCTTGTATATGAGACCTGTGGCATTTGTCTACAGTAACT 1118
Qy 661 GAAATATTAGGAGAGTGTGATGATGAGTGGGTTGGTGTGTTAATTTTTTTTAAAT 720
Db 1119 GAAATATTATGAGAGTGTGATGATGAGTGGGTTGGTGTGTTAATTTTTTTTAAAT 1178
Qy 721 TTTTACAGTTTGTGTTTAAAGATTTGTATGATTTTAAAGTCTGTGTCT 780
Db 1179 TTTTACAGTTTGTGTTTAAAGATTTGTATGATTTTAAAGTCTGTGTCT 1238
Qy 781 TGAACCTGAGACCTGAGGCGGACGAGAACCGGAGCTGCAAGACCTTCCGCGCTCTAA 840
Db 1239 TGAACCTGAGACCTGAGGCGGACGAGAACCGGAGCTGCAAGACCTTCCGCTCTAA 1298
Qy 841 AATGGCCCTGTATCTCTGAGACGCGGACATCACTGTGCTGAGAGATGCAATAGTAG 900
Db 1299 AATGGCCCTGTATCTCTGAGACGCGGACATCACTGTGCTGAGAGATGCAATAGTAG 1358
Qy 901 TAAGATAGCTGTGACTCCGGTCTTCTTAAACAACCTCTGAGATACCCCGGTGTCTCC 960
Db 1359 TAAGATAGCTGTGACTCCGGTCTTCTTAAACAACCTCTGAGATACCCCGGTGTCTCC 1418
Qy 961 GCTGTGCCCCATTAAACCACTTGGCGTGAAGATGTTGGTGGCGTCCAGAGCTGTGAATG 1020
Db 1419 GCTGTGCCCCATTAAACCACTTGGCGTGAAGATGTTGGTGGCGTCCAGAGCTGTGAATG 1478
Qy 1021 TATCGAGGACTTGTCAAGAGCTGGGCAACCTTGTGACTTGAAGCTGTAAACGCCCCAG 1080
Db 1479 TATCGAGGACTTGTCAAGAGCTGGGCAACCTTGTGACTTGAAGCTGTAAACGCCCCAG 1538
Qy 1081 GCCATTAAGTGTAAACCTGTGATTCGTGTGTGTTAAGCCTTTGTGCTGAATAGT 1140
Db 1539 GCCATTAAGTGTAAACCTGTGATTCGTGTGTGTTAAGCCTTTGTGCTGAATAGT 1598
Qy 1141 TGAATGTAAGTTTAAAGAGGTGAGATATGTTTAACTTGCATGCGGTGTTAAATGGGCG 1200
Db 1599 TGAATGTAAGTTTAAAGAGGTGAGATATGTTTAACTTGCATGCGGTGTTAAATGGGCG 1658
Qy 1201 GGGGCTTAAAGGATATTAATGCGCGTGGGCTAATCTTGGTTACATCTGACCTCATGGA 1260
Db 1659 GGGGCTTAAAGGATATTAATGCGCGTGGGCTAATCTTGGTTACATCTGACCTCATGGA 1718

1261 GGCTTGGAGGTGTTGGAGAATTTTCTGCTGTGCTAACTTGCTGGAACAGAGCTCTAA 1320
1719 GGGTTGGAGAGTGTGGAGAGATTTTCTGCTGTGCTAACTTGCTGGAACAGAGCTCTAA 1778
1321 CAGTACCTCTTGTTTGGAGGTTTCTGTGGGCTCATCCAGGCAAGTTAGTCTGAG 1380
1779 CAGTACCTCTTGTTTGGAGGTTTCTGTGGGCTCATCCAGGCAAGTTAGTCTGAG 1838
1381 AATTAAAGAGATTTACAAGTGGGAATTTGAAGCTTTTGAATCCCTGTGTGAGCTGTT 1440
1839 AATTAAAGAGATTTACAAGTGGGAATTTGAAGCTTTTGAATCCCTGTGTGAGCTGTT 1898
1441 TGATTTCTTGAATCTGGGTCAACAGCGCTTTTCCAGAAGAGTCAATCAAGCTTTGGA 1500
1899 TGATTTCTTGAATCTGGGTCAACAGCGCTTTTCCAGAAGAGTCAATCAAGCTTTGGA 1958
1501 TTTTTCACACCGGGGCGCGCTGCGCTGCTGTTGCTTTTGAAGTTTATAAAGATTA 1560
1959 TTTTTCACACCGGGGCGCGCTGCGCTGCTGTTGCTTTTGAAGTTTATAAAGATTA 2018
1561 ATGAGAGGAAGAAACCATCTGAGAGCGGGGGGTACTGCTGAATTTTCTGGCATGCACT 1620
2019 ATGAGAGGAAGAAACCATCTGAGAGCGGGGGGTACTGCTGAATTTTCTGGCATGCACT 2078
1621 GTGAGAGCGGTTGTGAGACACAAGAAATCGCTGCTACTGTTGCTTCCGTCGCGCGGC 1680
2079 GTGAGAGCGGTTGTGAGACACAAGAAATCGCTGCTACTGTTGCTTCCGTCGCGCGGC 2138
1681 GATTAATCCGACGGAGAGCAGCAGCAGCAGCAGAGAGAACCCAGCGCGCGCAGAGA 1740
2139 GATTAATCCGACGGAGAGCAGCAGCAGCAGCAGAGAGAACCCAGCGCGCGCAGAGA 2198
1741 GCAGAGCCCATGGAACCCGAGAGCGGCTGTGACCTTGGGAAATGAATGTTGTACAGGTG 1800
2199 GCAGAGCCCATGGAACCCGAGAGCGGCTGTGACCTTGGGAAATGAATGTTGTACAGGTG 2258
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2259 GCTGAACCTGTATCCAGAACTGAGACGCAATTTTGAACAATTAAGAGAGTGGCAGGGGCTA 2318
1861 AAGGGGGTAAAGAGAGAGCGGGGGGCTTTGTAGGCTACAGAGAGGCTAGGAATCTAATCT 1920
2319 AAGGGGGTAAAGAGAGAGCGGGGGGCTTTGTAGGCTACAGAGAGGCTAGGAATCTAATCT 2378
1921 TTTAGCTTAAAGACCAACACCGTCTGAGGTATTAATTTTCAACAGATCAAGATTAAT 1980
2379 TTTAGCTTAAAGACCAACACCGTCTGAGGTATTAATTTTCAACAGATCAAGATTAAT 2438
1981 TGCGCTAATGAGCTTGATCTGTGCGCAGAAAGTATTCATATAGAGCAGCTGACCACTTAC 2040
2439 TGCGCTAATGAGCTTGATCTGTGCGCAGAAAGTATTCATATAGAGCAGCTGACCACTTAC 2498
2041 TGCGTGCAGCCAGGGGATGATTTTGAAGAGGCTATTAAGGTATTAATGCAAGGTGGCACTT 2100
2499 TGCGTGCAGCCAGGGGATGATTTTGAAGAGGCTATTAAGGTATTAATGCAAGGTGGCACTT 2558
2101 AGGCCAAGTTGCAAGTACAAATCAGCAAACTTTGTAATTAATCAGAGATTTGTTGCTACATT 2160
2559 AGGCCAAGTTGCAAGTACAAATCAGCAAACTTTGTAATTAATCAGAGATTTGTTGCTACATT 2618
2161 TCTGGGAAACGGGGCCGAGGTGAGATAGATACGGAGGATTAAGGTGGCTTTAGATGATGAC 2220
2619 TCTGGGAAACGGGGCCGAGGTGAGATAGATACGGAGGATTAAGGTGGCTTTAGATGATGAC 2678
2221 ATGATAAATATGTGGCCGGGGGTGCTTGGCAATGACCGGGGTGTTATATATGATGTAAGG 2280
2679 ATGATAAATATGTGGCCGGGGGTGCTTGGCAATGACCGGGGTGTTATATATGATGTAAGG 2738
2281 TTTTACTGGCCCAATTTTACGGGTACGGTTTCTGTGGCAATACCAACCTTATCTTACAC 2340
2739 TTTTACTGGCCCAATTTTACGGGTACGGTTTCTGTGGCAATACCAACCTTATCTTACAC 2798

2341 GGTGTAAGCTTCTATGGGTTTAAACAATACCTGTGTGGAAGCCTGAGCATGTAAGGTT 2400
2799 GGTGTAAGCTTCTATGGGTTTAAACAATACCTGTGTGGAAGCCTGAGCATGTAAGGTT 2858
2401 CGGGGCTGTGCTTTTATCTGTGTGGAAGGGGGTGTGTGTGCCCCAAAAGCAGGCT 2460
2859 CGGGGCTGTGCTTTTATCTGTGTGGAAGGGGGTGTGTGTGCCCCAAAAGCAGGCT 2918
2461 TCAATTAAGAAATGCTTTTGAAGGATGATCCCTGGGATTCCTGTGAGGGTAACTCC 2520
2919 TCAATTAAGAAATGCTTTTGAAGGATGATCCCTGGGATTCCTGTGAGGGTAACTCC 2978
2521 AGGTGGCCACAATGTGGCTCCGACTGTGTGTTCTTCAATGATGTAAGAAAGGTGCT 2580
2979 AGGTGGCCACAATGTGGCTCCGACTGTGTGTTCTTCAATGATGTAAGAAAGGTGCT 3038
2581 GTGATTAAGCATTAACATGTATGTGCACTGCGAAGCAATTCAGTAGCAGCACTCTCGAAG 2640
3039 GTGATTAAGCATTAACATGTATGTGCACTGCGAAGCAATTCAGTAGCAGCACTCTCGAAG 3098
2641 TGCTGGAGCGGCAACCTGTCACTGTGTAAGACCAATTCAGTAGCAGCACTCTCGAAG 2700
3099 TGCTGGAGCGGCAACCTGTCACTGTGTAAGACCAATTCAGTAGCAGCACTCTCGAAG 3158
2701 GCTGGCCAGTGTGTGAGCATATATCTGACCCGCTGTTCTTGCATTTGGGTAACAG 2760
3159 GCTGGCCAGTGTGTGAGCATATATCTGACCCGCTGTTCTTGCATTTGGGTAACAG 3218
2761 AGGGGGGTGTTCTTCACTTACCAATGCAATTTAGTCACTAAGATATTCCTTGAAGCC 2820
3219 AGGGGGGTGTTCTTCACTTACCAATGCAATTTAGTCACTAAGATATTCCTTGAAGCC 3278
2821 GAGAGCATGTCCAAAGTGAACCTGAACGGGGTGTGAACATGAACATGAAGATCTGGAAG 2880
3279 GAGAGCATGTCCAAAGTGAACCTGAACGGGGTGTGAACATGAACATGAAGATCTGGAAG 3338
2881 GTGCTGAGTACGATGAGACCCGACAGGCTGACAGCCTGCGAGTGTGGCGTAAACAT 2940
3339 GTGCTGAGTACGATGAGACCCGACAGGCTGACAGCCTGCGAGTGTGGCGTAAACAT 3398
2941 ATTAGAACCAGCCTGTGATGCTGTGATGTGACCGAGAGCTGAGGCCGATCACTTGGTG 3000
3399 ATTAGAACCAGCCTGTGATGCTGTGATGTGACCGAGAGCTGAGGCCGATCACTTGGTG 3458
3001 CTGGCCTCGACCCGCGCTGAGTTTGGCTTACGATGAAGTAAAGTAAAGTTGAG 3052
3459 CTGGCCTCGACCCGCGCTGAGTTTGGCTTACGATGAAGTAAAGTAAAGTTGAG 3510

RESULT 9
US-10-432-989-1
Sequence 1, Application US/10432989
Publication No. US20040097455A1
GENERAL INFORMATION:
APPLICANT: Armendariz Borunda, Juan
APPLICANT: Aguilar Cordova, Saturno
TITLE OR INVENTION: Recombinant viral and non-viral vectors
TITLE OR INVENTION: containing the human gene of the urokinase plasminogen
TITLE OR INVENTION: activator and their utility in the treatment of various
TITLE OR INVENTION: types of fibrosis such as hepatic, renal, pulmonary,
TITLE OR INVENTION: pancreatic, heart fibrosis as well as hypertrophic scars
FILE REFERENCE: 5585-035-999(205/19071)
CURRENT APPLICATION NUMBER: US/10/432,989
CURRENT FILING DATE: 2003-10-24
PRIOR APPLICATION NUMBER: PCT/MX00/00050
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: MX011713
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 35935
TYPE: DNA

/ ORGANISM: Human adenovirus type 5
US-10-432-989-1

Query Match 100.0%; Score 3052; DB 19; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGTAGAGTATTTATACCCGGTGGTTCCTCAAGAGGCCACTCTTGAGTGCACCGAGT 60
DB CCGTAGAGTATTTATACCCGGTGGTTCCTCAAGAGGCCACTCTTGAGTGCACCGAGT 518
QY 459 CCGTAGAGTATTTATACCCGGTGGTTCCTCAAGAGGCCACTCTTGAGTGCACCGAGT 518
DB AGAGTTTCTCTCCGAGCCGCTCCGACACCGGACCTGAATAATGACATTTATCTGCC 578
QY 519 AGAGTTTCTCTCCGAGCCGCTCCGACACCGGACCTGAATAATGACATTTATCTGCC 578
DB 121 ACGGAGGTGTTATTAACGGAAGAAATGGCCGACGCTTTTGGACCAAGCTGATCGAAGAG 180
QY 579 ACGGAGGTGTTATTAACGGAAGAAATGGCCGACGCTTTTGGACCAAGCTGATCGAAGAG 638
DB 181 TACGTGGCTGATTAATTTTCACTCTTACAGCATTTTGAACCACTTACCGAAGCTGT 240
QY 639 TACGTGGCTGATTAATTTTCACTCTTACAGCATTTTGAACCACTTACCGAAGCTGT 698
DB 241 ATGATTTAGAGTGAGCGGCCCCCGGAAGATCCCAACGAGAGCGGTTTCCGAGATTTTTC 300
QY 699 ATGATTTAGAGTGAGCGGCCCCCGGAAGATCCCAACGAGAGCGGTTTCCGAGATTTTTC 758
DB 301 CCGACTCTGTAATGTTGGCGGTGACGAAAGGATTTGACTTCACTTTTCCGCGCGGC 360
QY 759 CCGACTCTGTAATGTTGGCGGTGACGAAAGGATTTGACTTCACTTTTCCGCGCGGC 818
DB 361 CCGGTTCTCCGAGCGGCTCACTTTTCCGAGCGGACCGGAGCGCGGACGAGAGGCT 420
QY 819 CCGGTTCTCCGAGCGGCTCACTTTTCCGAGCGGACCGGAGCGCGGACGAGAGGCT 878
DB 421 TGGGTCCGGTTTCTATGCGCAAACTTGTACCGGAGGTGATGATTTTCACTGCCACGAG 480
QY 879 TGGGTCCGGTTTCTATGCGCAAACTTGTACCGGAGGTGATGATTTTCACTGCCACGAG 938
DB 481 CTGGCTTTCCACCAGTGACACGAGATGAAGAGGTGAGAGGTTGTGTAGATTATG 540
QY 939 CTGGCTTTCCACCAGTGACACGAGATGAAGAGGTGAGAGGTTGTGTAGATTATG 998
DB 541 TGGAGCAACCCCGGCGACGCGTTGCAAGTCTTGTCAATACCGAGAGAAATCGGGGAC 600
QY 999 TGGAGCAACCCCGGCGACGCGTTGCAAGTCTTGTCAATACCGAGAGAAATCGGGGAC 1058
DB 601 CAGATATTAATGTTGCTTGTCTATATAGAGAACCTGTGSCATGTTGTCTACAGTAACT 660
QY 1059 CAGATATTAATGTTGCTTGTCTATATAGAGAACCTGTGSCATGTTGTCTACAGTAACT 1118
DB 661 GAAATTAATGAGGCAAGTGGTATAGAGTGTGGTTTGTGTGTAATTTTTTTTTTAACT 720
QY 1119 GAAATTAATGAGGCAAGTGGTATAGAGTGTGGTTTGTGTGTAATTTTTTTTTTAACT 1178
DB 721 TTTTACAGTTTGTGGTTTAAAGAAATTTGTATGTGATTTTTTTTAAAGGTCTGTGTC 780
QY 1179 TTTTACAGTTTGTGGTTTAAAGAAATTTGTATGTGATTTTTTTTAAAGGTCTGTGTC 1238
DB 781 TGAACCTGAGGCTGAGCCGAGCGAGCAACCGAGCGTGCAGAGCCTTACCGCGCGCTAA 840
QY 1239 TGAACCTGAGGCTGAGCCGAGCGAGCAACCGAGCGTGCAGAGCCTTACCGCGCGCTAA 1298
DB 841 AATGCGCGCTGCTATCTCTGAGACGCCGACATCACTGTGTCTAGAGAAATCAATAGTAG 900
QY 1299 AATGCGCGCTGCTATCTCTGAGACGCCGACATCACTGTGTCTAGAGAAATCAATAGTAG 1358
DB 901 TACGGAATAGCTGTGACTCCGCTCTTCAACAACACTCTCTGAGATCAACCGGAGGTCCC 960
QY 1359 TACGGAATAGCTGTGACTCCGCTCTTCAACAACACTCTCTGAGATCAACCGGAGGTCCC 1418
DB 961 GCTGTGCCCCATTAACCAAGTGTGCGTGAAGATGTTGTGGGCGTGCAGGCTGTGAATG 1020
QY |||||

DB 1419 GCTGTGCCCATTAACCACTTCCGTGAGAGTTGTGTGGCGCTGCCAGGCTGTGAATG 1478
QY 1021 TATCGAGGACTTGTCTTAACGAGCGCTGGCAACTTTGACCTGAGCTGAACGCCCGAG 1080
DB 1479 TATCGAGGACTTGTCTTAACGAGCGCTGGCAACTTTGACCTGAGCTGTGAACGCCCGAG 1538
QY 1081 GCCATAGGTGAACCTGTGATTCGCTGTGTGTTAAAGCCCTTTGTTGCTGAATGAT 1140
DB 1539 GCCATAGGTGAACCTGTGATTCGCTGTGTGTTAAAGCCCTTTGTTGCTGAATGAT 1598
QY 1141 TGATGTAACTTAATTAAGGAGTGAATATGTTTAACCTGATGCGGTTAAATGGGGC 1200
DB 1599 TGATGTAACTTAATTAAGGAGTGAATATGTTTAACCTGATGCGGTTAAATGGGGC 1658
QY 1201 GGGGCTTAAGGAGTATTAATGCGCGGTGCTAATCTTGTGTTACATCTGACCTCATGA 1260
DB 1659 GGGGCTTAAGGAGTATTAATGCGCGGTGCTAATCTTGTGTTACATCTGACCTCATGA 1718
QY 1261 GGGTGGGAGGTGTTGGAAGATTTTCTGTGTGCTGATTAAGCTTCTGAACAGAGCTCTTA 1320
DB 1719 GGGTGGGAGGTGTTGGAAGATTTTCTGTGTGCTGATTAAGCTTCTGAACAGAGCTCTTA 1778
QY 1321 CAGTACCTCTTGGTTTGGAGGTTTCTGTGGGGCTCATCCGAGCAAGTTAGTGTGAG 1380
DB 1779 CAGTACCTCTTGGTTTGGAGGTTTCTGTGGGGCTCATCCGAGCAAGTTAGTGTGAG 1838
QY 1381 AATTAAAGAGATTAACAAGTGGAAATTTGAAAGACTTTTGAATCTGTGTGAGCTGTT 1440
DB 1839 AATTAAAGAGATTAACAAGTGGAAATTTGAAAGACTTTTGAATCTGTGTGAGCTGTT 1898
QY 1441 TGATTTCTTGAATCTGGGTACACAGCGCTTTTCCAAAGAGAGTCAATCAAGACTTTGGA 1500
DB 1899 TGATTTCTTGAATCTGGGTACACAGCGCTTTTCCAAAGAGAGTCAATCAAGACTTTGGA 1958
QY 1501 TTTTTCACACCGGGGCGCGCTGCGGCTGTGCTTTTGTGATTTAAAGGATTA 1560
DB 1959 TTTTTCACACCGGGGCGCGCTGCGGCTGTGCTTTTGTGATTTAAAGGATTA 2018
QY 1561 ATGAGCGGAAGAAACCAATCTGAGCGGGGGTAACTGTGATTTTCTGACCATGATCT 1620
DB 2019 ATGAGCGGAAGAAACCAATCTGAGCGGGGGTAACTGTGATTTTCTGACCATGATCT 2078
QY 1621 GTGAGAGCGGTTGTGAGACCAAGAAATCGCTGCTACTGTGTTCTTCCGTCCCGCGC 1680
DB 2079 GTGAGAGCGGTTGTGAGACCAAGAAATCGCTGCTACTGTGTTCTTCCGTCCCGCGC 2138
QY 1681 GATAAATCCGACGGAAGGAGGAGGACGAGACGAGAGGAGGAGGCGGCGGCGAGGA 1740
DB 2139 GATAAATCCGACGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2198
QY 1741 GCAGAGCCATGGAACCCGAGAGCGGCTGTGACCTCTCGGAAATGAATGTTGTACAGGTG 1800
DB 2199 GCAGAGCCATGGAACCCGAGAGCGGCTGTGACCTCTCGGAAATGAATGTTGTACAGGTG 2258
QY 1801 GCTGAATCTGATCCAGAACTGAGACGCAATTTTGAACAATTAAGAGATGGGCGGCTTA 1860
DB 2259 GCTGAATCTGATCCAGAACTGAGACGCAATTTTGAACAATTAAGAGATGGGCGGCTTA 2318
QY 1861 AAGGGGGTAAAGAGGAGCGGGGGCTTGTGAGGCTTCAAGAGAGGCTAGAGATCTAGCT 1920
DB 2319 AAGGGGGTAAAGAGGAGCGGGGGCTTGTGAGGCTTCAAGAGAGGCTTCAAGAGATCTAGCT 2378
QY 1921 TTTAGCTTAATGACCAAGACCGCTCTGAGGTATTAATTTTCAACAGATCAAGATTAAT 1980
DB 2379 TTTAGCTTAATGACCAAGACCGCTCTGAGGTATTAATTTTCAACAGATCAAGATTAAT 2438
QY 1981 TGCCTTAATGAGCTTGAATCTGTGCGGCAAGAGTATTCATATAGAGCTGACCACTTAC 2040
DB 2439 TGCCTTAATGAGCTTGAATCTGTGCGGCAAGAGTATTCATATAGAGCTGACCACTTAC 2498
QY 2041 TGCCTGACGACGAGGAGTGAATTTTGAAGAGCTTATAGAGTATATGCAAAAGTGGCACTT 2100
DB 2499 TGCCTGACGACGAGGAGTGAATTTTGAAGAGCTTATAGAGTATATGCAAAAGTGGCACTT 2558

QY 2101 AGGCCAATTGCAAGTCAAGATGACAAACTTGTAAATATACAGAAATGTTGCTACATT 2160
DB 2559 AGGCCAATTGCAAGTCAAGATGACAAACTTGTAAATATACAGAAATGTTGCTACATT 2618
QY 2161 TCTGGGAACGGGGCCGAGGTGAGATAGATACGAGAGATAGAGTGGCTTTAGATGAGC 2220
DB 2619 TCTGGGAACGGGGCCGAGGTGAGATAGATACGAGAGATAGAGTGGCTTTAGATGAGC 2678
QY 2221 ATGATTAATATGTGGCCGGGGGTCTTGGCATGGAACGGGGGTGTTATTATGATGTAAGG 2280
DB 2679 ATGATTAATATGTGGCCGGGGGTCTTGGCATGGAACGGGGGTGTTATTATGATGTAAGG 2738
QY 2281 TTTTCTGGCCCCCAATTTTATGAGGTACGGTTTCTGGCCATACCAACTTATCTTACAC 2340
DB 2739 TTTTCTGGCCCCCAATTTTATGAGGTACGGTTTCTGGCCATACCAACTTATCTTACAC 2798
QY 2341 GGTGTAAGCTTCTATGAGTTTAACAAATACCTGTGTGGAAGCCTGGAACCGATGTAAGGTT 2400
DB 2799 GGTGTAAGCTTCTATGAGTTTAACAAATACCTGTGTGGAAGCCTGGAACCGATGTAAGGTT 2858
QY 2401 CGGGGCTGTGCTTTTACTGCTGCGAAGGGGGTGTGTCCGCCCAAAAGCAGGGCT 2460
DB 2859 CGGGGCTGTGCTTTTACTGCTGCGAAGGGGGTGTGTCCGCCCAAAAGCAGGGCT 2918
QY 2461 TCAATTAAGAAATGCTCTTGAAGAGGTACCTTGGGTATCTGTGAGAGGTAACTCC 2520
DB 2919 TCAATTAAGAAATGCTCTTGAAGAGGTACCTTGGGTATCTGTGAGAGGTAACTCC 2978
QY 2521 AGGGTGGCCCAAAATGTGGCTCCGACTGTGTGCTTCACTGATGTAAGAAAGCGTGT 2580
DB 2979 AGGGTGGCCCAAAATGTGGCTCCGACTGTGTGCTTCACTGATGTAAGAAAGCGTGT 3038
QY 2581 GTGATTAAGCAATAATGATGTATGTGGCAATCTGCCAGACAGGGCTCTCAGATGCTGACC 2640
DB 3039 GTGATTAAGCAATAATGATGTATGTGGCAATCTGCCAGACAGGGCTCTCAGATGCTGACC 3098
QY 2641 TGTCTGGGACGGCACTGTCACTGTGGAAGACATTCGTAAGCAGACCACTCTCCGACAG 2700
DB 3099 TGTCTGGGACGGCACTGTCACTGTGGAAGACATTCGTAAGCAGACCACTCTCCGACAG 3158
QY 2701 GCTGTGGCAAGTGTGTGACATTAACATCTGAACCGGCTGTTCTTGTGATTTGGGTAAACAG 2760
DB 3159 GCTGTGGCAAGTGTGTGACATTAACATCTGAACCGGCTGTTCTTGTGATTTGGGTAAACAG 3218
QY 2761 AGGGGGGTGTTCTTAACCTTAACCAATGCAATTTGAGTCACTAAGATATTTGCTGAAGCCC 2820
DB 3219 AGGGGGGTGTTCTTAACCTTAACCAATTTGAGTCACTAAGATATTTGCTGAAGCCC 3278
QY 2821 GAGAGCAATGTCACAGTGAACCTGGAACGGGGTGTGTGATGATGATGATGATGATGATGATG 2880
DB 3279 GAGAGCAATGTCACAGTGAACCTGGAACGGGGTGTGTGATGATGATGATGATGATGATGATG 3338
QY 2881 GTGCTGAGTACGATGAGAACCCGACACGAGTGCAGACCCCTGCGAGTGTGGGGTAAACAT 2940
DB 3339 GTGCTGAGTACGATGAGAACCCGACACGAGTGCAGACCCCTGCGAGTGTGGGGTAAACAT 3398
QY 2941 ATTAGGAACCAAGCTGTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 3000
DB 3399 ATTAGGAACCAAGCTGTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 3458
QY 3001 CTGGGCTGCAACCGGCGTGAATTTGGCTCTAGCGATGAAGATACAGATTTGAG 3052
DB 3459 CTGGGCTGCAACCGGCGTGAATTTGGCTCTAGCGATGAAGATACAGATTTGAG 3510

RESULT 10

US-10-766-307A-4
; Sequence 4, Application US/10766307A
; Publication No. US20040202663A1
; GENERAL INFORMATION:
; APPLICANT: Shanghai Suncay Biotech Co., LTD.
; TITLE OF INVENTION: Treatment for Metastatic Cancer

FILE REFERENCE: 121300.00003
; CURRENT APPLICATION NUMBER: US/10/766,307A
; CURRENT FILING DATE: 2004-01-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 35935
; TYPE: DNA
; ORGANISM: adenovirus
US-10-766-307A-4

Query Match 100.0%; Score 3052; DB 21; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGTAGTGTATTATATCCCGGTGAGTTCCTCAAGAGGCCACTTTAGTCCAGCGAGT 60
DB 459 CGGTAGTGTATTATATCCCGGTGAGTTCCTCAAGAGGCCACTTTAGTCCAGCGAGT 518
QY 61 AGAGTTTCTCTCCGAGCGGCTCCGACACCGGAGCTGAATAATGACATTTATCTGCC 120
DB 519 AGAGTTTCTCTCTCCGAGCGGCTCCGACACCGGAGCTGAATAATGACATTTATCTGCC 578
QY 121 ACGAGGTGTTATTAACGAAATAGCCGCACTCTTTGACACCTGATCGAAGAG 180
DB 579 ACGAGGTGTTATTAACGAAATAGCCGCACTCTTTGACACCTGATCGAAGAG 638
QY 181 TACTGGCTGATATCTTCCACTCTCTAGCCATTTGAACCACTTCACTTCAAGAACTGT 240
DB 639 TACTGGCTGATATCTTCCACTCTCTAGCCATTTGAACCACTTCACTTCAAGAACTGT 698
QY 241 ATGATTTAGAAGTGAAGGCCCGGAGATCCCAACGAGAGAGCGGTTTGGCAGATTTTTC 300
DB 699 ATGATTTAGAAGTGAAGGCCCGGAGATCCCAACGAGAGAGCGGTTTGGCAGATTTTTC 758
QY 301 CCGACTGTATATGTTGCGGTGACAGAGAGATGACTTACTCACTTTTCCGCGGCGC 360
DB 759 CCGACTGTATATGTTGCGGTGACAGAGAGATGACTTACTCACTTTTCCGCGGCGC 818
QY 361 CCGGTTTCTCCGAGCGGCTCACTTTCCCGGACGCGGACCGGAGAGAGAGAGCT 420
DB 819 CCGGTTTCTCCGAGCGGCTCACTTTCCCGGACGCGGACCGGAGAGAGAGAGCT 878
QY 421 TGGGTCCGTTTCTATATCCAAACCTTGTACCGAGGTGATGATCTTACCTGCCACAGG 480
DB 879 TGGGTCCGTTTCTATATCCAAACCTTGTACCGAGGTGATGATCTTACCTGCCACAGG 938
QY 481 CTGGCTTTCAACCCAGTGAACGAGAGATGAAGGGTGAAGAGTTTGTGTAGATTATG 540
DB 939 CTGGCTTTCAACCCAGTGAACGAGAGATGAAGGGTGAAGAGTTTGTGTAGATTATG 998
QY 541 TGAAGCAACCCCGGACAGGTGTGAGTCTTGTCACTTATCAACCGAGAAATACGGGGGAC 600
DB 999 TGAAGCAACCCCGGACAGGTGTGAGTCTTGTCACTTATCAACCGAGAAATACGGGGGAC 1058
QY 601 CAGATATTATGTGTGCTTGTGCTATATGAGACCTGTGCAATGTTGTCTACAGTAAGT 660
DB 1059 CAGATATTATGTGTGCTTGTGCTATATGAGACCTGTGCAATGTTGTCTACAGTAAGT 1118
QY 661 GAAATATTATGAGGAGTGGTATAGAGTGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
DB 1119 GAAATATTATGAGGAGTGGTATAGAGTGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1178
QY 721 TTTTACAGTTTGT 780
DB 1179 TTTTACAGTTTGT 1238
QY 781 TGAACCTGAGCCTGAGCCGAGCCAGAACCGAGACTGCAAGACTTACCCGCGCTCTTA 840
DB 1239 TGAACCTGAGCCTGAGCCGAGCCAGAACCGAGACTTACCCGCGCTCTTA 1298
QY 841 AATGGCGCTGTACTTCTGAGAGCGCCGACATCACTGTGTCTTGAAGAAATGCAATAGTAG 900

Db 1299 AATGGCGCTGCTATCCTGAGAACGCCGACATCACCTGTCTAGAGAAATGCAATAGTAG 1358
Qy 901 TACGGATAGCTGTGACTCCGGTCTTCTTAACACACCTCTGAGATACACCCGGTGGTCC 960
Db 1359 TACGGATAGCTGTGACTCCGGTCTTCTTAACACACCTCTGAGATACACCCGGTGGTCC 1418
Qy 961 GCTGTGCCCCCATTAACACAGTTGCGGTGAGATGTTGGTGGGGTGGCCGAGGCTGTGGAAATG 1020
Db 1419 GCTGTGCCCCCATTAACACAGTTGCGGTGAGATGTTGGTGGGGTGGCCGAGGCTGTGGAAATG 1478
Qy 1021 TATGAGAGACTTGTCTTAACGAGACCTGGCAACCTTGGACTTGAAGCTTAACGCCCCAG 1080
Db 1479 TATGAGAGACTTGTCTTAACGAGACCTGGCAACCTTGGACTTGAAGCTTAACGCCCCAG 1538
Qy 1081 GCCATAGGTGTAAACCTGTGATTCGTGTGTGTGTTAACGCTTTTGTGTCTGAATGAT 1140
Db 1539 GCCATAGGTGTAAACCTGTGATTCGTGTGTGTGTTAACGCTTTTGTGTCTGAATGAT 1598
Qy 1141 TGATGTAGTTTAAATTAAGGGTGAAGATAATGTTTAACTTGGATGGCGTGTAAATGGGGC 1200
Db 1599 TGATGTAGTTTAAATTAAGGGTGAAGATAATGTTTAACTTGGATGGCGTGTAAATGGGGC 1658
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Qy 1321 CAGTAACCTCTGTGTGTGTGAGAGTTCTGTGGGGCTCAATCCGAGCAAGTTAGTGTGAG 1380
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Qy 1381 AATTAAGAGAGATTAACAAGTGGAAATTTGAAGAGCTTTGAATCTGTGGTGAAGCTGT 1440
Db 1839 AATTAAGAGAGATTAACAAGTGGAAATTTGAAGAGCTTTGAATCTGTGGTGAAGCTGT 1898
Qy 1441 TGATTTCTTGAATCTGGGTCAACAGGCGCTTTTCCAGAGAAAGTCATCAAGACTTTGGA 1500
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Qy 1501 TTTTTCACACCGGGGCGCGCTGCGTGTGTCTTTTGAAGTTTAAAGAGATAA 1560
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Qy 1561 ATGAGCGAAGAAACCATCTGAGCGGGGGGTACCTGTGATTTTCTGCGCATGCACT 1620
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Qy 1741 GCAAGAGCCATGGAACCCGAGAGCGGCTGGAACCTCGGGAATGAATGTTGTACAGGTG 1800
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Db 2259 GCTGAACCTGATCCAGAACTGAGACGCAATTTTGAACAATTACAGAGATGGCAGGGGCTA 2318
Qy 1861 AAGGGGGTAAAGAGAGAGAGCGGGGGCTTGTAGGTAAAGAGAGAGCTTAAGAAATCTAGCT 1920
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Qy 2101 AGGCGAATTTGCAAGTACAGAGTACAGAACTTGTAAATATCAGAAATTTGTCTACATT 2160
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Db 2619 TCTGGAAACGGGGCCGAGAGTGAAGATAGATACGAGAGATAGGGTGGCTTTAGATGTAAGC 2678
Qy 2221 ATGATTAATATAGTGGCGGGGGTGGCTTGGCATGGAACGGGGGTGTTATTAAGATGTAAGG 2280
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Qy 2281 TTTACTGGCCCAATTTTAAAGCGTACGATTTTCTTGGCCCAATACCAACTTATCTACAC 2340
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Db 2919 TCAATTAAGAAATGCTCTTGTGAAGGATGTAACCTTGGGTAATCTGTCTGAGGGTAACTCC 2978
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Db 3099 TGCTGGAGCGCAACTGTCACTGTGAAAGCAATTCACGTAGCCAGCACTCTTGCAAG 3158
Qy 2701 GCTGGCAAGTGTGTGACATTAATGACACCGCTGTCTTGTGCAATTTGGGTAAACAGG 2760
Db 3159 GCTGGCAAGTGTGTGACATTAATGACACCGCTGTCTTGTGCAATTTGGGTAAACAGG 3218
Qy 2761 AGGGGGGTGTCCCACTTACCAATGCAATTTGATGTAACCTAAGATTAATGCTTGAAGCC 2820
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Db 3279 GAGAGCATGTCCAAAGGTGAACCTGAAAGGGGTGTTTGAACAATGACATGAAGATCTGAAAG 3338
Qy 2881 GTGCTGAGTACGATGAGAACCCGACCAAGGTGACAGACCTTGTGAGTGTGGCGTAAACAT 2940
Db 3339 GTGCTGAGTACGATGAGAACCCGACCAAGGTGACAGACCTTGTGAGTGTGGCGTAAACAT 3398
Qy 2941 ATTAGGAACAGAGCTGTGATGATGTGATGATGATGATGATGATGATGATGATGATGATG 3000
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Db 3459 CTGGCTTGACCCGCGCTGAGTGTGGCTTACGATGAAGATACAGATTGAG 3510


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RESULT 11
US-10-492-178-8
Sequence 8, Application US/10492178
Publication No. US20040247615A1
GENERAL INFORMATION:
APPLICANT: Emimi, Emilio A.
APPLICANT: Kaelow, David C.
APPLICANT: Bett, Andrew J.
APPLICANT: Shiver, John W.
APPLICANT: Nicolsia, Alfredo
APPLICANT: Lahm, Armin
APPLICANT: Luzago, Aleesandra
APPLICANT: Corcese, Riccardo
APPLICANT: Colloca, Stefano
TITLE OF INVENTION: HEPATITIS C VIRUS VACCINE
FILE REFERENCE: ITR00157P
CURRENT APPLICATION NUMBER: US/10/492,178
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: PCT/US02/32512
PRIOR FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 60/363,774
PRIOR FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: 60/328,655
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 35935
TYPE: DNA
ORGANISM: Adenovirus serotype 6
US-10-492-178-8

Query Match      100.0%; Score 3052; DB 21; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CGGTAGTGTATTTATACCGCGTGAATTCCTCAAGAGCCACTCTTAGTCCAGCAGT  60
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QY      61  AGAGTTTCTCTCCGAGCGCTCCGACACCGGGACTGAAATGACATATATCTGCC  120
DB      519  AGATTTTCTCTCCGAGCGCTCCGACACCGGGACTGAAATGACATATATCTGCC  578
QY      121  ACGGAGGTATTAACGGAATAATGCGCGCACTTTTGGACAGCTGATCGAAGAGG  180
DB      579  ACGGAGGTATTAACGGAATAATGCGCGCACTTTTGGACAGCTGATCGAAGAGG  638
QY      181  TACTGCGTGAATATCTTCACTCTAGCCATTTTGAACACACTACCTTACGACATGT  240
DB      639  TACTGCGTGAATATCTTCACTCTAGCCATTTTGAACACACTACCTTACGACATGT  698
QY      241  ATGATTTAGACGTACCGGCCCCGGAAGATCCCAAGAGAGGCGGTTTGGAGATTTTC  300
DB      699  ATGATTTAGACGTACCGGCCCCGGAAGATCCCAAGAGAGGCGGTTTGGAGATTTTC  758
QY      301  CCGACTCTGTAATGTGGCGGTGACGAGAGGATTTGACTTACTCATTTTCCGCGCGCC  360
DB      759  CCGACTCTGTAATGTGGCGGTGACGAGAGGATTTGACTTACTCATTTTCCGCGCGCC  818
QY      361  CCGGTTCTCCGAGACCGCTCACTTTCCTCCGACACCGGACACCGGAGAGAGAGCT  420
DB      819  CCGGTTCTCCGAGACCGCTCACTTTCCTCCGACACCGGAGAGAGAGAGCT  878
QY      421  TGGGTCCGTTTCTATGCAAACTTTGTAACCGAGGTGATGATCTTACCTGCCACGAG  480
DB      879  TGGGTCCGTTTCTATGCAAACTTTGTAACCGAGGTGATGATCTTACCTGCCACGAG  938
QY      481  CTGGCTTTCCACCGAGTACGAGAGGATGAAAGGGTGAAGAGGTTGTGTAGATTAATG  540
DB      939  CTGGCTTTCCACCGAGTACGAGAGGATGAAAGGGTGAAGAGGTTGTGTAGATTAATG  998
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QY      541  TGGAGACACCCCGGACGCTTGACAGTCTTGCTATATATCAACCGAGGAATACGGGGACC  600
DB      999  TGGAGACACCCCGGACGCTTGACAGTCTTGCTATATATCAACCGAGGAATACGGGGACC  1058
QY      601  CAGATATATATGTTGCTTGTCTATATGAGACCTGTGCGATGTTGTCTACAGTAAGT  660
DB      1059  CAGATATATATGTTGCTTGTCTATATGAGACCTGTGCGATGTTGTCTACAGTAAGT  1118
QY      661  GAAATATATGGGACGTGGGTGATGAGATGGGTGTTGGTGTATTTTTTTTTTAAT  720
DB      1119  GAAATATATGGGACGTGGGTGATGAGATGGGTGTTGGTGTATTTTTTTTTTAAT  1178
QY      721  TTTTACAGTTTGTGTTTAAAGATTTGTATGTGATTTTTTTTAAAGTCCGTGTC  780
DB      1179  TTTTACAGTTTGTGTTTAAAGATTTGTATGTGATTTTTTTTAAAGTCCGTGTC  1238
QY      781  TGAACCTGACCTGAGCCCGACCGAGACCGAGCTGCAAGACTTACCCGCGCTCTAA  840
DB      1239  TGAACCTGACCTGAGCCCGACCGAGACCGAGCTGCAAGACTTACCCGCGCTCTAA  1298
QY      841  AATGCGCCCTGCTATCTGAGAGCCCGACATCACTGTGCTAGAGAAATGATAGTAG  900
DB      1299  AATGCGCCCTGCTATCTGAGAGCCCGACATCACTGTGCTAGAGAAATGATAGTAG  1358
QY      901  TACGATAGCTGTGACTCCGCTCTTCTTAAACACACTCTGAGATACACCCGCTGTC  960
DB      1359  TACGATAGCTGTGACTCCGCTCTTCTTAAACACACTCTGAGATACACCCGCTGTC  1418
QY      961  GCTGTGCCCATTTAAACCAAGTGGCTGTGAGATTTGTGGGCGTGCAGAGCTGTGAATG  1020
DB      1419  GCTGTGCCCATTTAAACCAAGTGGCTGTGAGATTTGTGGGCGTGCAGAGCTGTGAATG  1478
QY      1021  TATGAGAGCTGTGTTAAGAGCTGCGGCAACCTTTGAGCTGATGATGAAAGCCCGAG  1080
DB      1479  TATGAGAGCTGTGTTAAGAGCTGCGGCAACCTTTGAGCTGATGATGAAAGCCCGAG  1538
QY      1081  GCCATTAAGTGTAAACCTGTGATTCGTGTGTGTATACGCTTGTGTGCTGATGAGT  1140
DB      1539  GCCATTAAGTGTAAACCTGTGATTCGTGTGTGTATACGCTTGTGTGCTGATGAGT  1598
QY      1141  TGATGTAAATTATTAAGGCTGATATGTTTAACTTGATGGCTGTAAATGGGGC  1200
DB      1599  TGATGTAAATTATTAAGGCTGATATGTTTAACTTGATGGCTGTAAATGGGGC  1658
QY      1201  GGGGCTTAAAGGGATTAATATGCGCGTGGGCTAATCTTGCTTACATCTGACCTATGGA  1260
DB      1659  GGGGCTTAAAGGGATTAATATGCGCGTGGGCTAATCTTGCTTACATCTGACCTATGGA  1718
QY      1261  GCGTTGGAGGTGTTGGAGATTTTCTGCTGTGCTAATCTGTGAGACAGACTCTAA  1320
DB      1719  GCGTTGGAGGTGTTGGAGATTTTCTGCTGTGCTAATCTGTGAGACAGACTCTAA  1778
QY      1321  CAGTACTCTTGGTTTGGAGGTTTCTGTGGGCTCATCCAGGCAAAATTAGTCTGAG  1380
DB      1779  CAGTACTCTTGGTTTGGAGGTTTCTGTGGGCTCATCCAGGCAAAATTAGTCTGAG  1838
QY      1381  AATTAAAGAGATTAACAAGTGGGAAATTGAAGACTTTTGAATACCTGTGTGAGCTGT  1440
DB      1839  AATTAAAGAGATTAACAAGTGGGAAATTGAAGACTTTTGAATACCTGTGTGAGCTGT  1898
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QY      1501  TTTTTCACACCGGGGGCGGCTGCGGCTGCTGTGCTTTTGAAGTTTATAAAGATTA  1560
DB      1959  TTTTTCACACCGGGGGCGGCTGCGGCTGCTGTGCTTTTGAAGTTTATAAAGATTA  2018
QY      1561  ATGAGCGAAGAAACCAATCTGAGCGGGGGTACCTGCTGATTTTCTGGCATGCACT  1620
DB      2019  ATGAGCGAAGAAACCAATCTGAGCGGGGGTACCTGCTGATTTTCTGGCATGCACT  2078
QY      1621  GTGAGAGCGGTTGTGAGACACAAGATCGCTGTACTGTGTCTTCCGTCCGCCGCGC  1680
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Db 2139 GATTAATCCGACGGAGAGCAGCAGCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2198
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|
Qy 1741 GCAGAGCCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
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|
Db 2139 GCAGAGCCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2258
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Qy 1801 GCTGAACGTATCCAGAACTGAGAGCAGATTTTGACAAATTAACAGAGATGGGAGGGGCTA 1860
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Db 2259 GCTGAACGTATCCAGAACTGAGAGCAGATTTTGACAAATTAACAGAGATGGGAGGGGCTA 2318
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Qy 1861 AAGGGGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
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Db 2319 AAGGGGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2378
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Qy 1921 TTTAGCTTAATGACAGACACCGTCTGAGTATTAATTAATTAATTAATTAATTAATTAATTAAT 1980
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|
Db 2379 TTTAGCTTAATGACAGACACCGTCTGAGTATTAATTAATTAATTAATTAATTAATTAATTAAT 2438
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|
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Qy 2041 TGCGCTGACAGCAGGGAGATTAATTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2100
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Db 2499 TGCGCTGACAGCAGGGAGATTAATTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2558
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Db 2619 TCTGGGAAACGGGGCCGAGAGTGAAGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2678
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RESULT 12
US-10-492-178-9
; Sequence 9, Application US/10492178
; Publication No. US20040247615A1
; GENERAL INFORMATION:
; APPLICANT: Emili, Emilio A.
; APPLICANT: Kaslow, David C.
; APPLICANT: Bell, Andrew J.
; APPLICANT: Shiver, John W.
; APPLICANT: Nicosia, Alfredo
; APPLICANT: Lahm, Armin
; APPLICANT: Luzzago, Alessandra
; APPLICANT: Cortese, Riccardo
; APPLICANT: Colloca, Stefano
; TITLE OF INVENTION: HEPATITIS C VIRUS VACCINE
; FILE REFERENCE: ITR0015YP
; CURRENT APPLICATION NUMBER: US/10/492,178
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: PCT/US02/32512
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 60/363,774
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/328,655
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 35935
; TYPE: DNA
; ORGANISM: Adenovirus serotype 5
US-10-492-178-9

Query Match 100.0%; Score 3052; DB 21; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGTAGATTAATTAATCCCGGTGAGTTCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
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Db 459 CGGTAGATTAATTAATCCCGGTGAGTTCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 518
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Qy 61 AGAGTTTCTCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
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Db 519 AGAGTTTCTCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 578
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Qy 121 ACGAGGTGTTATTAACGAGAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
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Db 579 ACGAGGTGTTATTAACGAGAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 638
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Qy 181 TACGTGATTAATCTTCCAGCTCTAGCAATTTTGAACCAACCTTACAGAGAGAGAGAGAG 240
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Db 639 TACTGCGTGAATATCTTCCACCTCCTAGCCATTTTGAACCACTACCTTCACGAACTGT 698
Qy 241 ATGATTTAGAGTGAACGGCCCCCGAAGATCCCAAGAGAGCGGTTTCGAGATTTTTC 300
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Qy 301 CCGACTCTGATATGTGGCGGTGCAAGAAAGGATTTGACTTCACTTTCGCGCGGCGC 360
Db 759 CCGACTCTGATATGTGGCGGTGCAAGAAAGGATTTGACTTCACTTTCGCGCGGCGC 818
Qy 361 CCGGTTCTCCGAGCGCCCTCACTTTCCCGAGACCCGAGACGCCGAGACAGAGGCTT 420
Db 819 CCGGTTCTCCGAGCGCCCTCACTTTCCCGAGACCCGAGACGCCGAGACAGAGGCTT 878
Qy 421 TGGGTCGGGTTTCTATGCAACCTTGTACCGGAGGTATGATCTTACCTGCAACGAG 480
Db 879 TGGGTCGGGTTTCTATGCAACCTTGTACCGGAGGTATGATCTTACCTGCAACGAG 938
Qy 481 CTGGCTTTCACCCAGTACGACGAGATGAAAGAGGTGAGAGTTGTGTAATATG 540
Db 939 CTGGCTTTCACCCAGTACGACGAGATGAAAGAGGTGAGAGTTGTGTAATATG 998
Qy 541 TGAAGACCCCGGAGCAAGGTTGCAAGTCTTGTCAATATCAACGAGAAATACGAGGACC 600
Db 999 TGAAGACCCCGGAGCAAGGTTGCAAGTCTTGTCAATATCAACGAGAAATACGAGGACC 1058
Qy 601 CAGATATATATGTTGCTTGTGCTATATAGAGACCTGAGGACGTTGTTCTACAGTAA 660
Db 1059 CAGATATATATGTTGCTTGTGCTATATAGAGACCTGAGGACGTTGTTCTACAGTAA 1118
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Qy 721 TTTTACAGTTTGTGTTTAAAGAAATTTTGTATGTGATTTTTTTTAAAGGTCTGTGTC 780
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Qy 781 TGAACCTGAGGCTGAGCCGAGCCGAGACCGGAGGCTGCAAGACCTACCCCGGCTCAA 840
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Db 1539 GCCATAGGTGTAACCTGTGATTCGTTGTGTGTTAAAGCCTTTGTTGCTGAATGAGT 1598
Qy 1141 TGATGTAGTTTAAATTAAGGGTGAATATGTTTAACTTGCAATGGCGGTTAAATGGGGC 1200
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Qy 1741 GCAGAGCCCATGGAACCCGAGAGCCGAGCTGGAACCTCGGGAATGAATGTTTGAACAGTGTG 1800
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Qy 1801 GCTGAATCTGTATCCAGAACTGAGACGCAATTTTGACATTTACAGAGATGGCAGAGGCTTA 1860
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Qy 2221 ATGATTAATATGTTGGCGGGGCTGCTTGGCATGAGACGGGGGTGTTATTAATGAATGAAG 2280
Db 2679 ATGATTAATATGTTGGCGGGGCTGCTTGGCATGAGACGGGGGTGTTATTAATGAATGAAG 2738
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Db 2739 TTTACTGCCCCCAATTTTTCAGCGATTCCTGTGCAATCAACCTTATCTTACAC 2798
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QY 2401 CGGGGCTGTGCTTTTAACTGCTGCTGGAAGGGGGTGTGTGCTCCGCCCAAAAGAGGAGCT 2460
DB 2859 CGGGGCTGTGCTTTTAACTGCTGCTGGAAGGGGGTGTGTGCTCCGCCCAAAAGAGGAGCT 2918
QY 2461 TCAATTAAGAAATGCTCTTTTGAAGAGTGTACTTTGGGTATCTGTCTGAGGGTAACTCC 2520
DB 2919 TCAATTAAGAAATGCTCTTTTGAAGAGTGTACTTTGGGTATCTGTCTGAGGGTAACTCC 2978
QY 2521 AGGGTGGCCCAATATGTCGCTCCGACTGTGTGTCTTCACTAGTGAAGAAAGCTGTGCT 2580
DB 2979 AGGGTGGCCCAATATGTCGCTCCGACTGTGTGTCTTCACTAGTGAAGAAAGCTGTGCT 3038
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DB 3039 GTGATTAAGCAATACATGCTATGTGGCAATGCGAGGA CAAGGGCTCTCAATATGCTGACC 3098
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DB 3099 TGCTCGGACGGCAACTGTCACTGCTGGAAGCAATTCAGTACGAGCACTCTCGCAAG 3158
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DB 3159 GCGTGGCCAGTGTGTTAGCATTAACATACTGACCCGCTGTCTTGTCAATTTGGGTAAACAG 3218
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DB 3219 AGGGGGGTGTCTTACCTTACCAATGCAATTTGATGCACTTAAGATATTTGCTGAGCCC 3278
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DB 3279 GAGAGCATGTCTCAAGTGAACCTGAAACGGGGTGTGTTGATGATGACATGACATGAAGATCTGAAAG 3338
QY 2881 GTGTGAGGTACGATGAGACCCGCAACGAGTGTGAGACCCCTGCAAGTGTGGCGGTAAACAT 2940
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DB 3399 ATTAGGAACCAAGCTGTGATGCTGATGTGACCGAGAGCTGAGAGCCCGATCACTTGGTG 3458
QY 3001 CTGGGCTGCAACCCGCGCTGAGTGTGCTCTGAGCGATGAAGATGAGATTGAG 3052
DB 3459 CTGGGCTGCAACCCGCGCTGAGTGTGCTCTGAGCGATGAAGATGAGATTGAG 3510

RESULT 13
US-10-433-681-1
; Sequence 1, Application US/10433681
; Publication No. US20040146856A1
; GENERAL INFORMATION:
; APPLICANT: IGGO, RICHARD
; APPLICANT: HOMICKO, KRISTIAN
; APPLICANT: FUERER, CHRISTOPHE
; TITLE OF INVENTION: ANTI-NEOPLASTIC AGENTS
; FILE REFERENCE: 604-687
; CURRENT APPLICATION NUMBER: US/10/433,681
; PRIOR FILING DATE: 2003-06-04
; PRIOR APPLICATION NUMBER: PCT/GB02/03211
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: GB 0117198.2
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 35935
; TYPE: DNA
; ORGANISM: Adenovirus type 5
US-10-433-681-1

Query Match 100.0%; Score 3052; DB 24; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 519 AGAGTTTCTCTCCGAGCGGCTCCGACACCGGGAGTGAATAAGACATATATCTGCGC 578
QY 121 ACGGAGGTGTATTAACGAAGAAATGAGCCGCACTTTTGGACAGCTGATCGAAGAG 180
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QY 241 ATGATTTAGACGTACGAGCCCGGCAAGATCCCAACGAGAGGCGGTTCGAGATTTTTC 300
DB 699 ATGATTTAGACGTACGAGCCCGGCAAGATCCCAACGAGAGGCGGTTCGAGATTTTTC 758
QY 301 CCGACTGTATATGTTGGCGGTGAGAGAGGATTTGACTTCACTTTTCGCGCGGC 360
DB 759 CCGACTGTATATGTTGGCGGTGAGAGAGGATTTGACTTCACTTTTCGCGCGGC 818
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QY 421 TGGGTCCGGTTTCTATGACCAAACTTGTACCGAGGTGATGATCTTACCTGCGACAGAG 480
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QY 481 CTGGCTTTCACCAACGATGACGACGAGATGAAGAGGTGAGAGTGTGTATTAATG 540
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QY 541 TGAAGCACCCCGGACAGGTTGACAGTCTTGTCTTATTCACCGAGAAATCGGGGAGC 600
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Db 1539 GCCATTAAGGTCTAAACCTGTGATTCGCTGTGTGTGAACGCTTTGTTGCTGATGAGT 1598
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Db 1779 CAGTACTCTTGTGTTTGAAGGTTTCTGTGGGCTCATCCAGCAAAAGTTAGTGTGAG 1838
Qy 1381 AATTAAAGGATTAACAAGTGGAAATTTGAAGGCTTTGAAATCTGTGTGTGAGCTGT 1440
Db 1839 AATTAAAGGATTAACAAGTGGAAATTTGAAGGCTTTGAAATCTGTGTGTGAGCTGT 1898
Qy 1441 TGATTTCTTGAATCTGTGCTACACAGCGCTTTTCCAGAAGAGTCAATCAAGACTTTGA 1500
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Qy 1501 TTTTTCACACCGGGGGCGCGCTGCGCTGTGTGCTTTTGAAGTTTAAAGATTA 1560
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Qy 1561 ATGAGGCAAGAAACCCATCTGAGCGGGGGGTAACCTGTGATTTTCTGGCATGCACT 1620
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Qy 1741 GCAGAGCCCATGGAACCCGAGAGCGCGCTGGAACCTGTGGGAATGAATGTTGACAGGTG 1800
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Db 2259 GCTGAACGTATCCAGAACTGAGACGCAATTTTGAACAATTAAGAGATGGCAGGGGCTA 2318
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Db 3459 CTGGCTGACACCGCGCTGATTTGCTTGAAGATGAAGATGAAGATTTGAG 3510

RESULT 14
US-10-612-285-1
; Sequence 1, Application US/10612285
; Publication No. US20050175589A1
; GENERAL INFORMATION:
; APPLICANT: IGO, RICHARD DEREK
; APPLICANT: FUERER, CHRISTOPHE
; APPLICANT: HOMICKO, KRISTIAN GYULA
; TITLE OF INVENTION: ANTI-NEOPLASTIC VIRAL AGENTS
; FILE REFERENCE: 604-689
; CURRENT APPLICATION NUMBER: US/10/612,285
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 10/433,681
; PRIOR FILING DATE: 2003-06-04

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PRIOR APPLICATION NUMBER: PCT/GB02/03211
PRIOR FILING DATE: 2002-07-12
PRIOR APPLICATION NUMBER: GB 0117198.2
PRIOR FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patent Ver. 3.2
SEQ ID NO: 1
LENGTH: 35935
TYPE: DNA
ORGANISM: Adenovirus type 5
US-10-612-285-1

Query Match      100.0%; Score 3052; DB 24; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 AGAGTTTCTCTCCGAGCCGCTCCGACACCGGAGCTGAATAATGACATATTAATCTGCC 120
DB 519 AGAGTTTCTCTCCGAGCCGCTCCGACACCGGAGCTGAATAATGACATATTAATCTGCC 578
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DB 579 ACCGAGGTGTATTAACCGAAGAAATGCGCCGCACTTTTGAGACCAGTGAATGCAAGAG 638
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DB 1179 TTTTACAGTTTGTAGTTTAAAGAAATTTGTATGTGATTTTAAAGAGTCTGTGTC 1238
QY 781 TGAACCTGAGCCTGAGCCGAGCAACCGAGCCTGCAAGACTACCCGCTCTTAA 840
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DB 1299 AATGGCCCTGCTATCTGTAGAGCCCGAGCACTACCTGTGTGTAGAGAAATGCAATAGTAG 1358
QY 901 TACGATATGCTGTGACTCCGCTCTTCTTAACACACTCTGAGATAGAACCCGAGTGTCCC 960
DB 1359 TACGATATGCTGTGACTCCGCTCTTCTTAACACACTCTGAGATAGAACCCGAGTGTCCC 1418
QY 961 GCTGTGCCCATTAACCAAGTTGCCGTGAGAGTGTGGGCGTCCGAGGCTGTGAATG 1020
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DB 1479 TATCGAGGACTGTGTTACGAGCCTGGGCAACCTTTGAGCTTGAGCTGTAAACGCCCCAG 1538
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QY 1441 TGATTTCTTGAATCTGTGTGACCAAGCGCTTTTCAAGAGAGTCAATCAAGACTTTTGA 1500
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QY 1561 ATGAGAGGAAAGAAACCAATCTGAGCGGGGGTACTGTGATTTTCTGCCATGCACT 1620
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QY 1621 GTGAGAGCGGTTGTGAGACCAAGAAATGCGCTGTCTGTGTGCTTCCGTCGCGCCGCGC 1680
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DB 2259 GCTGAACCTGATCCAGAACTGAGACGATTTTGAATTTACAGAGATGAGGACAGGGCTA 2318
QY 1861 AAGGGGTAAAGAGAGAGCGGGGCTTGTGAGCTTACAGAGAGGCTAGAAATCTAGCT 1920
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QY 1921 TTTTACCTTAATGACCAACACCGCTGTGATGTATTAATTTTCAACGATCAAGGATTAAT 1980
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Db 2379 TTATAGTTAATGACAGACCGGTCTGATGTATTAATTCTTTCAACAGATCAAGATATAT 2438
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Db 2499 TGGCTGACGACGAGGAGTATTTAGAGAGGCTATTAGGATATATGCAAAAGGTGCACTT 2558
Qy 2101 AGGCCAAGTTCAGACTACAGATCAAGCAACTTGTAAATACAGAAATGTTGCTTACATT 2160
Db 2559 AGGCCAAGTTCAGACTACAGATCAAGCAACTTGTAAATATACAGAAATGTTGCTTACATT 2618
Qy 2161 TCTGGGAAACGGGGCCGAGGTGAGATAGATACGAGAGATAGAGGCTTATAGATAGAC 2220
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Qy 2221 ATGATTAATATGTGGCCGAGGAGCTTGGCATGAGACGGGGGTGTTATATATGATAGTAAG 2280
Db 2679 ATGATTAATATGTGGCCGAGGAGCTTGGCATGAGACGGGGGTGTTATATGATAGTAAG 2738
Qy 2281 TTTAAGTGGCCCAATTTTAAAGCGGTATTCCTGACCAATACCAACTTATCTTACAC 2340
Db 2739 TTTAAGTGGCCCAATTTTAAAGCGGTATTCCTGACCAATACCAACTTATCTTACAC 2798
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Db 2859 CGGGGCTGTGCTTTTAACTGCTGTGAGAGGGGTGTGTGCTGCCCCCAAAAGAGGAGCT 2918
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Db 3219 AGGGGGGTGTTCTTACCTTACCAATGCAATTTGAGTCACTAAGATATTTCTTGAAGCC 3278
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Db 3279 GAGAGCATGTCCAAAGGTGAACCTGAACGGGGTGTGTCATGACCATGAGATGAGAG 3338
Qy 2881 GTGCTGAGTTCAGATGAGACCGGACCGAGTGCAGACCTGTGAGTGTGGGTTAAGCAT 2940
Db 3339 GTGCTGAGTTCAGATGAGACCGGACCGAGTGCAGACCTGTGAGTGTGGGTTAAGCAT 3398
Qy 2941 ATTAGGAACCAAGCTGTGATCTGATGTGACCGAGAGCTGAGGCGCATCACTTGGTG 3000
Db 3399 ATTAGGAACCAAGCTGTGATCTGATGTGACCGAGAGCTGAGGCGCATCACTTGGTG 3458
Qy 3001 CTGGCTTCACCCGCGCTGAGTTGGCTTACGATGAGATGAAATCAAGTTGAG 3052
Db 3459 CTGGCTTCACCCGCGCTGAGTTGGCTTACGATGAGATGAAATCAAGTTGAG 3510

RESULT 15
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; Sequence 732, Application US/10794514A
; Publication No. US20050112134A1
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas
; APPLICANT: Laus, Reiner
; APPLICANT: Diegel, Michael
; APPLICANT: Vidovic, Damir
; TITLE OF INVENTION: Compositions and Methods Employing Alternative
; TITLE OF INVENTION: Reading Frame Polypeptides for the Treatment of
; FILE REFERENCE: 11311.1003U
; CURRENT APPLICATION NUMBER: US/10/794,514A
; NUMBER OF SEQ ID NOS: 733
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 732
; LENGTH: 35938
; TYPE: DNA
; ORGANISM: Adeno Virus
US-10-794-514A-732
Query Match 100.0%; Score 3052; DB 22; Length 35938;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 459 CGTGTAGTGTATTATATACCCGGTGAAGTTCTCTCAAGAGGCCACTTGTAGTCCAGAGT 518
Qy 61 AGAGTTTCTCTCCGAGCCGCTCCGACACCGGAGCTGAAATATGACATTTATCTGCC 120
Db 519 AGAGTTTCTCTCCGAGCCGCTCCGACACCGGAGCTGAAATATGACATTTATCTGCC 578
Qy 121 ACGGAGGTATTATACGGAAGAAATGGCGCAGTCTTTTGAACAGCTGATCGAAGAG 180
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Qy 181 TACTGCTGATTAATCTTCAACTCTTACGATTTTGAACCACTTACCGAACTGT 240
Db 639 TACTGCTGATTAATCTTCAACTCTTACGATTTTGAACCACTTACCGAACTGT 698
Qy 241 ATGATTTAGACGTGACGGCCCCCGAAGATCCCAAGAGAGGGGTTTCCGAGATTTTC 300
Db 699 ATGATTTAGACGTGACGGCCCCCGAAGATCCCAAGAGAGGGGTTTCCGAGATTTTC 758
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Db 759 CCGACTCTGATATGTTGGCGGTGAGAGGAGATTAAGTCACTTTTCCGCGGCGC 818
Qy 361 CCGGTTCTCCGAGCCGCTCACTTTTCCCGGAGCCCGAGACCGGAGAGAGAGCT 420
Db 819 CCGGTTCTCCGAGCCGCTCACTTTTCCCGGAGCCCGAGAGCCGAGAGAGAGGCT 878
Qy 421 TGGGTCCGGTTTCTATGCCAAACCTTGTACCGAGGTGATGATCTTACCTGCCACAGG 480
Db 879 TGGGTCCGGTTTCTATGCCAAACCTTGTACCGAGGTGATGATCTTACCTGCCACAGG 938
Qy 481 CTGGCTTTCACCAAGTGAAGAGGATGAGAGGATGAGAGGATTTGTGTAGATTATG 540
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Qy 541 TGGAGACCCCGGAGCAGGTTGCAAGTCTTGTCAATATCAACCGAGGAATACGGGGAGC 600
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Qy 601 CAGATATTATGTGTTGCTTGTCTATATGAGACCTGTGCAATTTGTCTACAGTAACT 660
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QY	661	GAAATTTATGGGCACTGGGTGTATAGATGCTGGGTTTGCTGTGTAATTTTTTTTTTAAAT	720
Db	1119	GAAAATTATGGGCACTGGGTGTATAGAGGGGTGGGTTGGTGCTGTAAATTTTTTTTTTAAAT	1178
QY	721	TTTTACAGTTTGTGGCTTTAAAGAAATTTGTATTGTGATTTTTTTTTTAAAGAGCTCCGTGTC	780
Db	1179	TTTTACAGTTTGTGGCTTTAAAGAAATTTGTATTGTGATTTTTTTTTTAAAGAGCTCCGTGTC	1238
QY	781	TGAACCTGAGCCTGAGCCCGAGCCGAAACCGGAGCCTGCAAGACTTACCCTGCTCTAA	840
Db	1239	TGAACCTGAGCCTGAGCCCGAGCCGAAACCGGAGCCTGCAAGACTTACCCTGCTCTAA	1298
QY	841	AATGGCCGCTGCTATCTCTGAGACGCCCGACATCACTGTGTCTAGAGATGCAATAGTAG	900
Db	1299	AATGGCCGCTGCTATCTCTGAGACGCCCGACATCACTGTGTCTAGAGATGCAATAGTAG	1358
QY	901	TACGGATAGCTGTGATCTCCGGCTCTTAAACAACATCTGCTAGATATACCCGGGTGCTCC	960
Db	1359	TACGGATAGCTGTGATCTCCGGCTCTTAAACAACATCTGCTAGATATACCCGGGTGCTCC	1418
QY	961	GCTGTGCCCAATTAAACGAGTTGCCGTGAGAGTTGCTGGGCGTGGCCAGCCTGTGAAATG	1020
Db	1419	GCTGTGCCCAATTAAACGAGTTGCCGTGAGAGTTGCTGGGCGTGGCCAGCCTGTGAAATG	1478
QY	1021	TATCAGAGCATTTGCTTAAACGAGCCTGGGCAACTTTGGAATTGAGCTGTAAACGCCCCAG	1080
Db	1479	TATCAGAGCATTTGCTTAAACGAGCCTGGGCAACTTTGGAATTGAGCTGTAAACGCCCCAG	1538
QY	1081	GCCATPAAGGTGTAAACCTGTGATTTGGGTGTGTGTAAAGCTTTGTTTGTGTGAAATGAGT	1140
Db	1539	GCCATPAAGGTGTAAACCTGTGATTTGGGTGTGTGTAAAGCTTTGTTTGTGTGAAATGAGT	1598
QY	1141	TGATGTAAAGTTTAAATAAGGGGTAGATATGTATTAACTTGCATGGCGGTGTAAATGGGGC	1200
Db	1599	TGATGTAAAGTTTAAATAAGGGGTAGATATGTATTAACTTGCATGGCGGTGTAAATGGGGC	1658
QY	1201	GGGGCTTAAAGGGTATATATATGCGCCGTGGCTAACTTGTGTTACATCTGACTCATGGA	1260
Db	1659	GGGGCTTAAAGGGTATATATATGCGCCGTGGCTAACTTGTGTTACATCTGACTCATGGA	1718
QY	1261	GGCTTTGGGAGTGTTTGGAAAGATTTTTCGTGTGTGGTAACTTGTCTGGAAACGAACTCTTAA	1320
Db	1719	GGCTTTGGGAGTGTTTGGAAAGATTTTTCGTGTGTGGTAACTTGTCTGGAAACGAACTCTTAA	1778
QY	1321	CAGTACCTCTTGTTTTGGAGGTTTCTGTGGGGCTCATCCAGGCAAGTATGCTCAG	1380
Db	1779	CAGTACCTCTTGTTTTGGAGGTTTCTGTGGGGCTCATCCAGGCAAGTATGCTCAG	1838
QY	1381	AATTAAAGAGATTACAAGTGGAAATTTGAAGAAGCTTTTGAATCTGTGTGAGACTGT	1440
Db	1839	AATTAAAGAGATTACAAGTGGAAATTTGAAGAAGCTTTTGAATCTGTGTGAGACTGT	1898
QY	1441	TGATTTCTTGAATCTGGGTCACACAGGCGCTTTTCCAAGAAAGTCATCAAGACTTTTGA	1500
Db	1899	TGATTTCTTGAATCTGGGTCACACAGGCGCTTTTCCAAGAAAGTCATCAAGACTTTTGA	1958
QY	1501	TTTTTCCAACCCGGGGCGGCTGCGGCTGTGCTTTTGTGATTTTAAAGAGTAA	1560
Db	1959	TTTTTCCAACCCGGGGCGGCTGCGGCTGTGCTTTTGTGATTTTAAAGAGTAA	2018
QY	1561	ATGAGCGAAGAAACCAATCTGAGCGGGGGGTACTGCTGGAATTTTCTGGCCATGACTT	1620
Db	2019	ATGAGCGAAGAAACCAATCTGAGCGGGGGGTACTGCTGGAATTTTCTGGCCATGACTT	2078
QY	1621	GTGAGAGCGGTTGTGAGACACAAAGATCGCTGCTACTGTGTTCTTCGTTCCGCGCGGC	1680
Db	2079	GTGAGAGCGGTTGTGAGACACAAAGATCGCTGCTACTGTGTTCTTCGTTCCGCGCGGC	2138
QY	1681	GATTAATPACGAGCGAGGACAGCACAAGACAGAGAGAAACGAGCGGCGCGCGCAGGA	1740
Db	2139	GATTAATPACGAGCGAGGACAGCACAAGACAGAGAGAAACGAGCGGCGCGCGCAGGA	2198
QY	1741	GCAGGCCCATGGAACCCGAGAGCCGGGCTGGAACCTTGGGAAATGAATGTTGTACAGGTG	1800

Db	2199	GCAGAGCCCAATGGAAACCCGAGACCCGGCTCGAGACCTCCGGAATGATGTGTACAGGTG	2258
Qy	1801	GCTGCACTGATATCCAGAACTGGAACGCATTTTTCACATTTACAGAGGATGGCAGGGGCTTA	1860
Db	2259	GCTGCACTGATATCCAGAACTGGAACGCATTTTTCACATTTACAGAGGATGGCAGGGGCTTA	2318
Qy	1861	AAGGGGGTAAAGAGGGAGCGGGGGGCTTGTAGGCTTACAGAGAGGCTTAGAATCTTAGCT	1920
Db	2319	AAGGGGGTAAAGAGGGAGCGGGGGGCTTGTAGGCTTACAGAGAGGCTTAGAATCTTAGCT	2378
Qy	1321	TTTAGCTTAATGACCCAGACCGGTCGAGTGATTACTTTTCAACAGATCAAGATTAAT	1980
Db	2379	TTTAGCTTAATGACCCAGACCGGTCGAGTGATTACTTTTCAACAGATCAAGATTAAT	2438
Qy	1981	TGCCTTAATAGAGCTTGATCTGCTGGCGCAGAAATATTCATAGCAGCTGACCACTTAC	2040
Db	2439	TGCCTTAATAGAGCTTGATCTGCTGGCGCAGAAATATTCATAGCAGCTGACCACTTAC	2498
Qy	2041	TGCGTCGAGCCAGGGAGTGAATTTTGAAGAGGCTTAATAGGATATATGCAAGGTGSCACTT	2100
Db	2499	TGCGTCGAGCCAGGGAGTGAATTTTGAAGAGGCTTAATAGGATATATGCAAGGTGSCACTT	2558
Qy	2101	AGGCGCAATTTGCAAGTACAGATCAGCAAACTTGTAATATCAGGAATTTGCTCACTT	2160
Db	2559	AGGCGCAATTTGCAAGTACAGATCAGCAAACTTGTAATATCAGGAATTTGCTCACTT	2618
Qy	2161	TCTGGAAACGGGGCCGAGGTGAGATAGATACGGAGGATAGGGTGCCTTTAGATGTAC	2220
Db	2619	TCTGGAAACGGGGCCGAGGTGAGATAGATACGGAGGATAGGGTGCCTTTAGATGTAC	2678
Qy	2221	ATGATAAATATGTGGCCGGGGGGTGCTTGGCAGTGAACGGGGTGTTATTAAGATGTAAAG	2280
Db	2679	ATGATAAATATGTGGCCGGGGGGTGCTTGGCAGTGAACGGGGTGTTATTAAGATGTAAAG	2738
Qy	2281	TTTACTGGCCCCCAATTTTACGGGTACGGTTTTCTCTGGCCAAATACCAACTTATGCTACAC	2340
Db	2739	TTTACTGGCCCCCAATTTTACGGGTACGGTTTTCTCTGGCCAAATACCAACTTATGCTACAC	2798
Qy	2341	GGTGTAGCTTCAATGGGTTTAAACAATACCTGTGTGGAAGCCTGAGCCGATGTAAAGGTT	2400
Db	2799	GGTGTAGCTTCAATGGGTTTAAACAATACCTGTGTGTGGAAGCCTGAGCCGATGTAAAGGTT	2858
Qy	2401	CGGGGCTGTGCTTTTACTGCTGCTGGAAGGGGGTGTGTGTGCCCCAAAGCAGGGCT	2460
Db	2859	CGGGGCTGTGCTTTTACTGCTGCTGGAAGGGGGTGTGTGTGCCCCAAAGCAGGGCT	2918
Qy	2461	TCAATTAAAGAAATGCTCTTTTGAAGGTGTAACCTTGGGTATCTCTGTCTGAGGTTAACTCC	2520
Db	2919	TCAATTAAAGAAATGCTCTTTTGAAGGTGTAACCTTGGGTATCTCTGTCTGAGGTTAACTCC	2978
Qy	2521	AGGGTGGGCCAATGTGGGCTCCGACTGTGTGTGCTCACTGCTAATGAAAAGCGTGGCT	2580
Db	2979	AGGGTGGGCCAATGTGGGCTCCGACTGTGTGTGCTCACTGCTAATGAAAAGCGTGGCT	3038
Qy	2581	GTGATTTAAGATACATGATGTATGTGGCACTGCGAGACAGGGGCTCTCAGATGCTGACCC	2640
Db	3039	GTGATTTAAGATACATGATGTATGTGGCACTGCGAGACAGGGGCTCTCAGATGCTGACCC	3098
Qy	2641	TGCTCGGACGGCACTGTCACTGTCTGAGAGCAATTCAGTACGCCCACTTCCGACAG	2700
Db	3099	TGCTCGGACGGCACTGTCACTGTCTGAGAGCAATTCAGTACGCCCACTTCCGACAG	3158
Qy	2701	GGCCTGGGCAAGTTTGGACATAACATACGACCCGGCTTCCCTGATTTGGGTAAACAG	2760
Db	3159	GGCCTGGGCAAGTTTGGACATAACATACGACCCGGCTTCCCTGATTTGGGTAAACAG	3218
Qy	2761	AGGGGGGTGTTCCTACCTTACCAATGCAATTTAGTCACTAAGATATTTGCTTGAAGCCC	2820
Db	3219	AGGGGGGTGTTCCTACCTTACCAATGCAATTTAGTCACTAAGATATTTGCTTGAAGCCC	3278
Qy	2821	GAGAGCATGTTCAGAGGTGAACCTGGAACGGGGGTGTTGACATGACATGAAGATCTGGAAG	2880

Db	3279	GAGAGCATGTCCAAGTGAACCTGAACGGGGTGTTCATGACCATGAAGATCTGGAG	3338
Qy	2881	GTGCTGAGGTACGATGAGACCCGACACGAGTGCAGACCTGCGAGTGGGGTAAACAT	2940
Db	3339	GTGCTGAGGTACGATGAGACCCGACACGAGTGCAGACCTGCGAGTGGGGTAAACAT	3398
Qy	2941	ATTAGAACGAGCCTGTGATGCTGATGTGACCGAGGAGCTGAGGCCGATCACTTGGTG	3000
Db	3399	ATTAGAACGAGCCTGTGATGCTGATGTGACCGAGGAGCTGAGGCCGATCACTTGGTG	3458
Qy	3001	CTGGCTTGCAACCCGCGCTGAGTTGGCTCTAGCGATGAGATACAGATTGAG	3052
Db	3459	CTGGCTTGCAACCCGCGCTGAGTTGGCTCTAGCGATGAGATACAGATTGAG	3510

Search completed: October 28, 2005, 11:35:22
Job time : 8988 secs

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Db 401 ATCGATCTTACCTGCGCAGAGGCTGGCTTTCCACCAGCTACGACGAGATTGAAGAGGT 460

QY	61	GAGAGAGTTTGTTGTTAGATTATGTGTGAGACACCCCGGGCACCGGTTGACAGTCTTGTGCATTAT	120
Db	461	GAGAGGTTTGTTGATTAGATTATGTGTGAGACACCCCGGGCACCGGTTGACAGTCTTGTGCATTAT	520
QY	121	CACCGAGCAATTAACGGGGGAGCCACAGATATTATATGTTTGCTCTTGTCTATATAGAGACCGGT	180
Db	521	CACCGAGCAATTAACGGGGGAGCCACAGATATTATATGTTTGCTCTTGTCTATATAGAGACCGGT	580
QY	181	GGCATGTTTGTCTACAGTAAGTGAATAATATGAGCAGTGGGTGAATAGAGTGGTGGATTGG	240
Db	581	GGCATGTTTGTCTACAGTAAGTGAATAATATGAGCAGTGGGTGAATAGAGTGGTGGATTGG	640
QY	241	GTCGTGTAATTTTTTTTTTAATTTTTTAACGATTTTGTGGTTTAAAGAAATTTGTATTTGTGA	300
Db	641	GTCGTGTAATTTTTTTTTTAATTTTTTAACGATTTTGTGGTTTAAAGAAATTTGTATTTGTGA	700
QY	301	TTTTTTTAAAGGTCTGTGTCTGAACTGAGCCGAGCCGAGCCGAGCCAGAACCGAGGCGTG	360
Db	701	TTTTTTTAAAGGTCTGTGTCTGAACTGAGCCGAGCCGAGCCGAGCCAGAACCGAGGCGTG	760
QY	361	CAAGACCTACCCGCGCTCTAAATATGGCGCTGTACTCTGAGACGCCCCGACATCAACTG	420
Db	761	CAAGACCTACCCGCGCTCTAAATATGGCGCTGTACTCTGAGACGCCCCGACATCAACTG	820
QY	421	TGCTATAGAAATGCATATGTATGTAACGGAATAGCTGTGACTCCGGTCTTTTAAACAACCTC	480
Db	821	TGCTATAGAAATGCATATGTATGTAACGGAATAGCTGTGACTCCGGTCTTTTAAACAACCTC	880
QY	481	CTGAGATACACCCGGTGGTCCCGCTGACGCCCATTTAAACCAATGGCGTGAGATTGGTG	540
Db	881	CTGAGATACACCCGGTGGTCCCGCTGACGCCCATTTAAACCAATGGCGTGAGATTGGTG	940
QY	541	GCGCTGCGCAGGCTGTGTGAAATGTATCGAGACCTTGCTTAAACAGACCTTGGCAACTTTGG	600
Db	941	GCGCTGCGCAGGCTGTGTGAAATGTATCGAGACCTTGCTTAAACAGACCTTGGCAACTTTGG	1000
QY	601	ACTTGAGCTGTAAACGCCCAAGGCCATAAGGTGTAAACCTGTGATTTGGTGTGTGTAA	660
Db	1001	ACTTGAGCTGTAAACGCCCAAGGCCATAAGGTGTAAACCTGTGATTTGGTGTGTGTAA	1060
QY	661	GCGCTTGTGTGCAATGAGTGTGATGTAAATTAAGGGTGAATAATGTTTAAT	720
Db	1061	GCGCTTGTGTGCAATGAGTGTGATGTAAATTAAGGGTGAATAATGTTTAAT	1120
QY	721	TGCATGCGGTGTAAATGGGGCGGGGCTTAAAGGGTATATATCGCGGTGGCTAAATCT	780
Db	1121	TGCATGCGGTGTAAATGGGGCGGGGCTTAAAGGGTATATATCGCGGTGGCTAAATCT	1180
QY	781	TGTTTACATCTGACCTCATGAGAGGCTTGGGAGTGTGGAGATTTTTTGTGCTGTGCGTA	840
Db	1181	TGTTTACATCTGACCTCATGAGAGGCTTGGGAGTGTGGAGATTTTTTGTGCTGTGCGTA	1240
QY	841	ACTTGCTGGAACAGAGCTCTAAACGTAACCTCTTGTTTGGAGGTTTCTGTGGGGCTCAT	900
Db	1241	ACTTGCTGGAACAGAGCTCTAAACGTAACCTCTTGTTTGGAGGTTTCTGTGGGGCTCAT	1300
QY	901	CCAGAGCAAAATTAAGTGTGACAGAAATTAAGAGATTAACAATGGGAATTTTAAAGACTTT	960
Db	1301	CCAGAGCAAAATTAAGTGTGACAGAAATTAAGAGATTAACAATGGGAATTTTAAAGACTTT	1360
QY	961	TGAATATCTGTGTGAGGCTGTGTGAATCTTTGAAATCTGGGTCAACAGGCGCTTTTCCAG	1020
Db	1361	TGAATATCTGTGTGAGGCTGTGTGAATCTTTGAAATCTGGGTCAACAGGCGCTTTTCCAG	1420
QY	1021	AGAAAGTATCAAGACTTTTGGATTTTTCACAACCGGGGCGGGCTGTGGCTGTGTGCTT	1080
Db	1421	AGAAAGTATCAAGACTTTTGGATTTTTCACAACCGGGGCGGGCTGTGGCTGTGTGCTT	1480
QY	1081	TTTTTGAGTTTATTAAGGATTAATGAGACGAAGAAACCATCTGAGCGGGGGGTATACCTGC	1140
Db	1481	TTTTTGAGTTTATTAAGGATTAATGAGACGAAGAAACCATCTGAGCGGGGGGTATACCTGC	1540
QY	1141	TGGATTTTCTGGCCATGCACTGTGTGAGAGCGGTTGTGTAGACACAGAAATGCGCTGTAC	1200

Db	1541	TGAAATTTCTGGCCATGCAATCTGGAGACCGGTTTGAAACACAAAGAACTCGCTGCTAC	1600
Oy	1201	TGTATGCTTCCTGTCCTGCGCCCGGCATATAACGACCGAGAGCAGCAGCAGCAGGAGG	1260
Db	1601	TGTTGTCTTCCTCGCTCCGCGCCGCAATATATCCGACCGAGAGCAGCAGCAGCAGGAGG	1660
Oy	1261	AAGCCAGGCGCGCGCGCGCAGAGACAGAGCCCATGAAACCCGAGAGCCGCGCTGACCTTC	1320
Db	1661	AAGCCAGGCGCGCGCGCGCAGAGACAGAGCCCATGAAACCCGAGAGCCGCGCTGACCTTC	1720
Oy	1321	GGGAATGAATGTTGTACAGGTGCGTGAACGTATCCGAACCTGAGAGCAATTTTGAACAAT	1380
Db	1721	GGGAATGAATGTTGTACAGGTGCGTGAACGTATCCGAACCTGAGAGCAATTTTGAACAAT	1780
Oy	1381	TACAGAGATGCGGCAAGGCGCTAAAGGGGATTAAGAGGAGCAGGGGCGCTGTGAGCGTAC	1440
Db	1781	TACAGAGATGCGGCAAGGCGCTAAAGGGGATTAAGAGGAGCAGGGGCGCTGTGAGCGTAC	1840
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Db	1901	TTTTCAACAGATCAAGATTAATTTGCGCTAATGAGCTTGAATCTGCTGGCGCAAGATATTC	1960
Oy	1561	CATAGACAGCTGACCACTTACTAGCGCTGCAGCCAGGGGATGATTTTGAAGAGCGTATTAAG	1620
Db	1961	CATAGACAGCTGACCACTTACTAGCGCTGCAGCCAGGGGATGATTTTGAAGAGCGTATTAAG	2020
Oy	1621	GGTATATGCAAAAGGTGGCACTTAAGCGCAGATTGCAAGTACAGAAATCGAAACTTGTAA	1680
Db	2021	GGTATATGCAAAAGGTGGCACTTAAGCGCAGATTGCAAGTACAGAAACTTGTAA	2080
Oy	1681	TATACAGAAATTTGTGCTACATTTTCTGGGAAACGGGGCCGAGAGTGAAGTAAATACGAGGA	1740
Db	2081	TATACAGAAATTTGTGCTACATTTTCTGGGAAACGGGGCCGAGAGTGAAGTAAATACGAGGA	2140
Oy	1741	TAGGGTGGCCCTTTAGATGTAGCATGAATAAATATGTGGCCGGGGGTCTTGAGCATGACGCG	1800
Db	2141	TAGGGTGGCCCTTTAGATGTAGCATGAATAAATATGTGGCCGGGGGTCTTGAGCATGACGCG	2200
Oy	1801	GGTGGTATTAATGAAATGTAAAGTTTACTGACCCCAATTTTACCGGTACCGTATTTCTGTGC	1860
Db	2201	GGTGGTATTAATGAAATGTAAAGTTTACTGACCCCAATTTTACCGGTACCGTATTTCTGTGC	2260
Oy	1861	CAATACCAACCTTAATCTTAACGCGTGTAAAGCTTCTATGGGTTTAAACAATACCTGTGTGA	1920
Db	2261	CAATACCAACCTTAATCTTAACGCGTGTAAAGCTTCTATGGGTTTAAACAATACCTGTGTGA	2320
Oy	1921	AGCCTGAGACGGAATGAAGGTTGGGGCTGTGCTTTTACGTGCGCTGAAAGGGGGTGGT	1980
Db	2321	AGCCTGAGACGGAATGAAGGTTGGGGCTGTGCTTTTACGTGCGCTGAAAGGGGGTGGT	2380
Oy	1981	GTGTGCGCCCAAAAGCAGGCGCTCAATTAAGAAATGCTCTTTGAAAGGTGTACTTGTGG	2040
Db	2381	GTGTGCGCCCAAAAGCAGGCGCTCAATTAAGAAATGCTCTTTGAAAGGTGTACTTGTGG	2440
Oy	2041	TATCTGTCTGAGGGTAACTTCCAGGGTGGCCCAATATGTGGCTCCGACTGTGGTTGCTT	2100
Db	2441	TATCTGTCTGAGGGTAACTTCCAGGGTGGCCCAATATGTGGCTCCGACTGTGGTTGCTT	2500
Oy	2101	CATCTGTAGTAAAGCGGTGCTGTGAATTAAGCAATACATGTATGTGGCAATGCGAGGA	2160
Db	2501	CATCTGTAGTAAAGCGGTGCTGTGAATTAAGCAATACATGTATGTGGCAATGCGAGGA	2560
Oy	2161	CAGGGCGCTCTCAATGTCTGACTTGTGGAAGGCAATGCTACCTGCTGAAGACATTA	2220
Db	2561	CAGGGCGCTCTCAATGTCTGACTTGTGGAAGGCAATGCTACCTGCTGAAGACATTA	2620
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Db 2621 CGTAGCCAGCACTCTGCGCAAGGCTGCGCAGTGTTCGACATACATACGACCCGCTG 2680
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RESULT 2
AR310582 7090 bp DNA linear PAT 12-JUN-2003
LOCUS AR310582
DEFINITION Sequence 18 from patent US 6558948.
ACCESSION AR310582
VERSION AR310582.1 GI:31703596
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 7090)
AUTHORS Kochanek,S. and Schledner,G.
TITLE Permanent amniocytic cell line, its production and use for the
JOURNAL production of gene transfer vectors
FEATURES Patent: US 6558948-A 18 06-MAY-2003;
Location/Qualifiers
source 1..7090
/organism="unknown"
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ORIGIN
Query Match 100.0%; Score 2594; DB 6; Length 7090;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3225 GAGAGATTGTGTAGATTATGTGAGACACCCCGGCGACGGTTGCAAGTCTTGTCAATTAT 3284
Qy 121 CACCGGAGGAATACGGGGGACCCAGATATTATGTGTTGCTTTGCTATATGAGACTGT 180
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Qy 241 GTGTGGTAATTTTTTTTTTAATTTTACAGTTTGTGTGTTTAAAGATTTTGTATTGGA 300
Db 3405 GTGTGGTAATTTTTTTTTTAATTTTACAGTTTGTGTGTTTAAAGATTTTGTATTGGA 3464
Qy 301 TTTTAAAAAGGTCGTGTCTGTAACCTGAGCCTGAGCCGAGACCGAGACGCTG 360

Db 3465 TTTTAAAAAGGTCGTGTCTGTAACCTGAGCCTGAGCCGAGACCGAGAGGCTG 3524
Qy 361 CAAGACCTACCCGCGCTCTTAAATGAGCGCTGCTATCTGAGAGCGCCGACATACCTG 420
Db 3525 CAAGACCTACCCGCGCTCTTAAATGAGCGCTGCTATCTGAGAGCGCCGACATACCTG 3584
Qy 421 TGTCTAAGAAATGCAATAGTATGATGAGATAGCTGTGATCTCGGTCTTTCTAACACACCTC 480
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Qy 541 GGCCTGCCAGGCTGTGGAATGTATCGAGACTTGTAAACGAGCTGGGCACTTTGG 600
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D	4965	GGTGGTTATTAATGAATGAAGTTTACTGCGCCCAATTTTACCGGTACGGTTTCTGGC	5024
Q	1861	CAATATACCAACCTTTATCCACACGGGTGAAGCTTCATGCGGTTTAAACAATACCTGTGGA	1920
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D	5205	TATCTGTCTAGAGGTAACTCAGGGGTGCGCAAAATGTCGCTCCGACTGTGGTGTCTT	5264
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AX150263			
LOCUS			
Sequence 18 from Patent WO0136615.			
DEFINITION			
AX150263			
ACCESSION			
AX150263.1 GI:14348283			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
synthetic construct			
other sequences, artificial sequences.			
REFERENCE			
1			
Kochanek,S. and Schiedner,G.			
Permanent amniocyte cell line, the production thereof and its use			
for producing gene transfer vectors			
Patent: WO 0136615-A 18 25-MAY-2001,			
Kochanek, Stefan (DE)			
JOURNAL			
FEATURES			
Location/Qualifiers			
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Best Local Similarity 100.0%; Score 2594; DB 6; Length 7090;			
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ACCESSION BD268237.1
VERSION BD268237.1
KEYWORDS JP 2002534130-A/41.
SOURCE Synthetic construct
ORGANISM Synthetic construct
REFERENCE 1 (bases 1 to 7607)
AUTHORS Nemerow, G.R., Seggen, D.J.V., Hallenbeck, P.L., Stevenson, S.C. and Skripchenko, Y.
TITLE Adenovirus vector, packaging cell line, composition and method for production and use
JOURNAL Patent: JP 2002534130-A 41 15-OCT-2002;
NOVARTIS AG, THE SCRIPPS RESEARCH INSTITUTE
COMMENT OS Artificial Sequence
PN JP 2002534130-A/41
PD 15-OCT-2002
PF 14-JAN-2000 JP 2000593765
PI 14-JAN-1999 US 60/115920
PI GLEN ROBERT NEMEROW, DANIEL J VON SEGGEN, PAUL L HALLENBECK, PI SUSAN C STEVENSON, YELENA SKRIPCHENKO
PC C12N15/09, A61K35/76, A61K48/00, A61P35/00, A61P43/00, A61P43/00, PC C12N5/10,
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Query Match 100.0%; Score 2594; DB 6; Length 7607;
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1681	TATCAGCAATTGTTGCTACATTTCTGGGAAACGGGGCCGAGGTGAGATAGATACGAGCA	1740
3014	TATCAGCAATTGTTGCTACATTTCTGGGAAACGGGGCCGAGGTGAGATAGATACGAGCA	3073
1741	TAGGGTGCCCTTTAGATGATGACATATAATATGTGGCCCGGGGGGTGCTTGGCATGACG	1800
3074	TAGGGTGCCCTTTAGATGATGACATATAATATGTGGCCCGGGGGGTGCTTGGCATGACG	3133
1801	GGTGGTTATTTATGAAATGTAAAGGTTATCTGGCCCCCAATTTTAAACGGGTACGGTTTCTGTGC	1860
3134	GGTGGTTATTTATGAAATGTAAAGGTTATCTGGCCCCCAATTTTAAACGGGTACGGTTTCTGTGC	3193
1861	CAATACCAACCTTATCTTACAACGCTGTAACTTTATGAGGTTTAAACAATACCTGTGTGA	1920
3194	CAATACCAACCTTATCTTACAACGCTGTAACTTTATGAGGTTTAAACAATACCTGTGTGA	3253
1921	AGCCTGGACCCGATGTAAAGGTTCCGGGGCTGTGCTTTTACTGTGCTGTGAAAGGGGGTGT	1980
3254	AGCCTGGACCCGATGTAAAGGTTCCGGGGCTGTGCTTTTACTGTGCTGTGAAAGGGGGTGT	3313
1981	GGTGGCCCCCAAAACAGGGGCTTCAATTTAAAGAAAGCCCTTTTGAATAGGTATACCTTGGG	2040
3314	GGTGGCCCCCAAAACAGGGGCTTCAATTTAAAGAAAGCCCTTTTGAATAGGTATACCTTGGG	3373
2041	TATCCTGTCTGAGGGTAACTCCAGAGGTCGCGCAACATGTGCTCCGACTGTGGTGTCTT	2100
3374	TATCCTGTCTGAGGGTAACTCCAGAGGTCGCGCAACATGTGCTCCGACTGTGGTGTCTT	3433
2101	CATGCTAAGTAAAGCGTGGCTGTGATTTAAGCATTAACATGATGTGCGAACTGCGAGGA	2160
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2161	CAGGGCCCTCTCAGATGCTGACCTGCTCGGACGGCAACGTCAACCTGCTGAAAGACCATTC	2220
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3674	CACATAGATATTGCTTAGGCGCGAGAGCATGTCCAAAGGTGAACCGGAACGGGGTGTTTGA	3733
2401	CATGACCATGAAGATCTGAAAGGTGCTGAGGTACGATGAGACCCGCAACGAGTGCAGACC	2460
3734	CATGACCATGAAGATCTGAAAGGTGCTGAGGTACGATGAGACCCGCAACGAGTGCAGACC	3793
2461	CTGCGAGTGTGGCGGTAAACAATTTATAGAAACCAAGCTGTGATGCTGTGATGTGACCCGAGA	2520
3794	CTGCGAGTGTGGCGGTAAACAATTTATAGAAACCAAGCTGTGATGCTGTGATGTGACCCGAGA	3853
2521	GCTGAGGCCCATCACTTGTGTGCTGGCTGACCCGCGCTAGTGTGGCTTACGAGATGA	2580
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2581	AGATACAGATTGAG 2594	
3914	AGATACAGATTGAG 3927	

DEFINITION	Adenovirus vector, packaging cell line, composition and method for production and use.
ACCESSION	BD268208
VERSION	BD268208.1 GI:33077976
KEYWORDS	JP 2002534130-A/12.
SOURCE	synthetic construct
ORGANISM	synthetic construct
REFERENCE	other sequences; artificial sequences.
AUTHORS	1 (bases 1 to 11152)
TITLE	Nemerow,G.R., Seggem,D.J.V., Hallenbeck,P.L., Stevenson,S.C. and Skripchenko,Y.
JOURNAL	Adenovirus vector, packaging cell line, composition and method for production and use
COMMENT	Patent: JP 2002534130-A 12 15-OCT-2002; NOVARTIS AG, THE SCRIPPS RESEARCH INSTITUTE OS Artificial Sequence PN JP 2002534130-A/12 PD 15-OCT-2002 PF 14-JAN-2000 JP 2000593765 PR 14-JAN-1999 US 60/115920 PI GLEN ROBERT NEMEROW, DANIEL J VON SEGGERN, PAUL L HALLENBECK, PI SUSAN C STEVENSON, YELENA SKRIPCHENKO PC C12N15/09,A61K35/76,A61K48/00,A61J35/00,A61P43/00,A61P43/00, PC C12N5/10, PC C12N7/00,C12Q1/68,G01N35/53,G01N35/566,C12N15/00,C12N5/00 CC Description of Artificial Sequence: plasmid FT Key Location/Qualifiers FT source 1..11152 FT Location/Qualifiers
FEATURES	Location/Qualifiers 1..11152 /organism="synthetic construct" /mol_type="genomic DNA" /db_xref="taxon:32630"
ORIGIN	
Query Match	100.0%; Score 2594; DB 6; Length 11152;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 2594;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ATGCATCTTACCTCCACGAGGCTGGCTTCCACCCAGTGCAGCAGAGATGAAGAGGT 60
DB	1825 ATGCATCTTACCTCCACGAGGCTGGCTTCCACCCAGTGCAGCAGAGATGAAGAGGT 1884
QY	61 GAGAGTTTGTGTAGATTATGTGTGAGACACCCCGGGACAGGTTGCAGGTTCATTAT 120
DB	1885 GAGAGTTTGTGTAGATTATGTGTGAGACACCCCGGGACAGGTTGCAGGTTCATTAT 1944
QY	121 CACCGAGGAATTACGGGGAGCCCGAGATTATATGTTCGCTTTGCTATATGAGAACTGT 180
DB	1945 CACCGAGGAATTACGGGGAGCCCGAGATTATATGTTCGCTTTGCTATATGAGAACTGT 2004
QY	181 GGCATGTTTGTCTACAGTAAGTAAATTTATGGCAGTGGGTGATAGTGTGGTGGTTTG 240
DB	2005 GGCATGTTTGTCTACAGTAAGTAAATTTATGGCAGTGGGTGATAGTGTGGTGGTTTG 2064
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DB	2065 GTGTGTATATTTTTTTTAAATTTTACAGTTTGTGCTTTTAAAGAAATTTGTATTTGTGA 2124
QY	301 TTTTAAAAAGGCTCTGTGCTCTCAACCTGAGCTGAGCCCGAGCAGAAACCGGAGCCTG 360
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QY	361 CAGACCTACCCCGCGTCTTAAATGCGCTGTGATCTTGAGACGCGCCGACATCACCTG 420
DB	2185 CAGACCTACCCCGCGTCTTAAATGCGCTGTGATCTTGAGACGCGCCGACATCACCTG 2244
QY	421 TGTCTAAGAGATGCATATAGTATGATACGATGACGTGCTCGGTCCTTTCTTACACACCTC 480
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QY	481 CTGAGATACACCGCGTGTCCCGCTGTGCCCCATTAACCAAGTTGCGGTGAGAGTTGGTG 540

Db 2305 CTGAGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACAGTTGCCGTGAGAGTTGGTG 2364
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RESULT 6
AX356041

LOCUS AX356041 11152 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 12 from Patent WO0183729.
ACCESSION AX356041
VERSION AX356041.1 GI:18620603
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Nemerow, G.R., von Seggern, D.J. and Friedlander, M.
Vectors for ocular transduction and use thereof for genetic therapy
Patent: WO 0183729-A 12-08-NOV-2001;
Novartis AG (CH); The Scripps Research Institute (US); Nemerow,
Glen R. (US); Von Seggern, Daniel J. (US); Friedlander, Marcy
(US)
FEATURES
source Location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 2594; DB 6; Length 11152;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ATGATCTTACCTGCGCAGAGGCTGGCTTTCACCCAGTGAAGAGAGAGAGGCT 60
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121 CACCGAGGAATATACGGGGGACCCAGATATATGTTGGCTTGTATATGAGACCTGT 180
1945 CACCGAGGAATATACGGGGGACCCAGATATATGTTGGCTTGTATATGAGACCTGT 2004
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Db 2485 CGCCTTTTGTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2544
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Db	3745	AGCTGGA	CCGATGTAA	GGGTTCCGGGCTGTG	CCCTTTTACTGTGCTGTGA	AGGGGCTGTG	3804
Qy	1981	GTGTGCCCC	CAAAAGCAGG	GGCTTACAATTAA	GAATNGCCTCTTTGAA	AGGTGATCCTTG	2040
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Qy	2041	TATCCTGT	CTGAGGGTAA	CTCCAGGGTGC	CGCCACAAATGTGG	CTCCGACTGTGGTTGCTT	2100
Db	3865	TATCCTGT	CTGAGGGTAA	CTCCAGGGTGC	CGCCACAAATGTGG	CTCCGACTGTGGTTGCTT	3924
Qy	2101	CATCTAGT	GAAGAAAGCGT	GGCTGTGATTA	AAGCATPA	CACTGTGTGTGCA	2160
Db	3925	CATCTAGT	GAAGAAAGCGT	GGCTGTGATTA	AAGCATPA	CACTGTGTGTGCA	3984
Qy	2161	CAGGAGCC	CTCAGATGCT	GACCTGCTCGG	ACGGCACTGTCA	CCCTGTGCAAGACATTC	2220
Db	3985	CAGGAGCC	CTCAGATGCT	GACCTGCTCGG	ACGGCACTGTCA	CCCTGTGCAAGACATTC	4044
Qy	2221	CGTAGC	AGCCACTCTG	CCAAAGGCTG	GC	CAAGTGTTTAG	2280
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RESULT 7							
LOCUS	BD021940	11152 bp	DNA	linear	PAT 27-AUG-2002		
DEFINITION	BD021940	Packaging cell systems for use in promotion of the development of					
ACCESSION	BD021940	high-capacity adenoviral vectors.					
VERSION	BD021940.1	GI:22563163					
KEYWORDS	JP 2001505047-A/12.						
SOURCE	unidentified						
ORGANISM	unidentified						
REFERENCE	1 (bases 1 to 11152)						
AUTHORS	Memerow, G. R. and Seggern, D. J. V.						
TITLE	Packaging cell systems for use in promotion of the development of						
	high-capacity adenoviral vectors						

JOURNAL									
Patent: JP 2001505047-A 12 17-APR-2001;									
NOVARTIS AG, THE SCRIPSES RESEARCH INSTITUTE									
PN JP 2001505047-A/12									
COMMENT									
PD 17-APR-2001									
PF 24-SEP-1997 JP 1998515273									
PR 25-SEP-1996 US 08/719806									
PI GLEN R MEMBROW, DANIEL J VON SEGGERN									
PC C12N5/10, C07K14/075, C12N15/09//A61K31/711, A61K35/76, A61K48/00,									
PC A61K35/00									
PC C12N5/00, C12N15/00									
CC Strandedness: Double;									
CC Topology: Circular;									
FH Key Location/Qualifiers.									
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Source									
1. 11152									
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ORIGIN									
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Best Local Similarity 100.0%; Freq. No. 0;									
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY 1 ATGCATCTTACCTGCGACGAGCGTGGCTTCCACCAGTGCAGCAGAGATGAGAGGGT 60									
DB 1825 ATGCATCTTACCTGCGACGAGCGTGGCTTCCACCAGTGCAGCAGAGATGAGAGGGT 1884									
QY 61 GAGAGATTGTGTAGATTATGTGGAGCACCCCGGACAGGTTGACAGTCTTGTCAATTAT 120									
DB 1885 GAGAGATTGTGTAGATTATGTGGAGCACCCCGGACAGGTTGACAGTCTTGTCAATTAT 1944									
QY 121 CACCGAGGAATACGGGGACCCAGATATTATGTTCGCTTCTCTATATGAGACCTGT 180									
DB 1945 CACCGAGGAATACGGGGACCCAGATATTATGTTCGCTTCTCTATATGAGACCTGT 2004									
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QY 361 CAATACTTACCCGCGCTCTAAATGGCGCTGTATCTCGAAGAGCCGACATCACTG 420									
DB 2185 CAATACTTACCCGCGCTCTAAATGGCGCTGTATCTCGAAGAGCCGACATCACTG 2244									
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Oy 781 TGGTTACATCGACCTCATGAGAGCTTTGGAGATTTTCTGCTGCGTA 840
Db 2605 TGGTTACATCGACCTCATGAGAGCTTTGGAGATTTTCTGCTGCGTA 2664
Oy 841 ACTTGTGGAACAGAGCTTAAACAGTACTTGTGTTTGGAGTTTCTGCGGCTCAT 900
Db 2665 ACTTGTGGAACAGAGCTTAAACAGTACTTGTGTTTGGAGTTTCTGCGGCTCAT 2724
Oy 901 CCCAGGCAAAAGTTAGTCTGAGAAATTAAGAGATTAAGAGGGAATTTGAGAGCTTT 960
Db 2725 CCCAGGCAAAAGTTAGTCTGAGAAATTAAGAGATTAAGAGGGAATTTGAGAGCTTT 2784
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Oy 1021 AGAAGTCATGAAGCTTTGATTTTTCACACCGGGGCGGCTGCGGCTGTGCTT 1080
Db 2845 AGAAGTCATGAAGCTTTGATTTTTCACACCGGGGCGGCTGCGGCTGTGCTT 2904
Oy 1081 TTTTGAAGTTTATAAAGATTAATGAGAGAAACCATCTGAGCGGGGGTACCTGC 1140
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Oy 1141 TGAATTTTCTGCGCATCTGTGAGAGCGGTTGTGAGACAGAAATGCGCTGTAC 1200
Db 2965 TGAATTTTCTGCGCATCTGTGAGAGCGGTTGTGAGACAGAAATGCGCTGTAC 3024
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Db 3025 TGTGTCTTCCGTCCGCGCGGCGATTAACCGAGGAGAGACAGACAGACAGAGG 3084
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Db 3145 GGAATATATTTGTATACAGTGTGCTGAACTGTATCCAGAACTGAGACATTTTGA 3204
Oy 1381 TACGAGAGATGAGGCGGCTTAAAGGGGTAAAGAGGAGCGGGGGCTTGTGAGGCTAC 1440
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Oy 1621 GGTATATGCAAAAGGTGGCACTTAGCCGATTTGAGAGTACAAAGTACGAACTTTTAA 1680
Db 3445 GGTATATGCAAAAGGTGGCACTTAGCCGATTTGAGAGTACAAAGTACGAACTTTTAA 3504
Oy 1681 TATAGAAATTTTGTCTACATTTCTGGGAAAGGGGCGAGGTGAGATAGATACGAGGA 1740
Db 3505 TATAGAAATTTTGTCTACATTTCTGGGAAAGGGGCGAGGTGAGATAGATACGAGGA 3564
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Db 3565 TAGGCTGCGCTTTTGAATGATGATTAATATGTGCGCGGGGCTTGTGCAATGACCG 3624
Oy 1801 GGTGCTATTTATGAATGATGATTTAGCGCCCAATTTTACGGGTCTGCGC 1860

Db 3625 GGTGCTATTTATGAATGATGATTTAGCTTACTGCGCCCAATTTTACGGGTACGTTTCTGCGC 3684
Oy 1861 CAATACCAACCTTTATCCATACAGGTGTAAAGCTTATAGGTTTAAATATACCTGTGTGA 1920
Db 3685 CAATACCAACCTTTATCCATACAGGTGTAAAGCTTATAGGTTTAAATATACCTGTGTGA 3744
Oy 1921 AGCTTGGAACCAATGATGAGGTTTGGGGCTGTGCTTTTATCTGCTGTGGAAGGGGGTGT 1980
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Oy 1981 GTGTGCGCCCAAAAGAGGGGCTTCAATTAAGAAATGCTCTTTGAAAGGTATACCTTGG 2040
Db 3805 GTGTGCGCCCAAAAGAGGGGCTTCAATTAAGAAATGCTCTTTGAAAGGTATACCTTGG 3864
Oy 2041 TATCTGTCTGAGGGTAACTCAGAGGTGCGCCACAATGTGAGCTTCCGACTGTGTGCTT 2100
Db 3865 TATCTGTCTGAGGGTAACTCAGAGGTGCGCCACAATGTGAGCTTCCGACTGTGTGCTT 3924
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Db 4345 GCTGAGGCGCGATCACTTGGGTGTGCGCTGCAACCGGCGTGAATTTGCTTACCGATGA 4404
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Db 4405 AGATACAGATTGAG 4418

RESULT 8
AD5001 11570 bp DNA linear VRL 09-SEP-2004
LOCUS Adenovirus type 5 left 32% of the genome (coordinates 0% to 32.39%
DEFINITION as measured by <ad>)
ACCESSION X02996 J01967 J01968 J01970 J01971 J01972 J01974 J01976 J01977
VERSION J01978 J01979 J00515 V00025 V00026 V00027 V00029
KEYWORDS X02996.1 GI:58484
RNA polymerase III; terminal protein; terminal repeat; transfer
RNA.

SOURCE Human adenovirus type 5
ORGANISM Human adenovirus type 5
VIRUSES; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
REFERENCE 1 (bases 1 to 194)
AUTHORS Steenbergh, P.H., Maat, J., van Ormondt, H., and Sussenbach, J.S.
TITLE The nucleotide sequence at the termini of adenovirus type 5 DNA
JOURNAL Nucleic Acids Res. 4 (12), 4371-4389 (1977)

MEDLINE
PUBMED
78093872
2 (bases 1 to 1574)
Van Ormondt,H., Maat,J., De Waard,A. and Van der Eb,A.J.
TITLE
The nucleotide sequence of the transforming HpaI-B fragment of
adenovirus type 5 DNA
JOURNAL
Gene 4 (4), 309-328 (1978)
MEDLINE
PUBMED
79128735
3 (bases 1575 to 2809)
Maat,J. and Van Ormondt,H.
TITLE
The nucleotide sequence of the transforming HindIII-G fragment of
adenovirus type 5 DNA. The region between map positions 4.5 (HpaI
site) and 8.0 (HindIII site)
JOURNAL
Gene 6 (1), 75-90 (1979)
MEDLINE
PUBMED
80004833
478299
4
Petricaudet,M., Akusjarvi,G., Vitanen,A. and Pettersson,U.
TITLE
Structure of two spliced mRNAs from the transforming region of
human subgroup C adenoviruses
JOURNAL
Nucleic Acids Res. 7 (1979), 694-696 (1979)
MEDLINE
PUBMED
551290
5 (bases 10524 to 10636)
Thimmappa,B., Jones,N. and Shenk,T.
TITLE
A mutation which alters initiation of transcription by RNA
polymerase III on the Ad5 chromosome
JOURNAL
Cell 18 (4), 947-954 (1979)
MEDLINE
PUBMED
80090080
519773
6 (bases 1 to 6246)
Broker,T.R.
TITLE
Appendix d: nucleotide sequences, transcription and translation
analyses, and restriction endonuclease cleavage maps of group-c
human adenoviruses
(in) TOOLE,J. (Ed.):
DNA TUMOR VIRUSES: 937-1002;
Cold Spring Harbor Laboratory (1980)
JOURNAL
7 (bases 2804 to 4125)
Maat,J., van Beveren,C.P. and van Ormondt,H.
TITLE
The nucleotide sequence of adenovirus type 5 early region E1: the
region between map positions 8.0 (HindIII site) and 11.8 (SmaI
site)
JOURNAL
Gene 10 (1), 27-38 (1980)
MEDLINE
PUBMED
81005097
6250944
8
Petricaudet,M., Le Moulllec,J.M. and Pettersson,U.
TITLE
Predicted structure of two adenovirus tumor antigens
Proc. Natl. Acad. Sci. U.S.A. 77 (7), 3778-3782 (1980)
JOURNAL
81054654
MEDLINE
PUBMED
6253988
9 (bases 1 to 4125)
van Ormondt,H., Maat,J. and van Beveren,C.P.
TITLE
The nucleotide sequence of the transforming early region E1 of
adenovirus type 5 DNA
JOURNAL
Gene 11 (3-4), 299-309 (1980)
MEDLINE
PUBMED
81165537
6260576
10 (bases 10555 to 10733)
Fowlkes,D.M. and Shenk,T.
TITLE
Transcriptional control regions of the adenovirus VAI RNA gene
Cell 22 (2 Pt 2), 405-413 (1980)
JOURNAL
81088343
MEDLINE
PUBMED
7448868
11 (bases 1653 to 4043)
Boer,J.V., Polder,J.V., Bernard,R., Schrier,P.I., van den
Bosch,J., van der Eb,A.J. and van Ormondt,H.
TITLE
The 2.2 kb E1b mRNA of human Ad2 and Ad5 codes for two tumor
antigens starting at different AUG triplets
Cell 27 (1 Pt 2), 121-131 (1981)
JOURNAL
82115327
MEDLINE

PUBMED
7326748
12 (bases 4001 to 6246)
van Beveren,C.P., Maat,J., Dekker,B.M. and van Ormondt,H.
TITLE
The nucleotide sequence of the gene for protein Iva2 and of the 5'
leader segment of the major late mRNAs of adenovirus type 5
JOURNAL
Gene 16 (1-3), 179-189 (1981)
MEDLINE
PUBMED
82211779
7343420
13 (bases 325 to 604)
Hearling,P. and Shenk,T.
TITLE
Functional analysis of the nucleotide sequence surrounding the cap
site for adenovirus type 5 region E1a messenger RNAs
J. Mol. Biol. 167 (4), 809-822 (1983)
MEDLINE
PUBMED
83268691
6876165
deletion mutants
14 (bases 1 to 66)
Nagata,K., Guggenheim,R.A. and Hurwitz,J.
TITLE
Specific binding of a cellular DNA replication protein to the
origin of replication of adenovirus DNA
Proc. Natl. Acad. Sci. U.S.A. 80 (20), 6177-6181 (1983)
JOURNAL
84016017
MEDLINE
PUBMED
6336326
15 (bases 6242 to 11570)
Dekker,B.M. and van Ormondt,H.
TITLE
The nucleotide sequence of fragment HindIII-C of human adenovirus
type 5 DNA (map positions 17.1-31.7)
JOURNAL
Gene 27 (1), 115-120 (1984)
MEDLINE
PUBMED
84183604
6325298
16
Downey,J.F., Evelyn,C.M., Branton,P.E. and Bayley,S.T.
TITLE
Peptide maps and N-terminal sequences of polypeptides from early
region 1A of human adenovirus 5
J. Virol. 50 (1), 30-37 (1984)
JOURNAL
84138826
MEDLINE
PUBMED
6699947
6699947
REMARK
sites) cde start for E1a protein
sites) splice sites in E1a 13S mRNA
sites) splice sites and termini for E1b mRNAs
Notes on the presentation of ADENO in the EMBL data library: The
genetic map of Adeno is customarily presented from left to right,
the 0% position being left and the 100% position being right. The
two strands of Adeno are normally represented like this: r-strand:
3'-----5'
l-strand: 5'-----3'
0% 100%
This often causes confusion because the generally accepted way to
represent DNA molecules is:
5'-----3'
3'-----5'

Here Adeno virus sequences are always given in 5' to 3' direction
and the sequence of the l-strand is displayed irrespective of the
direction the viral transcription takes.
This sequence corresponds to bases 1 to 1560 of <ad2>, which serve
as some basis for the annotation of sites. The differences between
<ad2> and <ad5> are too many to report herein, however a printout
of those is available upon request from genbank. The map
coordinates in the sites presume 360 bases per map unit. Although
there are approximately 115 sequence differences between the two
strains over this region, no site difference exceeds 0.02% by this
calculation.
the sequence. represents the early mRNA transcripts e1a and e1b and
the intermediate mRNA transcript ix, all of which are transcribed
rightwardly off the r-strand; the iya2 and e2b mRNAs which are
transcribed leftwardly off the l-strand (indicated by '(C)' and
'comp strand' below); and the 5' end of the 28 kb major late mRNA.
the cap sites and possible promoter sequences for these are
summarized in the following table:
----- cap site ----- possible promoter region -----
----- tattata at bases 468-475 [6] e1b 1702 499

tatataa at bases 1672-1678 [6] ix 3582
tatataa at bases 3551-3557 [6] i1a2 5838 +/- 2 (c)
tatataa at bases 6018-6024 [10] as
with ad2, not all the transcripts from this region have been
characterized at the sequence level. the nine proteins given in
features table below are not the only possible gene products (see
the main adenovirus 2 entry).
large amounts of small rnas are produced from the vat and vai
genes late in development for unknown reasons. [5] and [6]
demonstrate that vai gene activity influences vai expression; that
the 5' flank affects the start site of the rna but that an
intragenic promoter (bases 10626 to 10690 below) determines whether
the rna is actually produced; and that there is striking similarity
between this rna and trna.

FEATURES
source

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(32k, regulation and transformation)"
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/db_xref="GOA:P03285"
/db_xref="UniProt/Swiss-Prot:P03285"
/translation="MRH1ICHG9VITTEMA5LIDQLIEVLAADNLPPSPFEPPTLH
ELYOLDVAPEDPNEBAVSQIFPD5VMAVOEGIDLTFPPAPSPSPPHLSRDEOP
EORALDGP5MNVLEVEVLDLTCHEGAPSPDEDEBEEFLVDYHEPHGHCRCYHA
RRNMGDDPDMCSLCYMRCTCMGFVYSPVSEPPPEPPEPRAPRRPMAAIIIRPPT

Query Match 100.0%; Score 2594; DB 14; Length 11570;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGATCTTACTCCGACGAGCTGGCTTTCCACCCCAATGACGACGAGATGAAGAGGT 60
917 ATGATCTTACTCCGACGAGCTGGCTTTCCACCCCAATGACGACGAGATGAAGAGGT 976
61 GAGAGTTTGTAGATTATGTGAGACACCCGAGGACGAGTTCAGATTTAT 120
977 GAGAGTTTGTAGATTATGTGAGACACCCGAGGACGAGTTCAGATTTAT 1036
121 CACCGAGGAATACGGGGGACCCAGATATTATGTGCTTGTCTATATGAGACCTGT 180
1037 CACCGAGGAATACGGGGGACCCAGATATTATGTGCTTGTCTATATGAGACCTGT 1096
181 GGCAATGTTGCTACAGTAATGAAATTATGGGCAATGAGTGTGGGTTTG 240
1097 GGCAATGTTGCTACAGTAATGAAATTATGGGCAATGAGTGTGGGTTTG 1156
241 GTGGGTAATTTTATTTTATTTTACAGTTTGTGGTTTAAAGATTGTTATGGA 300
1157 GTGGGTAATTTTATTTTATTTTACAGTTTGTGGTTTAAAGATTGTTATGGA 1216
301 TTTTAAAAAGGTCCTGTGTCTGAACTGAGCTGAGCCGAGCCAGAACCGAGGCTG 360
1217 TTTTAAAAAGGTCCTGTGTCTGAACTGAGCTGAGCCGAGCCAGAACCGAGGCTG 1276
361 CAAAGACTACCGCGGCTCTPAAATGGCGCTGCTATCTGAGACGCGCCAGATCACTTG 420
1277 CAAAGACTACCGCGGCTCTPAAATGGCGCTGCTATCTGAGACGCGCCAGATCACTTG 1336
421 TGTCTAGAGATGCAATAGTAGTAGCTGAGCTCGGCTCTTCTAACAACACTC 480

1337 TGTCTAGAGATGCAATAGTAGTAGCTGAGCTCGGCTCTTCTAACAACACTC 1396
481 CTGAGATACACCCGGGTGTCCCGCTGTGCCCATTTAAACAGATTGCGTGAAGTTGGTG 540
1397 CTGAGATACACCCGGGTGTCCCGCTGTGCCCATTTAAACAGATTGCGTGAAGTTGGTG 1456
541 GCGCGCGCAGGCTGTGAATGTATCGAGACTTGTCTTAAAGAGCTTGCGCACTTTGG 600
1457 GCGCGCGCAGGCTGTGAATGTATCGAGACTTGTCTTAAAGAGCTTGCGCACTTTGG 1516
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1517 ACTGAGCTGTAAAGCGCCAGCCCATAGAGGTATTAAGCTGTGAGTGTGGTTAA 1576
661 GCGCTTGTGTCTGAATGAGTGTATGATTTAAATTAAGGTGAGTAAATGTTTAACT 720
1577 GCGCTTGTGTCTGAATGAGTGTATGATTTAAATTAAGGTGAGTAAATGTTTAACT 1636
721 TGCAATGGGTGTAAATGGGCGCGGCTTAAAGGATATATATGCGCGCTGATCT 780
1637 TGCAATGGGTGTAAATGGGCGCGGCTTAAAGGATATATATGCGCGCTGATCT 1696
781 TGCTTACATCTGACCTCATGAGGCTTGGAGTGTGGAGATTTTCTGTGTGCGTA 840
1697 TGCTTACATCTGACCTCATGAGGCTTGGAGTGTGGAGATTTTCTGTGTGCGTA 1756
841 ACTGCTGGAACAGAGCTCTTAACAGTACTCTGTGTTTGGAGGTTTCTGTGGGCTCAT 900
1757 ACTGCTGGAACAGAGCTCTTAACAGTACTCTGTGTTTGGAGGTTTCTGTGGGCTCAT 1816
901 CCCAGCGAAATGTACTGTGCGAAATTAAAGAGATTACAGTGGAAATTTGAAGACTTT 960
1817 CCCAGCGAAATGTACTGTGCGAAATTAAAGAGATTACAGTGGAAATTTGAAGACTTT 1876
961 TGAATCTGTGAGAGCTGTATCTTGAATCTGGCTCAGACAGCGCTTTTCCAAG 1020
1877 TGAATCTGTGAGAGCTGTATCTTGAATCTGGCTCAGACAGCGCTTTTCCAAG 1936
1021 AGAAGCTATCAAGACTTTGATTTTTCACACCGGGGCGGCTGCGGCTGTGTGCTT 1080
1937 AGAAGCTATCAAGACTTTGATTTTTCACACCGGGGCGGCTGCGGCTGTGTGCTT 1996
1081 TTTTGAATTTTAAAGATTAATGAGCGGAAGAACCCATCTGAGCGGGGTAACCTGC 1140
1997 TTTTGAATTTTAAAGATTAATGAGCGGAAGAACCCATCTGAGCGGGGTAACCTGC 2056
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2057 TGATTTTCTGGCCATCTGTGAGAGCGGTTGAGACACAAATTCGCTGTAC 2116
1201 TGTGTCTTCCGTCGCGCGCGGATTAATCCGACGAGAGACAGCAGCAGCAGAGG 1260
2117 TGTGTCTTCCGTCGCGCGCGGATTAATCCGACGAGAGACAGCAGCAGCAGAGG 2176
1261 AAGCAGCGCGCGCGCAGAGAGCAGCCCATGGAACCCGAGAGCGGCTGACCTTC 1320
2177 AAGCAGCGCGCGCGCAGAGAGCAGCCCATGGAACCCGAGAGCGGCTGACCTTC 2236
1321 GGGATGAATGTTGTACAGGTGTGAACTGTATCCGAATCTAGAGGCAATTTGAAT 1380
2237 GGGATGAATGTTGTACAGGTGTGAACTGTATCCGAATCTAGAGGCAATTTGAAT 2296
1381 TACAGAGATGAGCGAGGCTTAAAGGGGTAAAGAGGAGCGGGGCTGTGAGCTAC 1440
2297 TACAGAGATGAGCGAGGCTTAAAGGGGTAAAGAGGAGCGGGGCTGTGAGCTAC 2356
1441 AGAGAGGCTGAGAACTTACCTTTAGCTTAAATGACCAACACCTGCTGAGTATTA 1500
2357 AGAGAGGCTGAGAACTTACCTTTAGCTTAAATGACCAACACCTGCTGAGTATTA 2416
1501 TTTTCAACAGATCAAGGATTAATGGCGTAAATGAGCTTGAATCTGTGCGCAGAAATTC 1560
2417 TTTTCAACAGATCAAGGATTAATGGCGTAAATGAGCTTGAATCTGTGCGCAGAAATTC 2476

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OY	1621	GGTATTATGCAAAAGGTGGCACTT	AGGCGCAGATTTGCAGATACAAAGATTCAGCAA	CTTGTAAA	1680
Db	2537	GGTATTATGCAAAAGGTGGCACTT	AGGCGCAGATTTGCAGATACAAAGATTCAGCAA	CTTGTAAA	2596
OY	1661	TATCAGCAATTGTTGCTACATTT	CTGGGAACGGGGCCGAGGTGGACATATACAGAGGA	1740	
Db	2597	TATCAGCAAAATGTTGCTACATTT	CTGGGAACGGGGCCGAGGTGGACATATACAGAGGA	2656	
OY	1741	TAGGGTGGCTTTTGA	TGTAGCAGATAAAATATGTGGCCGGGGGTGCTGGACATGACGG	1800	
Db	2657	TAGGGTGGCTTTTGA	TGTAGCAGATAAAATATGTGGCCGGGGGTGCTGGACATGACGG	2716	
OY	1801	GGTGGTTATTAATGATGTAAAGT	TTTACTGGCCCAATTTTAAAGCGGTACGGTTTTCTGTGC	1860	
Db	2717	GGTGGTTATTAATGATGTAAAGT	TTTACTGGCCCAATTTTAAAGCGGTACGGTTTTCTGTGC	2776	
OY	1861	CAATACCAACCTTATCTTACACACG	GTATAGCTTATAGGTTTAAACAATACCTGTGTGGA	1920	
Db	2777	CAATACCAACCTTATCTTACACACG	GTATAGCTTATAGGTTTAAACAATACCTGTGTGGA	2836	
OY	1921	AGCCGGAACCGATGTAAAGGGT	TCGGGGCTGTGCCTTTTACGTGCTGAGAAAGGGGGTGT	1980	
Db	2837	AGCCGGAACCGATGTAAAGGGT	TCGGGGCTGTGCCTTTTACGTGCTGAGAAAGGGGGTGT	2896	
OY	1981	GTGTGCCCCCAAAAGCAGGGCTT	CAATTTAAGAAATGCTCTTTGAAAGGTGTACTTTGGG	2040	
Db	2897	GTGTGCCCCCAAAAGCAGGGCTT	CAATTTAAGAAATGCTCTTTGAAAGGTGTACTTTGGG	2956	
OY	2041	TATCTGTGTGAGGGTAACTT	CAGGGTGGCCACAATGTGGCCCTCCGACTGTGGTGCCTT	2100	
Db	2957	TATCTGTGTGAGGGTAACTT	CAGGGTGGCCACAATGTGGCCCTCCGACTGTGGTGCCTT	3016	
OY	2101	CATGCTAGTAAAAAGCGTGGCTGT	ATTAAGCATTAACAATGTATGTGGCACTCGAGGA	2160	
Db	3017	CATGCTAGTAAAAAGCGTGGCTGT	ATTAAGCATTAACAATGTATGTGGCACTCGAGGA	3076	
OY	2161	CAGGGCTCTCAGATGTCTGACCT	GCTGCGACGGCACTGTCACTGTGAAAGCACTTCA	2220	
Db	3077	CAGGGCTCTCAGATGTCTGACCT	GCTGCGACGGCACTGTCACTGTGAAAGCACTTCA	3136	
OY	2221	CGTACCCAGCCACTTCCGCAAGG	CTGGCCCACTGTTTGAAGATTAACATCGAACCCGCTG	2280	
Db	3137	CGTACCCAGCCACTTCCGCAAGG	CTGGCCCACTGTTTGAAGATTAACATCGAACCCGCTG	3196	
OY	2281	TTCCCTTGCAATTTGGGTAA	CAGGAGGGGGTGTCTTACCTTAAACCAATTCGAATTTGA	2340	
Db	3197	TTCCCTTGCAATTTGGGTAA	CAGGAGGGGGTGTCTTACCTTAAACCAATTCGAATTTGA	3256	
OY	2341	CACATAAGATATTGCTTTAGACC	CCGAGACATGTCCAAAGTGAACCTGAAACGGGGTGTTTGA	2400	
Db	3257	CACATAAGATATTGCTTTAGACC	CCGAGACATGTGTCCAAAGTGAACCTGAAACGGGGTGTTTGA	3316	
OY	2401	CATGACCAATGAAGATCTGGAAG	GTCTGAGATGACATGACACCCGACACAGGTGACAGCC	2460	
Db	3317	CATGACCAATGAAGATCTGGAAG	GTCTGAGATGACATGACACCCGACACAGGTGACAGCC	3376	
OY	2461	CTGCGAGTGTGGCCGTTAAACA	TATTAGAAACAGCCTGTGATCTGTAGTGTGACCCGAGGA	2520	
Db	3377	CTGCGAGTGTGGCCGTTAAACA	TATTAGAAACAGCCTGTGATCTGTAGTGTGACCCGAGGA	3436	
OY	2521	GCTGAGGCCGATCACTTGTGTG	CTGCTGCACCCGCGCTGACGTTTGGCTTACGACATGA	2580	
Db	3437	GCTGAGGCCGATCACTTGTGTG	CTGCTGCACCCGCGCTGACGTTTGGCTTACGACATGA	3496	
OY	2581	AGATACAGATTAG	2594		
Db	3497	AGATACAGATTAG	3510		

RESULT 9					
BD268211		14455 bp	DNA	linear	PAT 17-JUN-2003
LOCUS	BD268211	14455 bp	DNA	linear	PAT 17-JUN-2003
DEFINITION	Adenovirus vector, packaging cell line, composition and method for production and use.				
ACCESSION	BD268211				
VERSION	BD268211.1 GI:33077979				
KEYWORDS	JP 2002534130-A/15.				
SOURCE	synthetic construct				
ORGANISM	synthetic construct				
REFERENCE	other sequence; artificial sequences.				
AUTHORS	1 (bases 1 to 14455) Nemerow,G.R., Seggern,D.J.V., Hallenbeck,P.L., Stevenson,S.C. and Skripchenko,Y.				
TITLE	Adenovirus vector, packaging cell line, composition and method for production and use				
JOURNAL	Patent: JP 2002534130-A 15 15-OCT-2002; NOVARTIS AG,THE SCRIPPS RESEARCH INSTITUTE				
COMMENT	OS Artificial Sequence PN JP 2002534130-A/15 PD 15-OCT-2002 PP 14-JAN-2000 JP 2000593765 PR 14-JAN-1999 US 60/115920 PI GLEN ROBERT NEMEROW,DANIEL J VON SEGGERN,PAUL L HALLENBECK, PI SUSAN C STEVENSON,YELENA SKRIPCHENKO PC C12N15/09,A61K35/76,A61K48/00,A61P35/00,A61P43/00,A61P43/00, PC C12N5/10, PC C12N7/00,C12O1/68,G01N13/53,G01N13/566,C12N15/00,C12N5/00 CC Description of Artificial Sequence: plasmid FT Key Location/Qualifiers FT source 1..14455 Location/Qualifiers FT 1..14455 /organism='Artificial Sequence'.				
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QY	1	ATCGATCTTACCTGSCCAGAGGCTGGCTTTCACCCAGTGCAGCAGAGATGAAGAGGGT	60		
DB	1825	ATCGATCTTACCTGCCAGAGGCTGGCTTTCACCCAGTGCAGCAGAGATGAAGAGGGT	18844		
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DB	1885	GAGAGATTGTGTAGATTATGTGAGACACCCGGGACAGGTTGCAGGCTTGTTCATTAT	19444		
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DB	1945	CACGGAGGAATTACGGGGGACCCGAGATTATATGTGTCGCTTTGCTATATAGAACCTGT	20044		
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DB	2005	GGCATGTTTGTCTACAGTAACTGAAAAATTATGGCAGTGGGTGATAGATGAGTGGGTTTG	20644		
QY	241	GTCGTGTAATTTTTTTTTTAAATTTTACAGTTTGTGTTTAAAGAAATTTGTATATGGA	300		
DB	2065	GTCGTGTAATTTTTTTTTTAAATTTTACAGTTTGTGTTTAAAGAAATTTGTATATGGA	21244		
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DB	2125	TTTTTTTAAAGATCCTGTGCTGTAACCTGAGCCTGAGCCGAGCAAAACCGAGACCTG	21844		
QY	361	CAAGACTTACCCGCGCTCTTAAATGGCGCCTGCTATCTGAGACGCCGACATCACTG	420		
DB	2185	CAAGACTTACCCGCGCTCTTAAATGGCGCCTGCTATCTGAGACGCCGACATCACTG	22444		
QY	421	TGCTTAGGAATGCATATGTAAGTACGATAGCTGACTCCGGTCTTCTTAAACACACTC	480		

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Db 2245 TGTCTAAGAAATGCAATATGTAAGATACCTGAGCTCGAGTCTTCTAACAACACTC 2304
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RESULT 10
AX356044
LOCUS AX356044 14455 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 15 from Patent WO0183729.
ACCESSION AX356044
VERSION AX356044.1 GI:18620606
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Nemerow, G.R., von Seggern, D.J. and Friedlander, M.
Vectors for ocular transduction and use thereof for genetic therapy
Patent: WO 0183729-A, 15 08-NOV-2001;
Novartis AG (CH) ; The Scripps Research Institute (US) ; Nemerow,
Glen R. (US) ; Von Seggern, Daniel J. (US) ; Friedlander, Marcy
(US)
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1945 CACCGAGGAATACGGGGGACCCAGATATTATGTTGCTTGTCTATATGAGACCTGT 2004
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Db		3565	TAGGTGGCCTTTAGATGATGATCATTAATAATGTGGCCCGGGGGCTTGACATGAAACGG	3624
OY		1801	GATGGTTATTATGATGTAAATGTAAAGTTACTGAGGCCCAATTTTAGCGGTACGTTTTCTGGC	1868
Db		3625	GATGGTTATTATGATGTAAATGTAAAGTTACTGAGGCCCAATTTTAGCGGTACGTTTTCTGGC	3684
OY		1861	CATTACCACAACCTTATCTTACACACGGTGAAGCTTCTATGGGTTTAACAATACCTGTGTGA	1920
Db		3665	CAATACCAACCTTATCTTACACACGGTGAAGCTTCTATGGGTTTAACAATACCTGTGTGA	3744
OY		1921	AGCGTCGACCGATGTAAAGGTTTCGGGGCTGGCCCTTTTACTGCGCTGTGAAGGGGGTGGT	1980
Db		3745	AGCGTCGACCGATGTAAAGGTTTCGGGGCTGGCCCTTTTACTGCGCTGTGAAGGGGGTGGT	3804
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Db		3865	TATCTCTGCTGAGGGTAACTCGAGGGTGGCCACAATGTGCCTCCGACTGTGTTGCTT	3924
OY		2101	CATGCTAGTGA AAAAGCGTGGCTGTGATTAAGCATTAACATGGTATGTGGCAACTGCGAGA	2160
Db		3925	CATGCTAGTGA AAAAGCGTGGCTGTGATTAAGCATTAACATGGTATGTGGCAACTGCGAGA	3984
OY		2161	CAGGGCCTCTCAGATGCTGACCTGCTCGGACGGCAACTGTCACTGTGTAAGAACCAATTCA	2220
Db		3985	CAGGGCCTCTCAGATGCTGACCTGCTCGGACGGCAACTGTCACTGTGTAAGAACCAATTCA	4044
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OY		2281	TTCCCTTGCAATTTGGGTTAA CAGAGGGGGGGTGTCTCTACCTTAACCAATGSCAATTTGAATCA	2340
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OY		2401	CATACCAATGAAGATCTGGAGGTGTCTGAAGTAAAGATGAACCCGGCACAGGTGTCAAGACC	2460
Db		4225	CATACCAATGAAGATCTGGAGGTGTCTGAAGTAAAGATGAACCCGGCACAGGTGTCAAGACC	4284
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Db		4285	CTGCGAGTGTGGCGGTAAACATATTAAAGAAACGAGCCTGTGA TGTGTGATGTGAACGAGGA	4344
OY		2521	GCTGAGGCCGATCACTTGTTGTGTGGCTGTGACCCCGCGCTGAATTTGGCTCTTACGATGA	2580
Db		4345	GCTGAGGCCGATCACTTGTTGTGTGGCTGTGACCCCGCGCTGAATTTGGCTCTTACGATGA	4404
OY		2581	AGATACAGATTGAG 2594	
Db		4405	AGATACAGATTGAG 4418	
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RESULT 11				
LOCUS	BD021943	14455 bp	DNA linear	PAT 27-AUG-2002
DEFINITION	Packaging cell systems for use in promotion of the development of high-capacity adenoviral vectors.			
ACCESSION	BD021943			
VERSION	BD021943.1	GI:22563166		
KEYWORDS	JP 2001505047-A/15.			
SOURCE	unidentified			
ORGANISM	unclassified			
unclassified.				

REFERENCE	1 (bases 1 to 1445)	Memerow,G.R. and Seggern,D.J.V.
AUTHORS		Packaging cell systems for use in promotion of the development of
TITLE		high-capacity adenoviral vectors
JOURNAL		Patent: JP 2001505047-A 15 17-Apr-2001;
COMMENT		NOVARTIS AG,THE SCRIPPS RESEARCH INSTITUTE
		PN JP 2001505047-A/15
		PD 17-APR-2001
		PF 24-SEP-1997 JP 1998515273
		PR 25-SEP-1996 US 08/719806
		PI GLEN R MEMEROW, DANIEL J VON SEGGERN
		PC C12N5/10,C07K14/075,C12N15/09//A61K31/711,A61K35/76,A61K48/00,
		PC A61P35/00,
		PC C12M5/00,C12N15/00
		CC Strandedness: Double;
		CC Topology: Circular;
FEATURES		Key
source		Location/Qualifiers
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		/mol_type="genomic DNA"
		/db_xref="taxon:32644"
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Best Local Similarity	100.0%;	Pred. No. 0;
Matches 2594;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	ATGCATCTTACTCTCCACGAGGCGTGGCTTCCACCCAGTGCAGACGATGAAGAGGCT 60
DB	1825	ATGCATCTTACTCTCCACGAGGCGTGGCTTCCACCCAGTGCAGACGATGAAGAGGCT 1884
QY	61	GAGAGTTTGTGTAGATTATGTGAGAGCACCCGCGGACGCTTCAGGTCTTGTTCATTAT 120
DB	1885	GAGAGTTTGTGTAGATTATGTGAGAGCACCCGCGGACGCTTCAGGTCTTGTTCATTAT 1944
QY	121	CACCGAGGAATACGGGGGACCCGAGATTATATGTGTTCGCTTTGCTATATAGAACCTGT 180
DB	1945	CACCGAGGAATACGGGGGACCCGAGATTATATGTGTTCGCTTTGCTATATAGAACCTGT 2004
QY	181	GGCATTGTTTGCTACAGTAGTGAATATTATGGGCAAGTGGTGAATAGTGGTGGTTTG 240
DB	2005	GGCATTGTTTGCTACAGTAGTGAATATTATGGGCAAGTGGTGAATAGTGGTGGTTTG 2064
QY	241	GTGTGTAAATTTTTTTTAAATTTTACAGTTTGTGAGTTTAAAGAAATTTTGTATTGTGA 300
DB	2065	GTGTGTAAATTTTTTTTAAATTTTACAGTTTGTGAGTTTGTGAGTTTAAAGAAATTTTGTATTGTGA 2124
QY	301	TTTTTTTAAAGGTCGTGTCTGTAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTG 360
DB	2125	TTTTTTTAAAGGTCGTGTCTGTAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTG 2184
QY	361	CAGAACCCTACCCGCGCTCTTAAATATGCGCTGTATCTTGAGAGCGCCGACATCATCTG 420
DB	2185	CAGAACCCTACCCGCGCTCTTAAATATGCGCTGTATCTTGAGAGCGCCGACATCATCTG 2244
QY	421	TGTTCTAAGAAATGCAATAGTAGTAGGATAGCTGTACTCCGTCCTTTTAAACAACCTC 480
DB	2245	TGTTCTAAGAAATGCAATAGTAGTAGGATAGCTGTACTCCGTCCTTTTAAACAACCTC 2304
QY	481	CTGAGATACACCCGGTGTCCCGCTGAGCCCATTTAAACAGATTGCGGTGAGATTTGGTG 540
DB	2305	CTGAGATACACCCGGTGTCCCGCTGAGCCCATTTAAACAGATTGCGGTGAGATTTGGTG 2364
QY	541	GGCGTGCACGAGCTGTGAAATGTATCGAGGACTTGCTTAAAGAGCCTGCGGCAACTTTGG 600
DB	2365	GGCGTGCACGAGCTGTGAAATGTATCGAGGACTTGCTTAAAGAGCCTGCGGCAACTTTGG 2424
QY	601	ACTTTGACTGTAAACGCGCCAGGCGCAATAGTGTAAACCTGTGATTTGCGTGTGTGTAA 660
DB	2425	ACTTTGACTGTAAACGCGCCAGGCGCAATAGTGTAAACCTGTGATTTGCGTGTGTGTAA 2484
QY	661	CGCCTTTGTGTGTGATGAGTTGATGTTAATTTAAATTAAGGTTGAGATATGTTTAACT 720

Db	2485	CGCCTTGTGTCGAAATGATGATGTAATTAATTAAGGGGTGAGTAATGTTTAACT	2544
QY	721	TGCATGGCGATTAAATGAGGCGGGGCTTAAAGGATATATATCGCCGCTGGGCTTAATCT	780
Db	2545	TGCATGGCGATTAAATGAGGCGGGGCTTAAAGGATATATATGCGCCGCTGGGCTTAATCT	2604
QY	781	TGGTTACATCTGACCTCATGAGGCTTGGGAGTGTTTGGAAAGATTTTTCCTGCTGCGCTTA	840
Db	2605	TGGTTACATCTGACCTCATGAGGCTTGGGAGTGTTTGGAAAGATTTTTCCTGCTGCGCTTA	2664
QY	841	ACTTGCTGGAAACAGAGCTCTAACAGTACCTCTGGTTTGGAGGTTTCTGTGGGCGCTCAT	900
Db	2665	ACTTGCTGGAAACAGAGCTCTAACAGTACCTCTGGTTTGGAGGTTTCTGTGGGCGCTCAT	2724
QY	901	CCGAGGCAAGATTAGTCTGCAGAAATTAAAGAGGATTCAAGTGGGAATTTGAAGACTTT	960
Db	2725	CCGAGGCAAGATTAGTCTGCAGAAATTAAAGAGGATTCAAGTGGGAATTTGAAGACTTT	2784
QY	961	TGAATTCCTGTGTGAGCTGTTTGATTTCTTTGAATCTGGGTCAACAGGCGCTTTTCAAG	1020
Db	2785	TGAATTCCTGTGTGAGCTGTTTGATTTCTTTGAATCTGGGTCAACAGGCGCTTTTCAAG	2844
QY	1021	AGAAAGTATCAAGACTTTGGATTTTTCACACCGGGGCGCGCTGGCGCTGCTGTGCTT	1080
Db	2845	AGAAAGTATCAAGACTTTGGATTTTTCACACCGGGGCGCGCTGGCGCTGCTGTGCTT	2904
QY	1081	TTTTGAGTTTATAAAGATAAATGAGACGAAGAAACCACTTGAGCGGGGCTTACCTCG	1140
Db	2905	TTTTGAGTTTATAAAGATAAATGAGACGAAGAAACCACTTGAGCGGGGCTTACCTCG	2964
QY	1141	TGGAATTTCTGGCCATGCACTGTGTGAGAGCGGTTGTGAGACACAGAAATCGCTCTGAC	1200
Db	2965	TGGAATTTCTGGCCATGCACTGTGTGAGAGCGGTTGTGAGACACAGAAATCGCTCTGAC	3024
QY	1201	TGTTGTCTTCCGTCCGCCCGCATTAATCCGACCGAGAGACAGACACACACAGAGAG	1260
Db	3025	TGTTGTCTTCCGTCCGCCCGCATTAATCCGACCGAGAGACAGACACACACAGAGAG	3084
QY	1261	AAGCAGGCGGGGCGGAGGAGGAGGAGCCCATGAAACCGAGAGCCGCGCTGAGCCCTC	1320
Db	3085	AAGCAGGCGGGGCGGAGGAGGAGGAGCCCATGAAACCGAGAGCCGCGCTGAGCCCTC	3144
QY	1321	GCGAATGAAATGTTTATACAGATGCGCTGAACTGTATCCAGAACTGAGAGCAATTTGA	1380
Db	3145	GCGAATGAAATGTTTATACAGATGCGCTGAACTGTATCCAGAACTGAGAGCAATTTGA	3204
QY	1381	TACAGAGATGGGCAAGGGGCTTAAGGGGGCTTAAGGGAGCGGGGCTTGTGAGGCTTAC	1440
Db	3205	TACAGAGATGGGCAAGGGGCTTAAGGGGGCTTAAGGGAGCGGGGCTTGTGAGGCTTAC	3264
QY	1441	AAGAGAGGCTAGAGATCTAAGCTTTAGCTTATATGACAGACACCGCTCTGAGTATTAAC	1500
Db	3265	AAGAGAGGCTAGAGATCTAAGCTTTAGCTTATATGACAGACACCGCTCTGAGTATTAAC	3324
QY	1501	TTTTCAACAGATCAAGGATTAATTCGCTTAATGAGGCTTGATCTGTGGCGCAAGATATTC	1560
Db	3325	TTTTCAACAGATCAAGGATTAATTCGCTTAATGAGGCTTGATCTGTGGCGCAAGATATTC	3384
QY	1561	CATAGAGCAGCTGACCACTTACTGCGCTGCAGCCAGGGGATGATTTTGAAGAGGCTATTAAG	1620
Db	3385	CATAGAGCAGCTGACCACTTACTGCGCTGCAGCCAGGGGATGATTTTGAAGAGGCTATTAAG	3444
QY	1621	GGTATTTGCAAAAGTGGGCACTTAAGGCGAGATTCGAAGTACAAAGATCAGCAAACTGTATAA	1680
Db	3445	GGTATTTGCAAAAGTGGGCACTTAAGGCGAGATTCGAAGTACAAAGATCAGCAAACTGTATAA	3504
QY	1681	TATCAGAGATTTGTGCTACATTTCTGGGAAACGGGGCCGAGGTGAGATATAGTACGAGAGA	1740
Db	3505	TATCAGAGATTTGTGCTACATTTCTGGGAAACGGGGCCGAGGTGAGATATAGTACGAGAGA	3564
QY	1741	TAGGATGGCCTTTAGATGTAGCATGATAAATATGTGGCGGGGGTGTCTTGCAATGACGG	1800

Db	3565	TAGGGTGGCCTTTAGATGTAAGCATGATAATTAATATGTGGCCGGGGGTCTTGGCATGACGG	3624
Qy	1801	GGTGTATTATTAGATATGTAAGTTTAACTGGCCCAATTTTACGGGTAACTGTTTCTGTGC	1860
Db	3625	GGTGTATTATTAGATATGTAAGTTTAACTGGCCCAATTTTACGGGTAACTGTTTCTGTGC	3684
Qy	1861	CAATACCAACCTTATCCTTACACGGGTGAAGCTCTATAGGTTTAACTATACCTGTGGGA	1920
Db	3685	CAATACCAACCTTATCCTTACACGGGTGAAGCTCTATAGGTTTAACTATACCTGTGGGA	3744
Qy	1921	AGCTTGACCGATGTAAAGGTTTCGGGCTGTGCCTTTTACTGTCTGAAAGGGGGTGT	1980
Db	3745	AGCTTGACCGATGTAAAGGTTTCGGGCTGTGCCTTTTACTGTCTGAAAGGGGGTGT	3804
Qy	1981	GTTGTGCCCCCAAAAGCGGGCTTCAATTAGAAATGCTCTTTGAAAGGTACCTTGGG	2040
Db	3805	GTTGTGCCCCCAAAAGCGGGCTTCAATTAGAAATGCTCTTTGAAAGGTATCTTGGG	3864
Qy	2041	TATCTGTGTAGAGGTAACTCCAGGGTGCACAATATGTGGCTCCGACTGTGGTTCCT	2100
Db	3865	TATCTGTGTAGAGGTAACTCCAGGGTGCACAATATGTGGCTCCGACTGTGGTTCCT	3924
Qy	2101	CATCTAGTGAATAAGCCTGGCTGTGATTAAACATACATGATATGTGGCACTGGCAGA	2160
Db	3925	CATCTAGTGAATAAGCCTGGCTGTGATTAAACATATGATATGTGGCACTGGCAGA	3984
Qy	2161	CAGGGCCCTTCAGATGTGACCTGTCTGGACGGCACTGTCACTGCTGAAAGCATTTCA	2220
Db	3985	CAGGGCCCTTCAGATGTGACCTGTCTGGACGGCACTGTCACTGCTGAAAGCATTTCA	4044
Qy	2221	CGTAGCCAGCACACTTCGCAAGGCTGTGGCCACATGTGTTGAGCATTAACATCTGACCCGCTG	2280
Db	4045	CGTAGCCAGCACACTTCGCAAGGCTGTGGCCACATGTGTTGAGCATTAACATCTGACCCGCTG	4104
Qy	2281	TTCTCTGCAATTGGGTGAACGGAAGGGGGGTGTCCTACCTTAACCAATTTGAAGTCA	2340
Db	4105	TTCTCTGCAATTGGGTGAACGGAAGGGGGGTGTCCTACCTTAACCAATTTGAAGTCA	4164
Qy	2341	CACTAAGATATTGTCTTGAGCCCGAAGCATGTCCAAAGGTGAACCTGAAACGGGGTGTGTA	2400
Db	4165	CACTAAGATATTGTCTTGAGCCCGAAGCATGTCCAAAGGTGAACCTGAAACGGGGTGTGTA	4224
Qy	2401	CATGACCATGAAGATCTGGAAGAGTGTGAGTAAAGTAGAGCCCGCACAGGTGACAGCC	2460
Db	4225	CATGACCATGAAGATCTGGAAGAGTGTGAGTAAAGTAGAGCCCGCACAGGTGACAGCC	4284
Qy	2461	CTGCGAGTGTGGCGGTAAACATATTAGGAACCAAGCTGTGATGTGTGAATGTGACCGAGA	2520
Db	4285	CTGCGAGTGTGGCGGTAAACATATTAGGAACCAAGCTGTGATGTGTGAATGTGACCGAGA	4344
Qy	2521	GCTGAGGCCCGATCACTTGTGTGTGCTGCACTCCGCGCTGAATTTGGCTCTAGCGATGA	2580
Db	4345	GCTGAGGCCCGATCACTTGTGTGTGCTGCACTCCGCGCTGAATTTGGCTCTAGCGATGA	4404
Qy	2581	AGATACAGATTGAG 2594	
Db	4405	AGATACAGATTGAG 4418	

RESULT 12					
CQ854906	CQ854906	32802 bp	DNA	linear	PAT 23-AUG-2004
LOCUS	Sequence 3 from Patent WO2004066947.				
DEFINITION	CQ854906				
ACCESSION	CQ854906				
VERSION	CQ854906.1	GI:51510466			
KEYWORDS	unidentified adenovirus				
SOURCE	unidentified adenovirus				
ORGANISM	viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus				
REFERENCE	1				
AUTHORS	Hu, F. and Wu, B.				
TITLE	Therapy for primary and metastatic cancers				
JOURNAL	Patent: WO 2004066947-A 3 12-AUG-2004;				

Shanghai Sunway Biotech Co Ltd (CN)
FEATURES Location/Qualifiers
Source 1..32802
/organism="unidentified adenovirus"
/mol_type="unassigned DNA"
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Query Match 100.0%; Score 2594; DB 6; Length 32802;
Beeb Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ATTCATCTTACCTGCGACGAGGCTGCTTCCACCACCGACGACGAGAGTGAAGAGGT 60
Db 917 ATTCATCTTACCTGCGACGAGGCTGCTTCCACCACCGACGACGAGAGTGAAGAGGT 976
Qy 61 GAGAGTTTGTAGATTATGTGAGACACCCCGGCGACGCTTGACAGTCTTTCATAT 120
Db 977 GAGAGTTTGTAGATTATGTGAGACACCCCGGCGACGCTTGACAGTCTTTCATAT 1036
Qy 121 CACCGAGAGATAGCGGGGACCCAGATATTATGTGCTTGTCTTATATAGACCTGT 180
Db 1037 CACCGAGAGATAGCGGGGACCCAGATATTATGTGCTTGTCTTATATAGACCTGT 1096
Qy 181 GGCAATGTTGCTACAGTAAGTGAATAATTATGGCAGTGGGTGATAGAGTGGTGG 240
Db 1097 GGCAATGTTGCTACAGTAAGTGAATAATTATGGCAGTGGGTGATAGAGTGGTGG 1156
Qy 241 GTGTGTATATTTTTTTTAAATTTTACAGTTTGTGTGTTAAAGAAATTTTGTATGTA 300
Db 1157 GTGTGTATATTTTTTTTAAATTTTACAGTTTGTGTGTTAAAGAAATTTTGTATGTA 1216
Qy 301 TTTTTTAAAGTCTGCTGTCTGAACCTGACCTGACCCGACGACGACCGAGGCTG 360
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Qy 361 CAAGACCTACCCGCGCTCTAAATAGGCGCTGCTATCTGAGAGCGCCGACATCCTG 420
Db 1277 CAAGACCTACCCGCGCTCTAAATAGGCGCTGCTATCTGAGAGCGCCGACATCCTG 1336
Qy 421 TGTCTAGAGATGCAATAGTATAGTACGATAGCTGATCTCCGCTCTTCTAACAACCTC 480
Db 1337 TGTCTAGAGATGCAATAGTATAGTACGATAGCTGATCTCCGCTCTTCTAACAACCTC 1336
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Db 1517 ACTTGAGCTGTAAACGCCCGACCATAGGTGTAACCTGTGATTCGCTGTGTGTTAA 1516
Qy 661 CGCCTTGTGTGCTGAATGAGTGTATGATTTAATTAAGGAGTGAATATGTTAACT 720
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Qy 781 TGGTTCATCTGACCTTCATGAGGCTTGAGAGTGTGTGAAGATTTTCTGCTGTGCTA 840
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Qy 841 ACTTGTGGAACAGAGCTCTTAACGTAACCTTGTGTTTGGAGGTTTCTGTGGGCTCAT 900
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Db 1877 TGAATTCCTGTGTAGAGCTGTTTGTATCTTGTGAATCTGGTCAACAGGCGCTTTCCAG 1936
Qy 1021 AGAAGTCAATCAAGACTTTGATTTTTTCCACACCGGGCGGCTGCGCTGTGCTT 1080
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Qy 1081 TTTTGAATTTTAAAGATTAATGAGCGGAAGAAACCATCTGAGCGGGGTAACTGTC 1140
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Qy 1381 TACAGAGATGGCGAGGCGCTAAAGGGGGTAAAGAGGAGCGGGGGCTGTGTGAGCTAC 1440
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Qy 1501 TTTTCAACAGATCAAGGATTAATTCGCTAATGAGCTTGATCTGTGCGCGAGAGTATTC 1560
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Qy 1561 CATAGAGAGCTGACCACTTAAGCTGACAGCCAGGGAGTATTTTGAAGAGCTATTAG 1620
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Qy 1681 TATCAGGAATTTGTTGCTACATTTCTGGGAAAGGGGCGGAGTGGAGATTAACGAGGA 1740
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Qy 1741 TAGGGTGGCTTTAGATGTAGCATGATTAATGTGCGCGGGGTGCTTGGCATGAGCGG 1800
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Qy 1861 CAATACCAACTTATCTCAACAGGTGTAAAGCTTCTATGSGTTTAAACAATACCTGTGGA 1920
Db 2777 CAATACCAACTTATCTCAACAGGTGTAAAGCTTCTATGSGTTTAAACAATACCTGTGGA 2836
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Qy 1981 GTGTGCGCCCAAAAGAGGCTTCAATTAAGAAATGCTCTTTGAAGAGTGTACTTGGG 2040

Db 2897 GTGTGCCCCAAAGCAGGGCTTCAATTAGAAATGCTCTTTGAAAAGGTGACCTTG3 2956
QY 2041 TATCCCTGTCGAGAGTTAATCCAGAGGGTGGCCAAATGTGGCCCTCGACTGTGGTCTT 2100
Db 2957 TATCCCTGTCGAGAGTTAATCCAGAGGGTGGCCAAATGTGGCCCTCGACTGTGGTCTT 3016
QY 2101 CATGCTAGTAAAGCGTGGCTGTGATTAGCATTAACATGATATGTGGCACTGCGAGA 2160
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QY 2161 CAGGGCTCTCAAGTGTGACCTGTGGACGGCAATGTGACCTGTGTAAGACCATTC 2220
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Db 3197 TTCCCTGCAATTTGGGTAAACAGAGGGGGTGTCTTACCTTACCAATGCAATTTGAGTCA 3256
QY 2341 CACTAAGATATTTGCTTGAAGCCGAGACATGTCCAAAGTGAACCTGAAACGGGGGTGTTGA 2400
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QY 2401 CATGACCATGAAGATCTGAAAGGTGTGAGGTGAGATGAGTAGAACCCGACCAAGTGCAGACC 2460
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QY 2461 CTGCGAGTGTGGCGGTAAACATATTATTAAGAACCAAGCTGTGATGCTGTGATGTGACCGAGA 2520
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QY 2521 GCTGAGGCCCGATCACTTGTGTGTGCTGTGACCCGCGCTGAGTTGGCTCTAGCGATGA 2580
Db 3437 GCTGAGGCCCGATCACTTGTGTGTGCTGTGACCCGCGCTGAGTTGGCTCTAGCGATGA 3496
QY 2581 AGATACAGATTGAG 2594
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RESULT 13
AX084506 33699 bp DNA linear PAT 28-FEB-2001
LOCUS AX084506 Sequence 3 from Patent WO0104282.
DEFINITION AX084506
ACCESSION AX084506.1 GI:13185914
VERSION
KEYWORDS
SOURCE Human adenovirus C
ORGANISM Human adenovirus C
VIRUSES; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
REFERENCE 1. Wold, W.S., Toch, K., Doronin, K. and Tollefson, A.E.
TITLE Replication-competent anti-cancer vectors
JOURNAL Patent: WO 0104282-A 3 18-JAN-2001;
Saint Louis University (US)
FEATRES location/Qualifiers
source 1. .33699
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ORIGIN
Query Match 100.0%; Score 2594; DB 6; Length 33699;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1097 GGCATGTTGTCTACAGTAAAGTAATAATATGGGCAAGTGGGTGATAGAGTGGGGTTG 1156
QY 241 GTGTGGTAATTTTTTTTTTAATTTTAACTTTTGTGTGTTTAAAGATTTGTATTGTGA 300
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QY 301 TTTTTTAAAGGTCCTGTGTCTGAACTTGAGCTTGAGCCGAGCCAGAACCGGAGCTTG 360
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Db 1517 ACTTGAAGCTGTAACCGCCAGGCCATTAAGGTGTAACCTGTGATTCGTGTGTGTTAA 1576
QY 661 GCGCTTGTGTGCTGAATGAGTTGATGTAAAGTTAATTAAGGTTGATGATGTTTAACT 720
Db 1577 GCGCTTGTGTGCTGAATGAGTTGATGTAAAGTTAATTAAGGTTGATGATGTTTAACT 1636
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LOCUS AY339865 35934 bp DNA linear VRL 13-AUG-2003

DEFINITION Human adenovirus C serotype 5, complete genome.

ACCESSION AY339865

VERSION AY339865.1 GI:33465830

KEYWORDS

SOURCE Human adenovirus C

ORGANISM Human adenovirus C

REFERENCE 1 (bases 1 to 35934)

AUTHORS McAllister,D.L., Lu,F., Thomas,B.K., Hutchins,B.M. and Sugerman,B.J.

TITLE Complete Nucleic Acid Sequence of the Adenovirus Type 5 Reference Material

JOURNAL BioProcessing (2003) In press

REFERENCE 2 (bases 1 to 35934)

AUTHORS Sugerman,B.J., McAllister,D.L. and Hutchins,B.M.

TITLE Direct Submision

JOURNML Submitted (09-JUN-2003) Processed Sciences, Canj Inc., Schering-Plough Corporation, 3525 John Hopkins Court, San Diego, CA 92121, USA

FEATURES

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Db 3017 CATGCTAGTGAAGAGCGTGTGTGATTAAGCATTAACATGTGTGTGCACTGCGAGGA 3076
Qy 2161 CAGGGGCTCTCAGATGCTGACTGTGCGAGCGCAACTGTCACTGCTGAAAGACCATTC 2220
Db 3077 CAGGGGCTCTCAGATGCTGACTGTGCGAGCGCAACTGTCACTGCTGAAAGACCATTC 3136

Qy 2221 CGTACCCAGCCACTCTGCCAAGGCTTGCCCACTGCTTGTGAGCATTAACATCTGACCCGCTG 2280
Db 3137 CGTACCCAGCCACTCTGCCAAGGCTTGCCCACTGCTTGTGAGCATTAACATCTGACCCGCTG 3196
Qy 2281 TTCCTTGCAATTTGGGTAAACAGAGAGGGGGTGTTCCTTACCTTAACCAATGCAATTTGAGTCA 2340
Db 3197 TTCCTTGCAATTTGGGTAAACAGAGAGGGGGTGTTCCTTACCTTACCAATGCAATTTGAGTCA 3256
Qy 2341 CACTAAGATATTTGCTTGAAGCCGAGAGCATGTCCAAGGTGAACCTGAACGGGGTGTGGA 2400
Db 3257 CACTAAGATATTTGCTTGAAGCCGAGAGCATGTCCAAGGTGAACCTGAACGGGGTGTGGA 3316
Qy 2401 CATGACCATGAAGATCTGAAAGGTGCTGAGGTGATGAGACCCGACACAGGTGACAGC 2460
Db 3317 CATGACCATGAAGATCTGAAAGGTGCTGAGGTGATGAGACCCGACACAGGTGACAGC 3376
Qy 2461 CTGAGAGTGTGGCGGTAAACATATTAGGAACGAGCTGTGATGCTGATGTGACCGAGGA 2520
Db 3377 CTGAGAGTGTGGCGGTAAACATATTAGGAACGAGCTGTGATGCTGATGTGACCGAGGA 3436
Qy 2521 GCTGAGGCCGATCATTTGTGCTGCGCTGCAACCGGCTGAGATTGCTTACGAGATGA 2580
Db 3437 GCTGAGGCCGATCATTTGTGCTGCGCTGCAACCGGCTGAGATTGCTTACGAGATGA 3496
Qy 2581 AGATACAGATTGAG 2594
Db 3497 AGATACAGATTGAG 3510

Search completed: October 30, 2005, 22:52:22
Job time : 11083 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 30, 2005, 17:47:52 ; Search time 1352 Seconds
(without alignments)
11357.847 Million cell updates/sec

Title: US-10-790-562-33_COPY_459_3052
Perfect score: 2594
Sequence: 1 atgatcttaccctccgcga.....cgatgaagatcagatcgag 2594

Scoring table: IDENTITY_NUC
Gapc 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : 'N_Geneseq_16Dec04:':
1: geneeqn19808:*
2: geneeqn19908:*
3: geneeqn20008:*
4: geneeqn20018:*
5: geneeqn20028:*
6: geneeqn20038:*
7: geneeqn20048:*
8: geneeqn20058:*
9: geneeqn20068:*
10: geneeqn20078:*
11: geneeqn20088:*
12: geneeqn20098:*
13: geneeqn20108:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2594	100.0	3408 9	ACC70006 Nucleotide
2	2594	100.0	7090 5	AAH20746 Plasmid S
3	2594	100.0	7607 3	AAAS9076 Nucleotide
4	2594	100.0	7607 6	ABA94278 Nucleotide
5	2594	100.0	7607 9	AA156864 DNA seq
6	2594	100.0	7607 10	ADB75124 Chromosome
7	2594	100.0	7607 10	ADFA8758 Plasmid P
8	2594	100.0	11152 2	AAV32373 Complete
9	2594	100.0	11152 3	AAAS9047 Nucleotide
10	2594	100.0	11152 6	ABA94256 Nucleotide
11	2594	100.0	11152 10	ADB75153 Plasmid P
12	2594	100.0	11152 12	ADFA8798 Plasmid P
13	2594	100.0	14455 2	AAV32374 Complete
14	2594	100.0	14455 2	AAAS9050 Nucleotide
15	2594	100.0	14455 6	ABA94259 Nucleotide
16	2594	100.0	14455 10	ADB75156 Plasmid P
17	2594	100.0	14455 10	ADFA8801 Plasmid P
18	2594	100.0	32802 13	ADFA8801 Plasmid P
19	2594	100.0	33699 4	AAAC85020 Adenovirus
20	2594	100.0	34448 4	AAAC85021 Adenovirus

21	2594	100.0	35934 8	ABZ82331 Human ade
22	2594	100.0	35935 2	AAV07258 Adenovirus
23	2594	100.0	35935 6	AAAC85026 Complete
24	2594	100.0	35935 6	ABZ82331 Human ade
25	2594	100.0	35935 6	ABZ82331 Human ade
26	2594	100.0	35935 8	ACA61116 Adenovirus
27	2594	100.0	35935 8	ACA61117 Adenovirus
28	2594	100.0	35935 10	ACA60761 Human ade
29	2594	100.0	35935 13	ADFA1672 Wild type
30	2594	100.0	35935 5	AAV32374 Complete
31	2594	100.0	37339 5	AAAS1612 Mouse ost
32	2582	99.5	33592 4	AAAC85018 Adenovirus
33	2582	99.5	33988 4	AAAC85023 Adenovirus
34	2582	99.5	34341 4	AAAC85019 Adenovirus
35	2582	99.5	34737 4	AAAC85024 Adenovirus
36	2582	99.5	35724 4	AAAC85022 Adenovirus
37	2582	99.5	35871 6	AAAD27972 Recombina
38	2582	99.5	36114 6	AAAC85025 Adenovirus
39	2498	96.3	35937 6	ABZ82331 Human ade
40	2498	96.3	35937 9	AACT70007 Nucleotide
41	2497.4	96.3	35759 10	ADFA6068 Adenovirus
42	2497.4	96.3	35759 13	ADFA6068 Adenovirus
43	2497	96.3	4853 10	ADFA6068 Adenovirus
44	2161	83.3	34303 2	AAV07261 Adenovirus
45	1830	70.5	2500 9	AAAC85140 Human ade

ALIGNMENTS

RESULT 1	ACCT70006	standard; cDNA; 3408 BP.
XX	ACCT70006;	
XX	29-JUL-2003	(first entry)
DE	Nucleotide sequence of the E1a protein of human adenovirus type 5.	
KW	Cancer; hyperproliferative disorder; viral vector; H19 promoter; H19 carcinoma; sarcoma; adenoma; ganglioblastoma; bladder carcinoma; E1a; gene; ss.	
XX	Human adenovirus type 5.	
XX	Key	Location/Qualifiers
FT	CDS	44..1029
FT		/*tag= a
FT		/product= "E1a protein"
FT	exon	/note= "contains an intron"
FT		44..598
FT		/*tag= b
FT		/number= 1
FT	intron	599..714
FT		/*tag= c
FT	exon	/number= 1
FT		715..1026
FT		/*tag= d
FT		/number= 2
XX		
PN	W02003035883-A2.	
XX		
PD	01-MAY-2003.	
XX		
PF	22-OCT-2002; 2002W0-IL000843.	
XX		
PR	22-OCT-2001; 2001US-00012131.	
XX		
PA	(YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.	
XX		
PI	Hochberg A, Ayesh S;	
XX		

DR MPI; 2003-441263/41.
XX P-PSDB; ABR55301.
PT Treating cancer or hyperproliferative disorder comprises administering a
PT conditionally replicative viral vector, where the viral nucleic acid
PT encoding a product essential for its replication is operably linked to
PT H19 regulatory sequence.
XX
XX Example; Fig 7; 122pp; English.
XX The specification describes a method of treating cancer or
XX hyperproliferative disorders. The method comprises administering a
XX conditionally replicative viral vector, where at least one of the viral
XX nucleic acids encoding a product essential for its replication is
XX operably linked to an H19 regulatory sequence. The method is useful for
XX treating cancer or hyperproliferative disorders. The cancer is selected
XX from many different types, for example, carcinoma, sarcoma, adenoma and
XX ganglioblastoma. Preferably, the cancer is bladder carcinoma. The present
XX sequence encodes the E1a protein of human adenovirus type 5. It was
XX linked to a H19 regulatory sequence, and used to produce vectors for use
XX in the method of the invention
SQ Sequence 3408 BP; 767 A; 764 C; 1007 G; 870 T; 0 U; 0 Other:
Query Match 100.0%; Score 2594; DB 9; Length 3408;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ATGCATCTTACCTGCGACGAGGCTGGCTTCCACCCAGTAGACGAGAGTAGAGAGGT 60
401 ATGCATCTTACCTGCGACGAGGCTGGCTTCCACCCAGTAGACGAGAGTAGAGAGGT 460
61 GAGAGTTGTGTAGATTATGTGAGACACCCCGGACGAGTTGACGAGTCTTGTCAATTAT 120
461 GAGAGTTGTGTAGATTATGTGAGACACCCCGGACGAGTTGACGAGTCTTGTCAATTAT 520
121 CACCGAGAGAAATACGGGGAGACCCAGATATATGTGTGCTTGTCTATATGAGACCTGT 180
521 CACCGAGAGAAATACGGGGAGACCCAGATATATGTGTGCTTGTCTATATGAGACCTGT 580
181 GGCATGTTGTCTACAGTAAGTAAGTAATTAATGAGGAGGAGTATGAGTGGGAGTTTG 240
581 GGCATGTTGTCTACAGTAAGTAAGTAATTAATGAGGAGGAGTATGAGTGGGAGTTTG 640
241 GTGTGTAATTTTTTTTAAATTTTAAAGTTTGTGTTTAAAGATTTGTATGTGA 300
641 GTGTGTAATTTTTTTTAAATTTTAAAGTTTGTGTTTAAAGATTTGTATGTGA 700
301 TTTTTTAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCGACAGAACCGGAGCCTG 360
701 TTTTTTAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCGACAGAACCGGAGCCTG 760
361 CAGAGCTTAACCGGCGCTCTAAATGAGGCGCTGATCCTGAGAGCCGACATCACTG 420
761 CAGAGCTTAACCGGCGCTCTAAATGAGGCGCTGATCCTGAGAGCCGACATCACTG 820
421 TGTCTAGAGAAATGCAATAGTAGTAGAGTAGCTGCTCCGCTCTTCTAAACACACCTC 480
821 TGTCTAGAGAAATGCAATAGTAGTAGAGTAGCTGCTCCGCTCTTCTAAACACACCTC 880
481 CTGAGATACACCGGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
881 CTGAGATACACCGGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 940
541 GCGCGTCGACGAGCTGGAATGATGAGAGACTGTGCTTAACGAGCCTGGGCAACTTTGG 600
941 GCGCGTCGACGAGCTGGAATGATGAGAGACTGTGCTTAACGAGCCTGGGCAACTTTGG 1000
601 ACTTGAGCTGTAAACCCCGAGGCAATTAAGTGTAAACCTGTGATTCGCTGTGTGTTAA 660
1001 ACTTGAGCTGTAAACCCCGAGGCAATTAAGTGTAAACCTGTGATTCGCTGTGTGTTAA 1060
661 CCGCTTTGTTGCTGATGATGATGATGATTTAAATTAAGGAGATTAATGTTTAACT 720

DB 1061 CCGCTTTGTTGCTGATGATGATGATGATGATTTAAATTAAGGAGATTAATGTTTAACT 1120
QY 721 TGCATGCGGTGTTAAATGAGGCGGCGCTTAAGAGGATATATATGCCGCTGAGCTAATCT 780
DB 1121 TGCATGCGGTGTTAAATGAGGCGGCGCTTAAGAGGATATATATGCCGCTGAGGCTAATCT 1180
QY 781 TGTGTACATCTGACCTCAACGAGGCTTGGAGAGTGTGGAAGATTTTCTGCTGTGCGTA 840
DB 1181 TGTGTACATCTGACCTCAACGAGGCTTGGAGAGTGTGGAAGATTTTCTGCTGTGCGTA 1240
QY 841 ACTTGCTGAACAGAGCTCTTAACAGTACCTCTGTTTGAAGTTCCTGTGGGCTCAT 900
DB 1241 ACTTGCTGAACAGAGCTCTTAACAGTACCTCTGTTTGAAGTTCCTGTGGGCTCAT 1300
QY 901 CCGAGCAAGATTAGTCTGCAAAATTAAGAGATTAACAAGTGGAAATTTGAAGAGCTTT 960
DB 1301 CCGAGCAAGATTAGTCTGCAAAATTAAGAGATTAACAAGTGGAAATTTGAAGAGCTTT 1360
QY 961 TGAATCTGTGTGAGCTGTTGATCTTGTGAATCTGGGTCACAGGCGCTTCCAG 1020
DB 1361 TGAATCTGTGTGAGCTGTTGATCTTGTGAATCTGGGTCACAGGCGCTTCCAG 1420
QY 1021 AGAGGTCAATCAAGACTTTGGAATTTTCCACACCGGCGCGCTGCGCTGTGCTT 1080
DB 1421 AGAGGTCAATCAAGACTTTGGAATTTTCCACACCGGCGCGCTGCGCTGTGCTT 1480
QY 1081 TTTTGAATTTTAAAGATTAATGAGAGCAAGAACCCCATCTGAGCGGGGGATACCTGC 1140
DB 1481 TTTTGAATTTTAAAGATTAATGAGAGCAAGAACCCCATCTGAGCGGGGGATACCTGC 1540
QY 1141 TGAATTTTCCGATCATCTGTGAGAGCGGCTGTGAGACAGAAATGCTGCTATC 1200
DB 1541 TGAATTTTCCGATCATCTGTGAGAGCGGCTGTGAGACAGAAATGCTGCTATC 1600
QY 1201 TGTGTCTTCCGCTCGCGCGCGATTAATCCGACGAGAGCAGCAGCAGCAGAGAGG 1260
DB 1601 TGTGTCTTCCGCTCGCGCGCGATTAATCCGACGAGAGCAGCAGCAGCAGAGAGG 1660
QY 1261 AAGCAGGCGGCGCGCAGAGCAGAGCCCATGGAACCCGAGAGCCGCTGAGCCCTC 1320
DB 1661 AAGCAGGCGGCGCGCAGAGCAGAGCCCATGGAACCCGAGAGCCGCTGAGCCCTC 1720
QY 1321 GCGAATGAATTTTAAAGGTCGCTGAACCTGTATCCAGAACTGAGAGCATTGTAACAT 1380
DB 1721 GCGAATGAATTTTAAAGGTCGCTGAACCTGTATCCAGAACTGAGAGCATTGTAACAT 1780
QY 1381 TACAGAGATGAGCAGGCGCTAAAGGCGGTTAAAGGAGCGGCGCTGTGAGGCTAC 1440
DB 1781 TACAGAGATGAGCAGGCGCTAAAGGCGGTTAAAGGAGCGGCGCTGTGAGGCTAC 1840
QY 1441 AGAGAGGCTAGGAATCTAGCTTTAGCTTAATGACAGACACCTCTCTGATGTATAC 1500
DB 1841 AGAGAGGCTAGGAATCTAGCTTTAGCTTAATGACAGACACCTCTCTGATGTATAC 1900
QY 1501 TTTTCAAGATCAAGATTAATGCGCTAATGAGTGTATCTGCTGGCAGAGATATTC 1560
DB 1901 TTTTCAAGATCAAGATTAATGCGCTAATGAGTGTATCTGCTGGCAGAGATATTC 1960
QY 1561 CATAGAGAGCTGACCACTTACTGCTCAGCAGAGGAGATATTTTGAAGGCTATTAG 1620
DB 1961 CATAGAGAGCTGACCACTTACTGCTCAGCAGAGGAGATATTTTGAAGGCTATTAG 2020
QY 1621 GGTATATGCAAAAGGTGCACTTAGGCTCAAGATTGCAAGTACAGAACTTGTAA 1680
DB 2021 GGTATATGCAAAAGGTGCACTTAGGCTCAAGATTGCAAGTACAGAACTTGTAA 2080
QY 1681 TATCAGAAATGTTCTCATTTCTGGGAAAGGGGCGGAGGAGATGATACGAGGA 1740
DB 2081 TATCAGAAATGTTCTCATTTCTGGGAAAGGGGCGGAGGAGATGATACGAGGA 2140
QY 1741 TAGGCTGCGCTTAATGATGATGATTAATATGTGCGCGGCGCTTGTGATGACGG 1800

Dp		2141	TAGGGTGGCCTTTAAGATGACGTAAATAATGTGGCCGGGGGGTGCTTGGCAATGCACCG	2200
Oy		1801	GGTGGTTATTATGAATGTAAAGGTTTACTGGCCCCCAATTTTAAGCGGTACGGTTTTCTGGC	1860
Dp		2201	GGTGGTTATTATGAATGTAAAGGTTTACTGGCCCCCAATTTTAAGCGGTACGGTTTTCTGGC	2260
Oy		1861	CAATTACCAACCTTATCTCAACAAGGTAAAGCTTCATAGGTTTAAACATTAACCTGTGCGA	1920
Dp		2261	CAATTACCAACCTTATCTCAACAAGGTAAAGCTTCATAGGTTTAAACATTAACCTGTGCGA	2320
Oy		1921	AGCCTGGAACCATGTAAAGGTTTCGGGGCTGTGCCCTTTTACTGTCTGTGGAAAGGGGATGCT	1980
Dp		2321	AGCCTGGAACCATGTAAAGGTTTCGGGGCTGTGCCCTTTTACTGTCTGTGGAAAGGGGATGCT	2380
Oy		1981	GTGTGGCCCCCAAAAGCAGGGGCTTCAATTAGAATATGCTCTTTGAAAAGTGTACCTTGGG	2040
Dp		2381	GTGTGGCCCCCAAAAGCAGGGGCTTCAATTAGAATATGCTCTTTGAAAAGTGTACCTTGGG	2440
Oy		2041	TATCTGTCTGAAGGGTTAATCTCAAGGTTCCGCACAAATGTGACTTCGCACTGTGGTTGCTT	2100
Dp		2441	TATCTGTCTGAAGGGTTAATCTCAAGGTTCCGCACAAATGTGACTTCGCACTGTGGTTGCTT	2500
Oy		2101	CATGTCTAGTAAAAAGCTGTGCTGTATTAAGCATTAACATGTGTAATGTGCAACTGCGAGGA	2160
Dp		2501	CATGTCTAGTAAAAAGCTGTGCTGTATTAAGCATTAACATGTGTAATGTGCAACTGCGAGGA	2560
Oy		2161	CAGGGCCTCTCAGATGCTGACCTGCTCGGACCGCAACTGTCACTGTCTGTAAGAACATTTCA	2220
Dp		2561	CAGGGCCTCTCAGATGCTGACCTGCTCGGACCGCAACTGTCACTGTCTGTAAGAACATTTCA	2620
Oy		2221	CGTAGCCAGCCACTCTCCGCAAGGCTCGGCCCAAGTGTTTAGCATTAACATATCTGACCCTG	2280
Dp		2621	CGTAGCCAGCCACTCTCCGCAAGGCTCGGCCCAAGTGTTTAGCATTAACATATCTGACCCTG	2680
Oy		2281	TTCCCTTGCAATTTGGGTAAACAGAGGGGGGTGTCTCTCACTTAACCAATGTGCAATTTGATCA	2340
Dp		2681	TTCCCTTGCAATTTGGGTAAACAGAGGGGGGTGTCTCTCACTTAACCAATGTGCAATTTGATCA	2740
Oy		2341	CACATAAGATATTTGCTTGAAGCCCGAAGACATGTCCAAGGTGAACCTGTAACGGGGTGTGGA	2400
Dp		2741	CACATAAGATATTTGCTTGAAGCCCGAAGACATGTCCAAGGTGAACCTGTAACGGGGTGTGGA	2800
Oy		2401	CATGACCATGAAGATCTGGAAGGTCTGAGGTACATGATGACCCGCACACAGGTGCAACACC	2460
Dp		2801	CATGACCATGAAGATCTGGAAGGTCTGAGGTACATGATGACCCGCACACAGGTGCAACACC	2860
Oy		2461	CTGGAGATGTGGCCGGTAAACATATTAGGAACACAGCTGTGATGTGATGTAACCGAGGA	2520
Dp		2861	CTGGAGATGTGGCCGGTAAACATATTAGGAACACAGCTGTGATGTGATGTAACCGAGGA	2920
Oy		2521	GCTGAGGCCCGCATCACTTGTGTCTGTGACCCGCGCTGAGTTTGGCTTACGCATGTA	2580
Dp		2921	GCTGAGGCCCGCATCACTTGTGTCTGTGACCCGCGCTGAGTTTGGCTTACGCATGTA	2980
Oy		2581	AGATACAGATTGAG	2594
Dp		2981	AGATACAGATTGAG	2994
RESULT 2				
AAH20746				
ID	AAH20746 standard; DNA; 7090 BP.			
XX	AAH20746;			
XX				
XX	13-AUG-2001 (first entry)			
XX				
DB	Plasmid SrtK146 DNA fragment.			
XX				
KW	Gene therapy; amniocyte; cytostatic; Ad5; B1A region; B1B region;			
XX	modified tropism; tumor; PCR primer; ss.			
OS	Synthetic.			

XX	WM0200136615-A2.
XX	
XX	25-MAY-2001.
XX	
XX	07-NOV-2000; 2000WO-EP010992.
XX	
XX	18-NOV-1999; 99DE-01055558.
XX	
XX	(KOCH/) KOCHANNEK S.
XX	
XX	Kochanek S, Schiedner G;
XX	
XX	WPI; 2001-343817/36.
XX	
XX	New permanent amniocyte cell lines, useful for producing viral gene
XX	therapy vectors or mutant adenoviruses, express the adenoviral E1A and
XX	E1B gene products.
XX	
XX	Example 1; Page 67-72; 72pp; German.
XX	
XX	This invention describes novel permanent amniocyte cell lines (A),
XX	containing at least one nucleic acid (I) that causes expression of the
XX	gene products (II) of the adenoviral E1A and E1B regions. (A) are used to
XX	produce gene therapy vectors, especially adeno, adeno-associated, retro
XX	or lentiviral vectors, particularly first- or second generation, large-
XX	capacity or deleted adenoviral vectors. (A) are also used to produce
XX	adenoviral mutants, optionally with modified tropism. The vectors may
XX	express a wide range of therapeutic proteins or antisense RNAs.
XX	Adenoviral mutants, unable to express the E1B 55 kDa protein, are useful
XX	for treating tumors, they replicate in the cells but not significantly in
XX	normal primary cells. (A) can be made efficiently, simply and
XX	reproducibly. The products of the invention have cytosolic activity.
XX	This sequence represents a PCR primer used in the amplification of
XX	Adenovirus Ad5 DNA which is described in the method of the invention
XX	
XX	Sequence 7090 BP; 1696 A; 1685 C; 1882 G; 1827 T; 0 U; 0 Other;
XX	
XX	Query Match 100.0%; Score 2594; DB 5; Length 7090;
XX	Best Local Similarity 100.0%; Pred. No. 0;
XX	Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX	
XX	1 ATGCATCTTACCTGCGACGAGGCTGCGCTTTCCACCAGTGAAGAGAGGCT 60
XX	3165 ATGCATCTTACCTGCGACGAGGCTGCGCTTTCCACCAGTGAAGAGAGGCT 3224
XX	
XX	61 GAGAGATTGTTGTTAGATTATGTTGAGACACCCCGGGACAGGTTGACAGTCTTTCATTAT 120
XX	3225 GAGAGATTGTTGTTAGATTATGTTGAGACACCCCGGGACAGGTTGACAGTCTTTCATTAT 3284
XX	
XX	121 CACCGGAGGAATACGGGGGACCCAGATTATATGTTGCTTGTCTATATAGAGACCTGT 180
XX	3285 CACCGGAGGAATACGGGGGACCCAGATTATATGTTGCTTGTCTATATAGAGACCTGT 3344
XX	
XX	181 GGCAATGTTTGTCTACAGTAAGTGAATAATATGAGCAGTGGGTGATAGAGTGTGGCTTTG 240
XX	3345 GGCAATGTTTGTCTACAGTAAGTGAATAATATGAGCAGTGGGTGATAGAGTGTGGCTTTG 3404
XX	
XX	241 GTGTGCTATATTTTATTTTATTTTACAGTTTGTGTGTTTAAAGATTGTGATTTTGCA 300
XX	3405 GTGTGCTATATTTTATTTTATTTTACAGTTTGTGTGTTTAAAGATTGTGATTTTGCA 3464
XX	
XX	301 TTTTAAAAAGTCTGTGTCTAATCTGAGCTGAGGCCGAGCCGAGAACCGGAGCCTG 360
XX	3465 TTTTAAAAAGTCTGTGTCTAATCTGAGCTGAGGCCGAGCCGAGAACCGGAGCCTG 3524
XX	
XX	361 CAAAGACCTACCCGCGTCTTAAATGCGCGCTGCTATCTGAGACGCGCCGACATCACCTG 420
XX	3525 CAAAGACCTACCCGCGTCTTAAATGCGCGCTGCTATCTGAGACGCGCCGACATCACCTG 3584
XX	
XX	421 TGTCTAAGAAATGCAATAGTATGTAACGATAGCTGTACTCCGTTCTTTTAAACACACTTC 480
XX	3585 TGTCTAAGAAATGCAATAGTATGTAACGATAGCTGTACTCCGTTCTTTTAAACACACTTC 3644

QY 481 CTGAGATACACCCGGTGGTCCCGTGTGCCCATTTAAACGATGGCCGTGAGATGGTG 540
Db 3645 CTGAGATACACCCGGTGGTCCCGTGTGCCCATTTAAACGATGGCCGTGAGATGGTG 3704
QY 541 GGGCTGCGCAGGCTGTGAAATGTATCGAGAGCTTGGCTTTAACGAGCTGGGCAACTTTGG 600
Db 3705 GGGCTGCGCAGGCTGTGAAATGTATCGAGAGCTTGGCTTTAACGAGCTGGGCAACTTTGG 3764
QY 601 ACTTGACACTGTAAACGCCCAAGGCATTAAGGTGTAAACCTGTGATTCGTGTGTGTTAA 660
Db 3765 ACTTGACACTGTAAACGCCCAAGGCATTAAGGTGTAAACCTGTGATTCGTGTGTGTTAA 3824
QY 661 CGCCTTGTGTGTGTAATGATGTGATGTAACTTTAATTAAGGGTGAGATTAATGTTTAACT 720
Db 3825 CGCCTTGTGTGTGTAATGATGTGATGTAACTTTAATTAAGGGTGAGATTAATGTTTAACT 3884
QY 721 TGCATGCGTGTAAATGCGGCGGGCTTTAAAGGCTATATAATGCGCGCTGGCTAATCT 780
Db 3885 TGCATGCGTGTAAATGCGGCGGGCTTTAAAGGCTATATAATGCGCGCTGGCTAATCT 3944
QY 781 TGGTTAATCTGACCTCAATGAGGCTTGGGAGTGTGGAGATTTTCTGCTGCGGTA 840
Db 3945 TGGTTAATCTGACCTCAATGAGGCTTGGGAGTGTGGAGATTTTCTGCTGCGGTA 4004
QY 841 ACTTGCTGGAACAGAGCTCTAACAGTACCTCTTGGTTTGGAGGTTTCTGTGGGCTCAT 900
Db 4005 ACTTGCTGGAACAGAGCTCTAACAGTACCTCTTGGTTTGGAGGTTTCTGTGGGCTCAT 4064
QY 901 CCCAGGCAAGTTAGTCTGCAAGATTTAAGAGATTAACAATGGGAATTTGAAGAAGCTTT 960
Db 4065 CCCAGGCAAGTTAGTCTGCAAGATTTAAGAGATTTAACAAGGGAATTTGAAGAAGCTTT 4124
QY 961 TGAATTCCTGTGGTGAAGCTGTTTGATCTTTGAATCTGGGTCAACGAGCGCTTTTCCAAG 1020
Db 4125 TGAATTCCTGTGGTGAAGCTGTTTGATCTTTGAATCTGGGTCAACGAGCGCTTTTCCAAG 4184
QY 1021 AGAAGTCAATCAAGCTTTGGATTTTTCACAACCGGGCGCGCTGCGCTGTGTGCTT 1080
Db 4185 AGAAGTCAATCAAGCTTTGGATTTTTCACAACCGGGCGCGCTGCGCTGTGTGCTT 4244
QY 1081 TTTTGAATTTTAAAGATTAATGAGCGAAGAAACCATCTGAGCGGGGGGTACCTGC 1140
Db 4245 TTTTGAATTTTAAAGATTAATGAGCGAAGAAACCATCTGAGCGGGGGGTACCTGC 4304
QY 1141 TGGATTTTCTGGCCATGATCTGTGAGAGCGGTTGTGAGACACAAGAACTGCTGTAC 1200
Db 4305 TGGATTTTCTGGCCATGATCTGTGAGAGCGGTTGTGAGACACAAGAACTGCTGTAC 4364
QY 1201 TGTGTCTTCCGTCCGCCCGCGGATTAATACGACGGAAGGAGCAGCAGCAGAGAG 1260
Db 4365 TGTGTCTTCCGTCCGCCCGCGGATTAATACGACGGAAGGAGCAGCAGCAGAGAG 4424
QY 1261 AAGCAGCGCGCGGGGCGAGAGCAGAGCCCATGGAACCCGAGACCCGGCTGGACCTTC 1320
Db 4425 AAGCAGCGCGCGGGGCGAGAGCAGAGCCCATGGAACCCGAGACCCGGCTGGACCTTC 4484
QY 1321 GGGGAATGAATGTGTACAGTGGCTGAACCTGTATCCAGAACTGAGACGATTTTGAAT 1380
Db 4485 GGGGAATGAATGTGTACAGTGGCTGAACCTGTGTATCCAGAACTGAGACGATTTTGAAT 4544
QY 1381 TACAGAGATGGGCAAGGGCTAAAGGGGTAAAGAGGAGCGGGGGCTTGTGAGGCTAC 1440
Db 4545 TACAGAGATGGGCAAGGGCTAAAGGGGTAAAGAGGAGCGGGGGCTTGTGAGGCTAC 4604
QY 1441 AAGAGAGCTAGAGATCTAGCTTTTATGCTTAAATGACCAAGACCGTCTGAGGTATTAG 1500
Db 4605 AAGAGAGCTAGAGATCTAGCTTTTATGCTTAAATGACCAAGACCGTCTGAGGTATTAG 4664
QY 1501 TTTTCAACAGATCAAGGATTAATGCGCTATAGAGCTTGAATCTGCTGGCGCAAGATATTC 1560
Db 4665 TTTTCAACAGATCAAGGATTAATGCGCTATAGAGCTTGAATCTGCTGGCGCAAGATATTC 4724

QY 1561 CATAGACAGCTGACCACTTACTGCTGACGCGAGGGAGATGATTTTGAAGGCTATTAG 1620
Db 4725 CATAGACAGCTGACCACTTACTGCTGACGCGAGGGAGATGATTTTGAAGGCTATTAG 4784
QY 1621 GGTATATGCAAGAGTGAACCTTAGGCGAGATTGCAAGTACAGATCAGCAAACTTGTAAA 1680
Db 4785 GGTATATGCAAGAGTGAACCTTAGGCGAGATTGCAAGTACAGATCAGCAAACTTGTAAA 4844
QY 1681 TATCAGGAATTTGTTGCTACATTTTCTGGGAAACGGGGCCGAGGTGAGATATATCCGAGGA 1740
Db 4845 TATCAGGAATTTGTTGCTACATTTTCTGGGAAACGGGGCCGAGGTGAGATATATCCGAGGA 4904
QY 1741 TAGGGTGGCCCTTAGATGTAGATGATTAATATGTGGCCGGGGGTGCTTGGCATGAGCG 1800
Db 4905 TAGGGTGGCCCTTAGATGTAGATGATTAATATGTGGCCGGGGGTGCTTGGCATGAGCG 4964
QY 1801 GGTGTATTATGATGATGTAAGTTTACTGCGCCCAATTTTACGGGTACGGTTTCTGGC 1860
Db 4965 GGTGTATTATGATGATGTAAGTTTACTGCGCCCAATTTTACGGGTACGGTTTCTGGC 5024
QY 1861 CAATACCAACCTTATCTTACACGCTGTACCTTCTATGGGTTTAACTACCTGTGGA 1920
Db 5025 CAATACCAACCTTATCTTACACGCTGTACCTTCTATGGGTTTAACTACCTGTGGA 5084
QY 1921 AGCCTGGAACGATGTAGGGTGGGGCTGACCTTTTACTGCTGTGGAAGGGGTGCT 1980
Db 5085 AGCCTGGAACGATGTAGGGTGGGGCTGACCTTTTACTGCTGTGGAAGGGGTGCT 5144
QY 1981 GTGTGCCCCCAAAAGCAGGGCTTCAATTAAAGAAATGCTTTGAAAGGTGTACTTGGG 2040
Db 5145 GTGTGCCCCCAAAAGCAGGGCTTCAATTAAAGAAATGCTTTGAAAGGTGTACTTGGG 5204
QY 2041 TATCTGTCTGAGGGTAACTTCAAGGTGCGGCAAAATGTGCGCTGCACTGTGTTGCTT 2100
Db 5205 TATCTGTCTGAGGGTAACTTCAAGGTGCGGCAAAATGTGCGCTGCACTGTGTTGCTT 5264
QY 2101 CATCTATGTGAAAACGAGGTGCTGATTAAGCATTAACATGATATGTGGCAACTGAGGA 2160
Db 5265 CATCTATGTGAAAACGAGGTGCTGATTAAGCATTAACATGATATGTGGCAACTGAGGA 5324
QY 2161 CAGGGCTCTCAGATGTGACCTGTGGAAGGCACTGTCACTGTGAGAACCATTTCA 2220
Db 5325 CAGGGCTCTCAGATGTGACCTGTGGAAGGCACTGTCACTGTGAGAACCATTTCA 5384
QY 2221 CGTAGCCAGCACTCTGCGCAAGGCTGTGGCCAGTGTGGAAGATTAACATGACCGGCTG 2280
Db 5385 CGTAGCCAGCACTCTGCGCAAGGCTGTGGCCAGTGTGGAAGATTAACATGACCGGCTG 5444
QY 2281 TTCTTGATTTGGGTAAACAGAGGGGGGTGTTCTTACCTTACCAATGCCAATTTGATCA 2340
Db 5445 TTCTTGATTTGGGTAAACAGAGGGGGGTGTTCTTACCTTACCAATGCCAATTTGATCA 5504
QY 2341 CACTAAGATATTGCTTGAACCCGAGAGCATGTCCAAAGGTGAACCTGAAACGGGGTGTGGA 2400
Db 5505 CACTAAGATATTGCTTGAACCCGAGAGCATGTCCAAAGGTGAACCTGAAACGGGGTGTGGA 5564
QY 2401 CATGACCAATGAAGATCTGGAAGGTCTGAGATACATAGAACCCGACACAGGTGAGACC 2460
Db 5565 CATGACCAATGAAGATCTGGAAGGTCTGAGATACATAGAACCCGACACAGGTGAGACC 5624
QY 2461 CTGCGAGTGTGGCGGTAAACATATTAGGAACCAAGCTGTGATGTGATGTCGAGGA 2520
Db 5625 CTGCGAGTGTGGCGGTAAACATATTAGGAACCAAGCTGTGATGTGATGTCGAGGA 5684
QY 2521 GCTGAGGCCGATCACTTGTGTGCTGCGCTGCAACCCGCGCTGAGTTTGGCTTACGATGA 2580
Db 5685 GCTGAGGCCGATCACTTGTGTGCTGCGCTGCAACCCGCGCTGAGTTTGGCTTACGATGA 5744
QY 2581 AGATACAGATTGAG 2594
Db 5745 AGATACAGATTGAG 5758

RESULT 3
ID AAA59076 standard; DNA; 7607 BP.
XX AAA59076;
AC
XX 07-NOV-2000 (first entry)
XX
XX Nucleotide sequence of plasmid GRES-EI-SV40-Hygro.
XX
XX Adenovirus; tripartite leader; adenovirus vector particle; gene delivery;
XX 88.
XX Synthetic.
XX MO200042208-A1.
XX
XX 20-JUL-2000.
XX
XX 14-JAN-2000; 2000MO-EP000265.
XX
XX 14-JAN-1999; 99US-0115920P.
XX
XX (NOVS) NOVARTIS AG.
XX (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX (SCRI) SCRIPPS RES INST.
XX
XX Nemerow GR, Von Seggern DJ, Hallenbeck PL, Stevenson SC,
XX Skripchenko Y;
XX WPI; 2000-476068/41.
XX
XX New nucleic acid comprising an adenovirus tripartite leader nucleotide
XX PT for producing high-capacity and targeted vectors for adenovirus-based
XX PT gene therapy.
XX
XX Example 6; Page 190-192; 212pp; English.
XX
XX The specification describes a nucleic acid molecule comprising an
XX CC adenovirus (AV) tripartite leader (TPL) nucleotide with a sequence
XX CC comprising two different TPL exons or three same or different TPL exons.
XX CC The nucleic acid is used to produce an adenovirus vector particle,
XX CC deliver an exogenous gene to a target cell, pseudotype recombinant viral
XX CC vectors, target an adenovirus vector to a cell, produce a modified
XX CC adenovirus, deliver a heterologous gene to an animal and produce a
XX CC gutless adenoviral vector particle. The present sequence represents
XX CC plasmid GRES-EI-SV40-Hygro, which is used in the course of the invention
XX
XX Sequence 7607 BP; 1838 A; 1733 C; 2001 G; 2035 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 2594; DB 3; Length 7607;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 ATGATCTTACCTGCGCAAGAGCTGGCTTCCACCGATGACGAGAGTAAGAGAGT 60
XX 1334 ATCATCTTACCTGCGCAAGAGCTGGCTTCCACCGATGACGAGAGTAAGAGAGT 1393
XX
XX 61 GAGAGTTTGTAGATTAATGTGAGACACCCGGGACGGTTGACAGTCTTGCATTAT 120
XX 1394 GAGAGTTTGTAGATTAATGTGAGACACCCGGGACGGTTGACAGTCTTGCATTAT 1453
XX
XX 121 CACCGGAGAAATACGGGGAGACCCAGATTAATGTGTTGCTTTGCTAATGAGACCTGT 180
XX 1454 CACCGGAGAAATACGGGGAGACCCAGATTAATGTGTTGCTTTGCTAATGAGACCTGT 1513
XX
XX 181 GGCATGTTTGTCTACAGTAAGTAATTAATGAGCACTGGTGTATAGAGCTGGTTG 240
XX 1514 GGCATGTTTGTCTACAGTAAGTAATTAATGAGCACTGGTGTATAGAGCTGGTTG 1573
XX
XX 241 GTGTGTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTGA 300
XX 1574 GTGTGTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTGA 1633

QY 301 TTTTAAAAAGGCTCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGAGCTTG 360
DB 1634 TTTTAAAAAGGCTCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGAGCTTG 1693
QY 361 CAAGACCTAACCCCGCGCTCTTAAATGGGCGCTGCTATCTCTAGAGCCCGACATCACTTG 420
DB 1694 CAAGACCTAACCCCGCGCTCTTAAATGGGCGCTGCTATCTCTAGAGCCCGACATCACTTG 1753
QY 421 TGCTAGAGAAATGCAATAGTAGTACGAGTACGAGTCTGAGCTCCGCTCTTCTAACAACCTG 480
DB 1754 TGCTAGAGAAATGCAATAGTAGTACGAGTACGAGTCTGAGCTCCGCTCTTCTAACAACCTG 1813
QY 481 CTGAGATACACCCGCTGCTCCGCTGTGCTCCCATTAACAGAGTCCGCTGAGAGTGGTG 540
DB 1814 CTGAGATACACCCGCTGCTCCGCTGTGCTCCCATTAACAGAGTCCGCTGAGAGTGGTG 1873
QY 541 GGGCGTCCGAGGCTGTGGAATGTAATCGAGAGCTTGCTTAACGAGACCTGGGCAACCTTTGG 600
DB 1874 GGGCGTCCGAGGCTGTGGAATGTAATCGAGAGCTTGCTTAACGAGACCTGGGCAACCTTTGG 1933
QY 601 ACTGAGCTGTAAACGCCCGAGCCATTAAGGTGTAAACCTGTGATGGTGTGTTAA 660
DB 1934 ACTGAGCTGTAAACGCCCGAGCCATTAAGGTGTAAACCTGTGATGGTGTGTTAA 1993
QY 661 CGCCTTGTGTTGCTGAATGAGTTGATGTAAATTAATTAAGGCTGAGATAATGTTAACT 720
DB 1994 CGCCTTGTGTTGCTGAATGAGTTGATGTAAATTAATTAAGGCTGAGATAATGTTAACT 2053
QY 721 TGCAATGCGGTGTTAAATGGGCGGGGCTTAAAGGCTATTAATGCGGCTGGCTAATCT 780
DB 2054 TGCAATGCGGTGTTAAATGGGCGGGGCTTAAAGGCTATTAATGCGGCTGGCTAATCT 2113
QY 781 TGCTTACATCTGACCTCATGAGAGCTTGGAGTGTGGAAGATTTTCTGCTGCGTA 840
DB 2114 TGCTTACATCTGACCTCATGAGAGCTTGGAGTGTGGAAGATTTTCTGCTGCGTA 2173
QY 841 ACTTGTGGAACAGAGCTCTAACAGTACTTGTGTTGAGGTTTCTGTGGGCTCAT 900
DB 2174 ACTTGTGGAACAGAGCTCTAACAGTACTTGTGTTGAGGTTTCTGTGGGCTCAT 2233
QY 901 CCCAGGAAAGTAAAGTGTGAGAAATTAAGAGAGTTTCAATGGGATTTGAAGAGCTTT 960
DB 2234 CCCAGGAAAGTAAAGTGTGAGAAATTAAGAGAGTTTCAATGGGATTTGAAGAGCTTT 2293
QY 961 TGAATCTGTGAGAGCTTTGATCTTGAATCTGAGTCAACGAGCGCTTTCCAAAG 1020
DB 2294 TGAATCTGTGAGAGCTTTGATCTTGAATCTGAGTCAACGAGCGCTTTCCAAAG 2353
QY 1021 AGAAGTCAATCAAGACTTTGATTTTTCACACCGGGGCGCGTGCCTGCTGCTT 1080
DB 2354 AGAAGTCAATCAAGACTTTGATTTTTCACACCGGGGCGCGTGCCTGCTGCTT 2413
QY 1081 TTTTGAATTTTAAAGATTAATGAGCGAAGAAACCTTCTGAGCGGGGGTAACTGTC 1140
DB 2414 TTTTGAATTTTAAAGATTAATGAGCGAAGAAACCTTCTGAGCGGGGGTAACTGTC 2473
QY 1141 TGAATTTTCTGCGCATCTGTGAGAGCGGTGTGAGACACAAGATTCGCTGTAC 1200
DB 2474 TGAATTTTCTGCGCATCTGTGAGAGCGGTGTGAGAGCGGTGTGAGAGCGGTGTGAC 2533
QY 1201 TGTGTCTTCCGTCGCGCGCGGAGTAATACGAGAGAGACAGACAGACAGAGAGG 1260
DB 2534 TGTGTCTTCCGTCGCGCGCGGAGTAATACGAGAGAGAGACAGACAGACAGAGAGG 2593
QY 1261 AAGCCAGCGCGCGCGGAGAGACAGAGCCAGTGAACCCGAGAGCGGCTGAGACCTTC 1320
DB 2594 AAGCCAGCGCGCGCGGAGAGACAGAGCCAGTGAACCCGAGAGCGGCTGAGACCTTC 2653
QY 1321 GGAAGTAATGTTGTACAGGTGCTGAACCTGTATCAAGACTGAGACGATTTTGAAT 1380
DB 2654 GGAAGTAATGTTGTACAGGTGCTGAACCTGTATCAAGACTGAGACGATTTTGAAT 2713

QY	1381	TACGAGATGGCGAGGGCTAAAGGGGGTTAAAGGAGACCGGGGGCTTTGTGAGGCTAC	1440
DB	2714	TACAGAGATGGCGAGGGCTAAAGGGGGCTAAAGAGGGAGCGGGGGGCTTGTGAGGCTAC	2773
QY	1441	AGAGAGGCTTAGGAATCTAGCTTTTAGCTTAATGACACACCGTCTGAGGTATTAC	1500
DB	2774	AGAGAGGCTTAGGAATCTAGCTTTTAGCTTAATGACACAGACCCGTCTGAGGTATTAC	2833
QY	1501	TTTTCAACAGATCAAGGATTAATTCGCTTAATGAGCTTGAATCTGCTGGCGCAGAAATTC	1560
DB	2834	TTTTCAACAGATCAAGGATTAATTCGCTTAATGAGCTTGAATCTGCTGGCGCAGAAATTC	2893
QY	1561	CATGAGAGCTGACCACTTACTGCTGACGCCAGGGGATGATTTTGAAGGAGCTATTAG	1620
DB	2894	CATGAGAGCTGACCACTTACTGCTGACGCCAGGGGATGATTTTGAAGGAGCTATTAG	2953
QY	1621	GCTATTATGCCAAGGTGGCACTTAGCCAGATTCGCAAGTACAGATACAGCAAACTTGTAA	1680
DB	2954	GCTATTATGCCAAGGTGGCACTTAGCCAGATTCGCAAGTACAGATACAGCAAACTTGTAA	3013
QY	1681	TATCAGAAATGTTGCTPACATTTCTGGGAAACGGGGCCGAGGTGAGATAGATACGAGGA	1740
DB	3014	TATCAGAAATGTTGCTPACATTTCTGGGAAACGGGGCCGAGGTGAGATAGATACGAGGA	3073
QY	1741	TAGGGTGGCTTTTAGATGATGACATGATTAATATGTGCCCCGGGGTGTCTTGGCATGGAACGG	1800
DB	3074	TAGGGTGGCTTTTAGATGATGACATGATTAATATGTGCCCCGGGGTGTCTTGGCATGGAACGG	3133
QY	1801	GGTGGTTATTATATGAAATGTAAGGTTTACTGGCCCCCAATTTTACGGGTACGGTTTCTGAC	1860
DB	3134	GGTGGTTATTATATGAAATGTAAGGTTTACTGGCCCCCAATTTTACGGGTACGGTTTCTGAC	3193
QY	1861	CAATACCAACCTTAATCTTACACACGGGTGTAAGCTTCTATAGGTTTAAACAATCCTGTGTGA	1920
DB	3194	CAATACCAACCTTAATCTTACACACGGGTGTAAGCTTCTATAGGTTTAAACAATCCTGTGTGA	3253
QY	1921	AGCTGTGACCGATGTAAGGTTTCGGGGCTGTGCTTTTACGTGCTGAGAAAGGGGGTGT	1980
DB	3254	AGCTGTGACCGATGTAAGGTTTCGGGGCTGTGCTTTTACGTGCTGAGAAAGGGGGTGT	3313
QY	1981	GTGTGGCCCCCAAAACAGGGCTTCAATTAAGAAATGCTCTTTAAAGGTGTACCTTGGG	2040
DB	3314	GTGTGGCCCCCAAAACAGGGCTTCAATTAAGAAATGCTCTTTAAAGGTGTACCTTGGG	3373
QY	2041	TATCCTGTCTGAGGTTAACTCCAGGGGTCCGACAAATGTGGCTTCGACTGTGTTGCTT	2100
DB	3374	TATCCTGTCTGAGGTTAACTCCAGGGGTCCGACAAATGTGGCTTCGACTGTGTTGCTT	3433
QY	2101	CATGCTAAGTAAAGCGTGGCTGTGTATTAAGCATTAACATGTAATGTGGCAACTCCAGGA	2160
DB	3434	CATGCTAAGTAAAGCGTGGCTGTGTATTAAGCATTAACATGTAATGTGGCAACTCCAGGA	3493
QY	2161	CAGGGCTCTCGAATGCTGACCTGCTCGGACGGCAACGTACACCTGCTGAAAGCACTTCA	2220
DB	3494	CAGGGCTCTCGAATGCTGACCTGCTCGGACGGCAACGTACACCTGCTGAAAGCACTTCA	3553
QY	2221	CGTAGCCAGCACTCTCCGAAAGGCTGTGCAAGTGTTTGAGATTAACAATCTGACCGCTG	2280
DB	3554	CGTAGCCAGCACTCTCCGAAAGGCTGTGCAAGTGTTTGAGATTAACAATCTGACCGCTG	3613
QY	2281	TTCTCTTGCAATTTGGGTAAACGAGAGGGGGTGTCTTACCTTACCAATGCAATTTGAATCA	2340
DB	3614	TTCTCTTGCAATTTGGGTAAACGAGAGGGGGTGTCTTACCTTACCAATGCAATTTGAATCA	3673
QY	2341	CACCTAAGATTAATGCTTTGAACCCGAGATGTCATTCGCAAGGTAAACCTGAACGGGGTGTGA	2400
DB	3674	CACCTAAGATTAATGCTTTGAACCCGAGATGTCATTCGCAAGGTAAACCTGAACGGGGTGTGA	3733
QY	2401	CATGACCATGAAGATCTGGAAGGTGTCTGAGTACATGAGACACCGCACCAAGTGTGACACC	2460
DB	3734	CATGACCATGAAGATCTGGAAGGTGTCTGAGTACATGAGACACCGCACCAAGTGTGACACC	3793
QY	2461	CTGCGAGTGTGGCGGTAAACATTAATGGAACCAAGCTGTGATGTGTGAATGTGAACGAGGA	2520

Db	3794	CTGGAGTGTGGCGGCTAAACATATTAGGAACGAGCCGTGATGCTGATGTGACCCGAGCA	3853
Oy	2521	GCTGAGGCCGCGATACCTTGGTGTGCTGGCCTGACACCCGGCGTGAAGTTGGCTCTAGCGATGA	2580
Db	3854	GCTAGAGCCCGCATCATCTTGGTGTGCTGGCGCTGCACCCGGCGTGAAGTTGGCTCTAGCGATGA	3913
Oy	2581	AGATACAGATTGAG	2594
Db	3914	AGATACAGATTGAG	3927
RESULT 4			
ABAA94278	ID	ABA94278 standard; DNA; 7607 BP.	
XX	AC	ABA94278;	
XX	DT	13-MAR-2002 (first entry)	
XX	DE	Nucleotide sequence of plasmid GRES-E1-SV40-Hygro.	
XX	XX	Adenovirus; inverte terminal repeat sequence; ITRS; ocular disease;	
XX	XX	fiber protein; photoreceptor; rhodopsin; stargardt disease gene; STDG1;	
XX	XX	ophthalmological; antiinflammatory; antidiabetic; cyostatic;	
XX	XX	gene therapy; tripartite leader; TPL, ss.	
XX	OS	Synthetic.	
XX	PN	WO200183729-A2.	
XX	PD	08-NOV-2001.	
XX	PF	30-APR-2001; 2001WO-EP004863.	
XX	PR	01-MAY-2000; 2000US-00562934.	
XX	PA	(NOVS) NOVARTIS AG.	
XX	PA	(SCHI) SCHRIPPS RES. INST.	
XX	PA	(NEME/) NEMEROW G. R.	
XX	PA	(VSEB/) VON SEGGERN D. J.	
XX	PA	(FRIE/) FRIEDLANDER M.	
XX	PI	Nemerow GR, Von Seggern DJ, Friedlander M;	
XX	DR	WPI; 2002-082846/11.	
XX	PT	Polynucleotide for making vectors, useful for treating ocular diseases,	
XX	PT	e.g., retinitis pigmentosa, comprises adenovirus inverte terminal repeat	
XX	PT	sequences, packaging signal and photoreceptor-specific promoter.	
XX	PS	Example 5; Page 139-141; 149pp; English.	
XX	XX	The invention provides an isolated polynucleotide comprising adenovirus	
XX	XX	(AV) inverte terminal repeat sequences (ITRS), AV packaging signal	
XX	XX	operatively linked to ITRS and a photoreceptor-specific promoter. A	
XX	XX	recombinant AV vector (AVV) comprising the polynucleotide is useful for	
XX	XX	targeted delivery of a gene product to the eye (especially to the	
XX	XX	vitreous cavity), for treating an ocular disease, e.g., retinal	
XX	XX	degenerative disease, retinitis pigmentosa, Stargardt's disease, diabetic	
XX	XX	retinopathies, retinal vascularizations, and retinoblastoma, of a mammal	
XX	XX	preferably human. The AVV comprises a fiber protein that specifically or	
XX	XX	selectively binds to receptors that are expressed on cells (preferably a	
XX	XX	photoreceptor in the eye). Preferably, the recombinant virus comprise a	
XX	XX	fiber protein from an adenovirus type D subgroup or is a chimeric protein	
XX	XX	containing a portion of the N-terminus of an adenovirus type 2 or type 5	
XX	XX	penton, and the therapeutic product is a trophic factor, an anti-	
XX	XX	apoptotic factor, gene encoding a rhodopsin protein, a wild-type	
XX	XX	stargardt disease gene (STDG1), an anti-cancer agent and a protein that	
XX	XX	regulates expression of a photoreceptor specific gene product. The viral	
XX	XX	nucleic acid of AAV comprises ITRS and packaging signal derived from AAV	
XX	XX	subgroup B or C, especially an AV type 2 or type 5. AAV is also useful	
XX	XX	for targeted gene therapy, where the vector comprises an AV type 37 fiber	

CC protein or its portion, and selectively transduces photoreceptors and
CC delivers a gene product encoded by AYV. The present sequence represents
CC the nucleotide sequence of plasmid GRS-B1-SV40-Hygro

Sequence 7607 BP, 1838 A, 1733 C, 2001 G, 2035 T, 0 U, 0 Other;

Query Match 100.0%; Score 2594; DB 6; Length 7607;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATCGATCTTACCTGCGCAGAGCGCTTTCCACCCAGTACGACGAGATGAAGAGGT 60
DB 1334 ATCGATCTTACCTGCGCAGAGCGCTTTCCACCCAGTACGACGAGATGAAGAGGT 1393
QY 61 GAGGAGTTTGTTAGATTATGTGGAGCAACCCGGGCAAGTTGCAAGTCTTTGATTAT 120
DB 1394 GAGGAGTTTGTTAGATTATGTGGAGCAACCCGGGCAAGTTGCAAGTCTTTGATTAT 1453
QY 121 CACCGGAGAGTAACGGGGGAGCCAGATATATATGTTTGGCTTATATGAGACCTGT 180
DB 1454 CACCGGAGAGTAACGGGGGAGCCAGATATATATGTTTGGCTTATATGAGACCTGT 1513
QY 181 GGCATGTTTGTCTACAGTAAGTAATAATTATGGGAGTGGGATAGAGTGGGTTTG 240
DB 1514 GGCATGTTTGTCTACAGTAAGTAATAATTATGGGAGTGGGATAGAGTGGGTTTG 1573
QY 241 GTGTGTAATTTTTTTTTTAATTTTTTAACAGTTTGTGTTTAAAGAAATTTGTATTTGA 300
DB 1574 GTGTGTAATTTTTTTTTTAATTTTTTAACAGTTTGTGTTTAAAGAAATTTGTATTTGA 1633
QY 301 TTTTTTAAAGGTCCTGTCTGAACTTGAGCCGAGCCGAGCAGAAACCGAGGCTTG 360
DB 1534 TTTTTTAAAGGTCCTGTCTGAACTTGAGCCGAGCCGAGCAGAAACCGAGGCTTG 1693
QY 361 CAAGACCTACCCGCGCTCTAAATATGGGCGCTGATCTTGAGAGCGCCGACATCACCTG 420
DB 1694 CAAGACCTACCCGCGCTCTAAATATGGGCGCTGATCTTGAGAGCGCCGACATCACCTG 1753
QY 421 TGCTTGAAGATGCAATATGATAGTAAGATAGCTGTGACTCCGGTCTTTCTAACACACTC 480
DB 1754 TGCTTGAAGATGCAATATGATAGTAAGATAGCTGTGACTCCGGTCTTTCTAACACACTC 1813
QY 481 CTGAGATACACCCGGTGTCTCCGCTGTGCCCCCATTAACCAATGTCCTGTGAGAGTTGGT 540
DB 1814 CTGAGATACACCCGGTGTCTCCGCTGTGCCCCCATTAACCAATGTCCTGTGAGAGTTGGT 1873
QY 541 GGGCGTCGCGAGGCTGTGATATGATCGAGGACTTGCTTAAGGAGCTGGGCAACTTTGG 600
DB 1874 GGGCGTCGCGAGGCTGTGATATGATCGAGGACTTGCTTAAGGAGCTGGGCAACTTTGG 1933
QY 601 ACTTGAAGCTGTAAACGCCCAAGCCATTAAGGTGTAAACCTGTGATTCGTGTGCTTAA 660
DB 1934 ACTTGAAGCTGTAAACGCCCAAGCCATTAAGGTGTAAACCTGTGATTCGTGTGCTTAA 1993
QY 661 CGCCTTTGTTTGTGTAATGATGATGATTAATAAAGGTGAGATTAATGTTAACT 720
DB 1994 CGCCTTTGTTTGTGTAATGATGATGATTAATAAAGGTGAGATTAATGTTAACT 2053
QY 721 TGCAATGGGCTGTAAATGGGGGGGGCTTAAAGGATATATAATGGCGGTGGCTAACT 780
DB 2054 TGCAATGGGCTGTAAATGGGGGGGGCTTAAAGGATATATAATGGCGGTGGCTAACT 2113
QY 781 TGGTTACATCTGACCTCATGAGGCTTGGAGGTGTTTGAAGATTTTCTGTGTGCTGA 840
DB 2114 TGGTTACATCTGACCTCATGAGGCTTGGAGGTGTTTGAAGATTTTCTGTGTGCTGA 2173
QY 841 ACTTGTCTGAAACAGAGCTCTTAACAGTACCTCTTGTTTGAAGTTTCTGTGGGCTCAT 900
DB 2174 ACTTGTCTGAAACAGAGCTCTTAACAGTACCTCTTGTTTGAAGTTTCTGTGGGCTCAT 2233
QY 901 CCCAGGCAAAAGTTAGTCTGAGAAATTAAGAGGATTAACAAGTGGGATTTGAAGGCTTT 960
DB 2234 CCCAGGCAAAAGTTAGTCTGAGAAATTAAGAGGATTAACAAGTGGGATTTGAAGGCTTT 2293
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QY 961 TGAATCTGTGTGAGCTGTTTGAATCTTTGATCTGGGTACACGAGCCTTTTCCAG 1020
DB 2294 TGAATCTGTGTGAGCTGTTTGAATCTTTGATCTGGGTACACGAGCCTTTTCCAG 2353
QY 1021 AGAAGTCAATCAAGCTTTGGATTTTTCACACCGGGGGGGCTGGGCTGTGTGGCT 1080
DB 2354 AGAAGTCAATCAAGCTTTGGATTTTTCACACCGGGGGGGCTGGGCTGTGTGGCT 2413
QY 1081 TTTTGAATTTTAAAGATTAATGAGACGGAAGAACCCATCTGAGCCGGGGGTACTGC 1140
DB 2414 TTTTGAATTTTAAAGATTAATGAGACGGAAGAACCCATCTGAGCCGGGGGTACTGC 2473
QY 1141 TGAATTTCTGGCCATGATCTGTGAGAGAGGCTTTGAGACACAAGATGCTGTCTAC 1200
DB 2474 TGAATTTCTGGCCATGATCTGTGAGAGAGGCTTTGAGACACAAGATGCTGTCTAC 2533
QY 1201 TGTGTCTTCGTCGCGCCGGCGATTAATCCGAGGAGAGAGCAGACGACGAGAGG 1260
DB 2534 TGTGTCTTCGTCGCGCCGGCGATTAATCCGAGGAGAGAGCAGACGACGAGAGG 2593
QY 1261 AAGCAGCGCGCGCGGCGAGAGCAGAGCCCATGGAACCCGAGAGCCGCGCTGACCTC 1320
DB 2594 AAGCAGCGCGCGCGGCGAGAGCAGAGCCCATGGAACCCGAGAGCCGCGCTGACCTC 2653
QY 1321 GGGAAATGATGTTGTACAGTGTGCTGAACTGTATCAAGACTGAGACGATTTGACAT 1380
DB 2654 GGGAAATGATGTTGTACAGTGTGCTGAACTGTATCAAGACTGAGACGATTTGACAT 2713
QY 1381 TACAGAGATGGGAGGGGGCTAAAGGGGGTAAAGGGGAGGGGGGGCTTGGAGGCTAC 1440
DB 2714 TACAGAGATGGGAGGGGGCTAAAGGGGGTAAAGGGGAGGGGGGGCTTGGAGGCTAC 2773
QY 1441 AGAGAGGCTAGGAATCTAGCTTTTATGCTTAATGACAGACACCGTCTGATGATTAC 1500
DB 2774 AGAGAGGCTAGGAATCTAGCTTTTATGCTTAATGACAGACACCGTCTGATGATTAC 2833
QY 2834 TTTTCAACAGATCAAGATTAATTTGGCTTAATGAGCTTATCTGCTGCGCAGAAATATTC 2893
DB 1501 TTTTCAACAGATCAAGATTAATTTGGCTTAATGAGCTTATCTGCTGCGCAGAAATATTC 1560
QY 2894 CATAGAGAGCTGACCACTTACTGCTGACCGAGGGGATGATTTTGAAGAGCTATTAG 1620
DB 1561 CATAGAGAGCTGACCACTTACTGCTGACCGAGGGGATGATTTTGAAGAGCTATTAG 1680
QY 1621 GGTATATGCAAAAGGTGCACTTGAAGCCAGATTGCAAGTACAAAGATCAGCAAACTGTAAA 1680
DB 2954 GGTATATGCAAAAGGTGCACTTGAAGCCAGATTGCAAGTACAAAGATCAGCAAACTGTAAA 3013
QY 1681 TATCAGGAATTTGTTCTACATTTCTGGGAACGGGCGAGGTGAGATGATACGAGGA 1740
DB 3014 TATCAGGAATTTGTTCTACATTTCTGGGAACGGGCGAGGTGAGATGATACGAGGA 3073
QY 1741 TAGGTGCTTTTATGATGATGATGATTAATATGTGGCCGGGGGTGCTTGGCATGGAAG 1800
DB 3074 TAGGTGCTTTTATGATGATGATGATTAATATGTGGCCGGGGGTGCTTGGCATGGAAG 3133
QY 1801 GGTGTTATTAATGATGATGATTTTACTGGCCCAATTTTAAAGCGGTACGTTTCTGGC 1860
DB 3134 GGTGTTATTAATGATGATGATTTTACTGGCCCAATTTTAAAGCGGTACGTTTCTGGC 3193
QY 1861 CAATACCAACCTTATCTTACACGAGGTGAAGCTTATGAGGTTTAACAATACCTGTGGA 1920
DB 3194 CAATACCAACCTTATCTTACACGAGGTGAAGCTTATGAGGTTTAACAATACCTGTGGA 3253
QY 1921 AGCTTGAACCGATGATGAAGGTTGGGGGTGTCCTTTTAACTGCTGTGGAAGGGGTGGT 1980
DB 3254 AGCTTGAACCGATGATGAAGGTTGGGGGTGTCCTTTTAACTGCTGTGGAAGGGGTGGT 3313
QY 1981 GTGTGCGCCCAAAAGAGAGGCTTCAATTAAGAAATGCTCTTTGAAGAGGTACCTTGGG 2040
DB 3314 GTGTGCGCCCAAAAGAGAGGCTTCAATTAAGAAATGCTCTTTGAAGAGGTACCTTGGG 3373
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OY 2041 TATCTGTCTGAGGTAACCTCCAGGGGTGCGCACATGNGGCTCCGAGTGTGTTGCT 2100
XX |||
DB 3374 TATCTGTCTGAGGTAACCTCCAGGGGTGCGCACATGNGGCTCCGAGTGTGTTGCT 3433
OY 2101 CATGCTAGTGAAGAACGCTGCTGTGATTAAAGCATTAACATGATGTGGCAACCTGCGAGGA 2160
XX |||
DB 3434 CATGCTAGTGAAGAACGCTGCTGTGATTAAAGCATTAACATGATGTGGCAACCTGCGAGGA 3493
OY 2151 CAGGGCCCTCTGAGATGCTGACCTGTGCGACCGGCAATGTCACCTGCTGAACACATTTCA 2220
XX |||
DB 3494 CAGGGCCCTCTGAGATGCTGACCTGTGCGACCGGCAATGTCACCTGCTGAACACATTTCA 3553
OY 2221 CGTACCCAGCCACTCTCCGAAAGGCTGTGGCCATGTTTGAGCATTAACATTAAGCCGCTG 2280
XX |||
DB 3554 CGTACCCAGCCACTCTCCGAAAGGCTGTGGCCATGTTTGAGCATTAACATTAAGCCGCTG 3613
OY 2281 TTCCTTGGATTGGTAAACAGAGAGGGGGGTGTCTTCACTTACCAATGCAATTTGAGTCA 2340
XX |||
DB 3614 TTCCTTGGATTGGTAAACAGAGAGGGGGGTGTCTTCACTTACCAATGCAATTTGAGTCA 3673
OY 2341 CACTAAGATATTGCTTGAAGCCCGAGAGCATGTCCAAAGTGAACCTGAAGGGGTGTTTGA 2400
XX |||
DB 3674 CACTAAGATATTGCTTGAAGCCCGAGAGCATGTCCAAAGTGAACCTGAAGGGGTGTTTGA 3733
OY 2401 CATGACCATGAAGATCTGGAGAGGTGCTGAGTAGATGAGACCCGACACAGGTGAGAC 2460
XX |||
DB 3734 CATGACCATGAAGATCTGGAGAGGTGCTGAGTAGATGAGACCCGACACAGGTGAGAC 3793
OY 2461 CTGCGAGTGTGGCGGTAAACATATTAGGAACAGAGCTGTGATGCTGATGAGCCGAGGA 2520
XX |||
DB 3794 CTGCGAGTGTGGCGGTAAACATATTAGGAACAGAGCTGTGATGCTGATGAGCCGAGGA 3853
OY 2521 GCTGAGGCCCGGATCACTTGTGCTGCTGCGACCCGCGGTGAGTTGGCTCAGAGATGA 2580
XX |||
DB 3854 GCTGAGGCCCGGATCACTTGTGCTGCTGCGACCCGCGGTGAGTTGGCTCAGAGATGA 3913
OY 2581 AGATACAGATTGAG 2594
XX |||
DB 3914 AGATACAGATTGAG 3927
XX |||

RESULT 5
AAL56864
ID AAL56864 strand: DNA; 7607 BP.
XX
AC AAL56864;
XX
DT 06-NOV-2003 (fixet entry)
XX
DE DNA sequence of the plasmid GRES-EI-SV40-Hygro construct.
XX
XX Fibre shaft modification: adenoviral vector; cell entry pathway; penton;
XX CAR; coxsackie adenovirus receptor; heparin sulphate proteoglycan; HSP;
XX gene therapy; fibre knob; ds.
XX
OS Rhesus macaque polyoma virus.
OS Unidentified adenovirus.
OS OS
OS WO2003062400-A2.
XX
XX 31-JUL-2003.
XX
XX 24-JAN-2003; 2003WO-US002295.
XX
XX 24-JAN-2002; 2002US-0350388P.
XX
XX 26-JUN-2002; 2002US-0391967P.
XX
XX (SCRI) SCRIPS RES INST.
XX
XX (NOVS) NOVARTIS AG.
XX
XX Kaleko M, Nemerow GR, Smith T, Stevenson SC;
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DR WPI; 2003-627459/59.
XX
XX New modified adenovirus capsid protein, useful as a base vector for
PT producing redirected adenoviruses.
XX
XX Disclosure; Page 141-143; 132pp; English.
XX
XX This invention relates to novel fibre shaft modifications in adenoviral
CC vectors. Adenoviral vector-mediated gene therapy aims to transduce a
CC specific targeted tissue or organ, accordingly gene therapy requires the
CC ablation of normal virus tropism. If successful, systemic vector delivery
CC into a peripheral vein would be targeted to the desired location in the
CC body without any associated side effects, which would permit lower, less
CC toxic vector doses that are also potentially less immunogenic. The
CC present invention describes capsid modifications, specifically fibre
CC shaft mutations that when expressed on adenoviral particles ablates
CC binding to heparin sulphate proteoglycans (HSP) thus providing targeted
CC vectors. Furthermore, when this is combined with modifications of other
CC adenoviral proteins involved in the cell entry pathway such as the fibre
CC knob, penton or CAR (coxsackie adenovirus receptor) proteins, the vectors
CC become fully detargeted. As such, these fully ablated particles can be
CC used in vivo as base vectors for producing redirected adenoviruses with
CC the desired cell specificity. This polynucleotide sequence is the plasmid
CC GRES-EI-SV40-Hygro construct used to provide complementation of the
CC adenoviral EI function of the invention
XX
XX Sequence 7607 BP; 1838 A; 1733 C; 2001 G; 2035 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 2594; DB 9; Length 7607;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ATCGATCTTACTCTGCGACAGAGGCTGGCTTCCACCCAGTAGACGAGAGTAAGAGGT 60
DB 1334 ATCGATCTTACTCTGCGACAGAGGCTGGCTTCCACCCAGTAGACGAGAGTAAGAGGT 1393
OY 61 GAGGAGTTTGTGTTAGATTATGATGAGAGCACCAGGCGAGTTGACAGGCTTGTCTATTAT 120
DB 1394 GAGGAGTTTGTGTTAGATTATGATGAGAGCACCAGGCGAGTTGACAGGCTTGTCTATTAT 1453
OY 121 CACCGAGGAATACGGGGGACCCAGATATTATGTTGCTTTGCTTATATGAGACCTGT 180
DB 1454 CACCGAGGAATACGGGGGACCCAGATATTATGTTGCTTTGCTTATATGAGACCTGT 1513
OY 181 GGCATGTTGCTACAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 240
DB 1514 GGCATGTTGCTACAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 1573
OY 241 GTGTGTAATTTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 300
DB 1574 GTGTGTAATTTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 1633
OY 301 TTTTAAAGTCTGCTGTCTGACCTGAGCCGAGCCGAGCCGAGCCGAGCCGAGCCGAGCCG 360
DB 1634 TTTTAAAGTCTGCTGTCTGACCTGAGCCGAGCCGAGCCGAGCCGAGCCGAGCCGAGCCG 1693
OY 361 CAAGACCTAACCCGCGCTCTAAATGAGGCGCTGATCTGAGAGCCGAGCATACCTG 420
DB 1694 CAAGACCTAACCCGCGCTCTAAATGAGGCGCTGATCTGAGAGCCGAGCATACCTG 1753
OY 421 TGTCTAGAGAAATGCAATAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG 480
DB 1754 TGTCTAGAGAAATGCAATAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG 1813
OY 481 CTGAGATACACCCGCTGCTCCGCTGTGCGCCCATTTAAACCACTTGCCTGAGAGTTGGTG 540
DB 1814 CTGAGATACACCCGCTGCTCCGCTGTGCGCCCATTTAAACCACTTGCCTGAGAGTTGGTG 1873
OY 541 GGCCTGCGCAGGCTGTGAATGTATCGAGGACTTGTCTTAACGAGGCTGGGCAACCTTTGG 600
DB 1874 GGCCTGCGCAGGCTGTGAATGTATCGAGGACTTGTCTTAACGAGGCTGGGCAACCTTTGG 1933
OY 601 ACTTGAGCTGTAAACGCCCCAGGCCATTAAGGTGTAAACCTGTGATTTGGGTGTGTAA 660
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Db 1934 ACTTGAAGCTGTAAGAGCCCGGAGGCAATAGAGTGTAAAGCTGTGATGGGTGTGTATTA 1993
Qy 661 CGCCTTGTGTTGCTGAATGAGTGTATGATGTTATTAAGGGTGAATATGTTTAACT 720
Db 1994 CGCCTTGTGTTGCTGAATGAGTGTATGATGTTATTAAGGGTGAATATGTTTAACT 2053
Qy 721 TGCATGGGCTGTAAATGGGGCGGGCTTAAAGGGTATTAATGCGCGCTGGGCTTAATCT 780
Db 2054 TGCATGGGCTGTAAATGGGGCGGGCTTAAAGGGTATTAATGCGCGCTGGGCTTAATCT 2113
Qy 781 TGTGTACATGACCTCACTGAGAGCTTGGAGAGTGTGTTGGAAGATTTTTCGTGTCGCTA 840
Db 2114 TGTGTACATGACCTCACTGAGAGCTTGGAGAGTGTGTTGGAAGATTTTTCGTGTCGCTA 2173
Qy 841 ACTTGTGGAACAGAGCTCTAAACAGTACCTCTTGGTTTGGAGTTTCTGTGGGCTCAT 900
Db 2174 ACTTGTGGAACAGAGCTCTAAACAGTACCTCTTGGTTTGGAGTTTCTGTGGGCTCAT 2233
Qy 901 CCCAGGCAAGTTAGTCTGACAGATTTAAGAGAGATTACAGTGGGAATTTGAAAGCTTT 960
Db 2234 CCCAGGCAAGTTAGTCTGACAGATTTAAGAGAGATTACAGTGGGAATTTGAAAGCTTT 2293
Qy 961 TGAATCTGTGTGAGGCTGTGATTTGATTTGATCTGGGTGACAGAGGCGCTTTCCAG 1020
Db 2294 TGAATCTGTGTGAGGCTGTGATTTGATTTGATCTGGGTGACAGAGGCGCTTTCCAG 2353
Qy 1021 AGAAGGTATCAGAGCTTTGGATTTTTCACACCGGGGCGGCTGCGCTGTGTGCTT 1080
Db 2354 AGAAGGTATCAGAGCTTTGGATTTTTCACACCGGGGCGGCTGCGCTGTGTGCTT 2413
Qy 1081 TTTTGAAGTTTATTAAGATTAATGAGACGAAGAAACCATTTGACGGGGGGTATCTGTC 1140
Db 2414 TTTTGAAGTTTATTAAGATTAATGAGACGAAGAAACCATTTGACGGGGGGTATCTGTC 2473
Qy 1141 TGGATTTTCTGAGCATCTGTGAGAGAGGGGTTGTGACACAGAAATGCGCTGTCTAC 1200
Db 2474 TGGATTTTCTGAGCATCTGTGAGAGAGGGGTTGTGAGACACAGAAATGCGCTGTCTAC 2533
Qy 1201 TGTGTCTTCCGTCGCGCCGCGAGTAATACCGACGAGAGAGCAGACAGACAGAGAG 1260
Db 2534 TGTGTCTTCCGTCGCGCCGCGAGTAATACCGACGAGAGAGCAGACAGACAGAGAG 2593
Qy 1261 AAGCGAGCGCGCGGCGAGAGAGAGCCCATGGAACCCGAGAGCCGCGCTGTGACCTTC 1320
Db 2594 AAGCGAGCGCGCGGCGAGAGAGAGCCCATGGAACCCGAGAGCCGCGCTGTGACCTTC 2653
Qy 1321 GGAATGMAATGTTGACAGTGGCTGAACCTGATTCAGAACTGAGAGGCAATTTTGACAA 1380
Db 2654 GGAATGMAATGTTGACAGTGGCTGAACCTGATTCAGAACTGAGAGGCAATTTTGACAA 2713
Qy 1381 TACAGAGAGTGGGAGGGGCTTAAAGGGGTAAAGAGAGCGGGGGCTTGTGAGGCTAC 1440
Db 2714 TACAGAGAGTGGGAGGGGCTTAAAGGGGTAAAGAGAGCGGGGGCTTGTGAGGCTAC 2773
Qy 1441 AGAGAGAGCTGGAATCTAGCTTTTAACTTAATGACAGACACCGTCTGTAGTGTATAC 1500
Db 2774 AGAGAGAGCTGGAATCTAGCTTTTAACTTAATGACAGACACCGTCTGTAGTGTATAC 2833
Qy 1501 TTTTCAACAGATCAAGATTAATGCGCTAATGAGCTTATCTGCGTGGCGGAGAAATATTC 1560
Db 2834 TTTTCAACAGATCAAGATTAATGCGCTAATGAGCTTATCTGCGTGGCGGAGAAATATTC 2893
Qy 1561 CATAGAGAGCTGACCACTTACTGGCTGACACGAGGGAGTATTTTGAAGAGCTATTAG 1620
Db 2894 CATAGAGAGCTGACCACTTACTGGCTGACACGAGGGAGTATTTTGAAGAGCTATTAG 2953
Qy 1621 GGTATATGCAAAAGGTGGCACTTAAGCCAGATTGCAAGTACAGCAATTTGTAA 1680
Db 2954 GGTATATGCAAAAGGTGGCACTTAAGCCAGATTGCAAGTACAGCAATTTGTAA 3013
Qy 1681 TATCAGGAATTTGTGCTACATTTCTGGGAAGGGGCGAGGTGAGATAGATACGAGAGA 1740

Db 3014 TATCAGGAATTTGTGCTACATTTCTGGGAAGGGGCGAGGTGAGATAGATACGAGAGA 3073
Qy 1741 TAGGGTGGCCTTTAGATGTAGCATGATTAATATGTGGCGGGGGGTCTTGGCATGAGACG 1800
Db 3074 TAGGGTGGCCTTTAGATGTAGCATGATTAATATGTGGCGGGGGGTCTTGGCATGAGACG 3133
Qy 1801 GGTGTTATTTATGATATGTAAGGTTTACGCGCCCAATTTTACGGGTACGGTTTCTGGC 1860
Db 3134 GGTGTTATTTATGATATGTAAGGTTTACGCGCCCAATTTTACGGGTACGGTTTCTGGC 3193
Qy 1861 CAATACCAACCTTATCTACACGGGTGTAAGCTTCTATGAGGTTTAAACAATACCTGTGTGA 1920
Db 3194 CAATACCAACCTTATCTACACGGGTGTAAGCTTCTATGAGGTTTAAACAATACCTGTGTGA 3253
Qy 1921 AGCCTGACCGATGTAAAGGTTTGGGGGCTGTGCTTTTATCTGTGCTGGAAGGGGGTGT 1980
Db 3254 AGCCTGACCGATGTAAAGGTTTGGGGGCTGTGCTTTTATCTGTGCTGGAAGGGGGTGT 3313
Qy 1981 GTGTGCGCCCAAAAGCAGGGGCTTCAATTAAGAAATGCTCTTTTGAAGGTATCCTTGG 2040
Db 3314 GTGTGCGCCCAAAAGCAGGGGCTTCAATTAAGAAATGCTCTTTTGAAGGTATCCTTGG 3373
Qy 2041 TATCCTGTCTGAGGGTAACTCAGGGGTGCGCAATGTGGGCTCGACTGTGTGCTT 2100
Db 3374 TATCCTGTCTGAGGGTAACTCAGGGGTGCGCAATGTGGGCTCGACTGTGTGCTT 3433
Qy 2101 CATGTAGTGAAGAGCGGTGTGATTTAGCATTAACATGATGTGCAACTGCGAGGA 2160
Db 3434 CATGTAGTGAAGAGCGGTGTGATTTAGCATTAACATGATGTGCAACTGCGAGGA 3493
Qy 2161 CAGGGGCTCTAGATGTGACCTGTCTGAGAGGCACTGTCACTGTGGAAGACATTTCA 2220
Db 3494 CAGGGGCTCTAGATGTGACCTGTCTGAGAGGCACTGTCACTGTGGAAGACATTTCA 3553
Qy 2221 CGTAGCCAGCCACTCTGCAAGAGGCTGGCCAGTGTGAGATTAACATGACCGGCTG 2280
Db 3554 CGTAGCCAGCCACTCTGCAAGAGGCTGGCCAGTGTGAGATTAACATGACCGGCTG 3613
Qy 2281 TTCCTTGTGATTTGGGTAAACAGAGAGGGGGTGTCTTCACTTAACCAATGCAATTTGAGTCA 2340
Db 3614 TTCCTTGTGATTTGGGTAAACAGAGAGGGGGTGTCTTCACTTAACCAATGCAATTTGAGTCA 3673
Qy 2341 CACTTAAGTATTTGCTTGAAGCCGAGAGACATGTCAGAGTGAACCTGAACGGGGTCTTTGA 2400
Db 3674 CACTTAAGTATTTGCTTGAAGCCGAGAGACATGTCAGAGTGAACCTGAACGGGGTCTTTGA 3733
Qy 2401 CATGACCATGAAGATCTGGAAGGTGTGAGGTAGATGAGACCGGACACAGGTGACAGCC 2460
Db 3734 CATGACCATGAAGATCTGGAAGGTGTGAGGTAGATGAGACCGGACACAGGTGACAGCC 3793
Qy 2461 CTGCGAGTGTGGCGGTAAACATATTAGGAACCAAGCTGTGATGCTGATGTCGAGCA 2520
Db 3794 CTGCGAGTGTGGCGGTAAACATATTAGGAACCAAGCTGTGATGCTGATGTCGAGCA 3853
Qy 2521 GCTGAGGCGCCGATCACTTGTGTGCTGTGCTGCAACCGGCTGAAGTTTGGCTTACGAGTGA 2580
Db 3854 GCTGAGGCGCCGATCACTTGTGTGCTGTGCTGCAACCGGCTGAAGTTTGGCTTACGAGTGA 3913
Qy 2581 AGATACAGATTGAG 2594
Db 3914 AGATACAGATTGAG 3927

RESULT 6
ADB75124
ID ADB75124 standard; DNA; 7607 BP.
XX ADB75124;
AC ADB75124;
XX
XX
XX 04-DEC-2003 (first entry)
DT
XX
XX Chromosomal insertion pGR5-2.B1.
XX

Db 2294 TGAATCCCTGATGAGCTGTTGATCTTTGAATCTGAGTCAACAGGCGCTTTCCAG 2353
Qy 1021 AGAAGCTCATTAAGACTTTTGGATTTTTCACACCGGGGCGGCTGCGGCTGCTGTTGCTT 1080
Db 2254 AGAAGGCTATCMAACTTTGATTTTTCACACCGGGGCGGCTGCGGCTGCTGTTGCTT 2413
Qy 1081 TTTTGAAGTTTATTAAGATTAATGAGAGCAAGAAACCATCTGAGCGGGGGGTAACTGCG 1140
Db 2414 TTTTGAAGTTTATTAAGATTAATGAGAGCAAGAAACCATCTGAGCGGGGGGTAACTGCG 2473
Qy 1141 TGAATTTTCTGCGCATCTGTGAGAGCGGTTGTGAGACAAAGATGCGCTGCTAC 1200
Db 2474 TGAATTTTCTGCGCATCTGTGAGAGCGGTTGTGAGACAAAGATGCGCTGCTAC 2533
Qy 1201 TGTGTCTTCCGCTCCGCGCGGCAATATACGAGAGAGACAGACAGACAGAGAGG 1260
Db 2534 TGTGTCTTCCGCTCCGCGCGGCAATATACGAGAGAGACAGACAGACAGAGAGG 2593
Qy 1261 AAGCCAGCGCGCGGAGAGAGAGCCCATGGAACCCGAGAGCGGCGCTGGAACCTC 1320
Db 2594 AAGCCAGCGCGCGGAGAGAGAGCCCATGGAACCCGAGAGCGGCGCTGGAACCTC 2653
Qy 1321 GGGATATATGTTGTATAGAGTGTGAGCTGATCTGACAACTGAGAGCGCATTTGACAA 1380
Db 2654 GGGATATATGTTGTATAGAGTGTGAGCTGATCTGACAACTGAGAGCGCATTTGACAA 2713
Qy 1381 TACAGAGATGAGGAGGAGGCTAAAGGGGGTAAAGAGGAGCGGGGGCTTGTAGGCTAC 1440
Db 2714 TACAGAGATGAGGAGGAGGCTAAAGGGGGTAAAGAGGAGCGGGGGCTTGTAGGCTAC 2773
Qy 1441 AGAGGAGGCTAGGAATCTAGCTTTAGCTTAAATGACAGACCGCTCTGAGTATTTAC 1500
Db 2774 AGAGGAGGCTAGGAATCTAGCTTTAGCTTAAATGACAGACCGCTCTGAGTATTTAC 2833
Qy 1501 TTTTCAACAGATCAAGATTAATGCGCTAAATGAGCTTGATCTGCGCGAGAGTATTC 1560
Db 2834 TTTTCAACAGATCAAGATTAATGCGCTAAATGAGCTTGATCTGCGCGAGAGTATTC 2893
Qy 1561 CATAGAGACGTCACCTTACTGCTGACGACCGAGGAGTATTTAGAGGCTATTTAG 1620
Db 2894 CATAGAGACGTCACCTTACTGCTGACGACCGAGGAGTATTTAGAGGCTATTTAG 2953
Qy 1621 GGTATATGCAAGGTGACCTTAGGCGAGANTGCAATGACATCAAGTCAAGCAACTGTAAA 1680
Db 2954 GGTATATGCAAGGTGACCTTAGGCGAGANTGCAATGACATCAAGTCAAGCAACTGTAAA 3013
Qy 1681 TATCAGGAATTTGTTCTACATTTCTGGAAACGGGGCGAGGTGAGATAGATACGAGGA 1740
Db 3014 TATCAGGAATTTGTTCTACATTTCTGGAAACGGGGCGAGGTGAGATAGATACGAGGA 3073
Qy 1741 TAGGGTGGCTTTAGATGATGATGATTAATATGTGGCGGGGGTGTCTTGACATGACGG 1800
Db 3074 TAGGGTGGCTTTAGATGATGATGATTAATATGTGGCGGGGGTGTCTTGACATGACGG 3133
Qy 1801 GGTGGTTATTAATTAATGATGATTTACTGGCGCCCAATTTTAGGGGTACGGTTTCTGCGC 1860
Db 3134 GGTGGTTATTAATTAATGATGATTTACTGGCGCCCAATTTTAGGGGTACGGTTTCTGCGC 3193
Qy 1861 CAATACCAACCTTATCTTACACGAGTGAAGCTTCTATGAGGTTTAAACAATACCTGTGGA 1920
Db 3194 CAATACCAACCTTATCTTACACGAGTGAAGCTTCTTATGAGGTTTAAACAATACCTGTGGA 3253
Qy 1921 AGCTTGAGACGATGTAAGGGTTCGGGGCTGTGCTTTTACTGTGCTGAAGGGGGTGT 1980
Db 3254 AGCTTGAGACGATGTAAGGGTTCGGGGCTGTGCTTTTACTGTGCTGAAGGGGGTGT 3313
Qy 1981 GGTGGCGCCCAAAAGCAAGGGCTTCAATTAAGAAATGCTCTTTGAAAGGTGTACTTGGG 2040
Db 3314 GGTGGCGCCCAAAAGCAAGGGCTTCAATTAAGAAATGCTCTTTGAAAGGTGTACTTGGG 3373
Qy 2041 TATCTGTCTGAGGGTAACTCAAGGGTGGCCCAATGATGGCTCGACGTGTGGTCTT 2100
Db 3374 TATCTGTCTGAGGGTAACTCAAGGGTGGCCCAATGATGGCTCGACGTGTGGTCTT 3433

Qy 2101 CATGCTAGTGAAGACGTGCTGTGATTAAGCATPAACATGATATGTCGAACCTGAGAGA 2160
Db 3434 CATGCTAGTGAAGACGTGCTGTGATTAAGCATPAACATGATATGTCGAACCTGAGAGA 3493
Qy 2161 CAGGGCCCTCAGATGCTGACCTGCTGAGAGGCACTGTCACTGCTGAGAACCATTTCA 2220
Db 3494 CAGGGCCCTCAGATGCTGACCTGCTGAGAGGCACTGTCACTGCTGAGAACCATTTCA 3553
Qy 2221 CGTAGCAGACCACTCTGCAAGGCTGCGCAGTGTGTTGAGCATPAACATGACCCGCTG 2280
Db 3554 CGTAGCAGACCACTCTGCAAGGCTGCGCAGTGTGTTGAGCATPAACATGACCCGCTG 3613
Qy 2281 TTCCTTGATTTGGGTAAACAGAGAGGAGGAGTGTCTTCACTTACCAATGCAATTTGAGTCA 2340
Db 3614 TTCCTTGATTTGGGTAAACAGAGAGGAGGAGTGTCTTCACTTACCAATGCAATTTGAGTCA 3673
Qy 2341 CACTPAAGATATTGCTTGAAGCCCGAGACATGTCCAAAGTGAACCTGAACGGGGTGTGGA 2400
Db 3674 CACTPAAGATATTGCTTGAAGCCCGAGACATGTCCAAAGTGAACCTGAACGGGGTGTGGA 3733
Qy 2401 CATGACCATGAAAGATCTGAAAGGTGCTGAGGTACATGAGACCCGACACAGGTGACAGC 2460
Db 3734 CATGACCATGAAAGATCTGAAAGGTGCTGAGGTACATGAGACCCGACACAGGTGACAGC 3793
Qy 2461 CTGCAAGTGTGCGGTAAACATATTAGAAACAGCCTGTGATGCTGATGATGACCGAGGA 2520
Db 3794 CTGCAAGTGTGCGGTAAACATATTAGAAACAGCCTGTGATGCTGATGATGACCGAGGA 3853
Qy 2521 GCTGAGGCCCGATCACTTGTGTGCTGAGCTGCAACCCGCGTGAAGTTTGCTTACGATGA 2580
Db 3854 GCTGAGGCCCGATCACTTGTGTGCTGAGCTGCAACCCGCGTGAAGTTTGCTTACGATGA 3913
Qy 2581 AGATPACAGATTGAG 2594
Db 3914 AGATPACAGATTGAG 3927

RESULT 7
ADP48758
ID ADP48758 standard; DNA; 7607 BP.
XX
AC ADP48758;
XX
DT 12-FEB-2004 (first entry)
XX
DE Plasmid pGR5-2.E1.
XX
KW cytostatic; anti-HIV; gene therapy; HIV gene expression inhibitor;
KW HIV gene expression activation; adenovirus tripartite leader; TPL;
KW gutless adenoviral vector particle;
KW helper-independent fiberless recombinant adenovirus vector;
KW packaging cell line; pseudotyping; adenovirus vector; gene therapy;
KW hereditary disorder; tumour; HIV infection; GR5-2.E1; ds.
XX
OS Synthetic.
OS Human adenovirus type 5.
XX
PN US2003157688-A1.
XX
PD 21-AUG-2003.
XX
PF 14-JAN-2000; 2000US-00482682.
XX
PR 14-JAN-1999; 99US-0115920P.
PR 26-JUN-2000; 2000US-00423783.
XX
XX (VSEG/) VON SEGGERN D J.
PA (NEME/) NEMEROW G R.
PA (HAL/) HALENBECK P.
PA (STEV/) STEVENSON S.
PA (SKRI/) SKRIPCHENKO Y.
XX

PI Von Seggern DJ, Nemerow GR, Hallenbeck P, Stevenson S;
PI Skripchenko Y;
DR WPI, 2003-843463/78.
XX
XX Novel isolated nucleic acid molecule useful for delivering heterologous
PT gene to human or any animal, or for producing gutless adenoviral vector
PT particle.
PS
PS Example 6; SEQ ID NO 48; 157bp; English.

XX The invention describes an isolated nucleic acid molecule (I) comprising
CC an adenovirus tripartite leader (TPL) nucleotide, the TPL nucleotide
CC sequence comprising a first and second different TPL exons or first,
CC second and third same or different TPL exons, the TPL exons chosen from
CC complete or partial TPL exon 1, complete TPL exon 2 and complete TPL exon
CC 3. (i) is useful for delivering a heterologous gene to a human or any
CC animal, or for producing a gutless adenoviral vector particle. A
CC recombinant adenovirus particle (II) is useful for delivery of an
CC exogenous gene to a target cell which involves contacting the cell with
CC an amount of (II) sufficient to infect the cell. A helper-independent
CC fiberless recombinant adenovirus vector genome (III) is useful for
CC producing an adenovirus vector particle containing (III) which involves
CC providing a packaging cell line which complements replication and
CC packaging of the genome and (III) which is deficient in expressing
CC sufficient functional fiber protein to support assembly of fiber
CC containing particles and harvesting the particle produced by the cell
CC line. (III) is useful for pseudotyping recombinant viral vectors which
CC involves complementing a missing fiber gene of (III) or helper-dependent
CC fiberless recombinant adenovirus vector genome by expressing in packaging
CC cells a fiber gene from a different adenoviral serotype than the
CC recombinant adenovirus vector. (III) is also useful for specifically
CC targeting an adenovirus vector to a cell of choice. (I) is useful for
CC gene therapy. (II) is useful for treating diseases such as hereditary
CC disorder, and for reducing proliferation of tumour cells in a subject
CC to disrupt HIV infection. This sequence represents construct GBS-2.B1, a
CC plasmid inserted into the chromosomal DNA of lung carcinoma line A59.
XX
XX Sequence 7607 BP; 1838 A; 1733 C; 2001 G; 2035 T; 0 U; 0 Other;

Query Match 100.0%; Score 2594; DB 10; Length 7607;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCGATCTTACTGCGCAGAGGCTGCTTTCACCCAGTACGACGAGATGAAAGGGT 60
DB 1334 ATCGATCTTACTGCGCAGAGGCTGCTTTCACCCAGTACGACGAGATGAAAGGGT 1393
QY 61 GAGGAGTTGTGTAGATTATGTGAGACACCCGGGACAGTTGCAAGTCTTGTCAATTAT 120
DB 1394 GAGGAGTTGTGTAGATTATGTGAGACACCCGGGACAGTTGCAAGTCTTGTCAATTAT 1453
QY 121 CACCGGAGAAATACGGGGGACCCAGATATTAATGTGCTTGTCTATATGAGACCTGT 180
DB 1454 CACCGGAGAAATACGGGGGACCCAGATATTAATGTGCTTGTCTATATGAGACCTGT 1513
QY 181 GGCATGTTGTCTACAGTAAGTAAATATATGAGGAGTGGTATGATGAGTGGGTTTG 240
DB 1514 GGCATGTTGTCTACAGTAAGTAAATATATGAGGAGTGGTATGATGAGTGGGTTTG 1573
QY 241 GTGTGTAATTTTTTTTTTAATTTTTTACAGTTTGTGTTTAAAGATTTTTGTATTTGCA 300
DB 1574 GTGTGTAATTTTTTTTTTAATTTTTTACAGTTTGTGTTTAAAGATTTTTGTATTTGCA 1633
QY 301 TTTTTTTTAAAGAGTCTGTGTCTGAACCTGAGCCTTGAAGCCGAGAACGGAGCCCTG 360
DB 1634 TTTTTTTTAAAGAGTCTGTGTCTGAACCTGAGCCTTGAAGCCGAGAACGGAGCCCTG 1693
QY 361 CAAGACCTTACCCGCGCTCTTAAATAGGCGCTGTCTATCTCTGAGACGCCGACATCACTTG 420
DB 1694 CAAGACCTTACCCGCGCTCTTAAATAGGCGCTGTCTATCTCTGAGACGCCGACATCACTTG 1753
QY 421 TGTCTAGAGAAATGCAATAGTATGAGATGAGTGTGATCTCCGCTCTTCAACACACTTC 480

DB 1754 TGTCTAGAGAAATGCAATAGTATGAGATGAGTGTGATCTCCGCTCTTCAACACACTTC 1813
QY 481 CTGAGATACACCCGGGTGTCTCCGCTGTGCCCCATTAACCAAGTTGCCGTGAGAGTTGGTG 540
DB 1814 CTGAGATACACCCGGGTGTCTCCGCTGTGCCCCATTAACCAAGTTGCCGTGAGAGTTGGTG 1873
QY 541 GCGCTGCCAGGCTGTGGAATGTATGAGAGACTTGCTTAAACGAGCCGTGGCAACTTTGG 600
DB 1874 GCGCTGCCAGGCTGTGGAATGTATGAGAGACTTGCTTAAACGAGCCGTGGCAACTTTGG 1933
QY 601 ACTTGAGCTGTAAACGCCCAAGCCATTAAGTGTAACCTGTGATTCGTTGTGTTAA 660
DB 1934 ACTTGAGCTGTAAACGCCCAAGCCATTAAGTGTAACCTGTGATTCGTTGTGTTAA 1993
QY 661 CGCCTTGTGTGTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
DB 1994 CGCCTTGTGTGTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2053
QY 721 TGCATGCGCTGTAAATGAGGCGCGGCTTAAAGGTAATATGCGCGGCTAATCT 780
DB 2054 TGCATGCGCTGTAAATGAGGCGCGGCTTAAAGGTAATATGCGCGGCTAATCT 2113
QY 781 TGGTTACATCTGACCTCATATGAGGCTTGGAGTGTGTAAGATTTTCTGCTGTGCTGA 840
DB 2114 TGGTTACATCTGACCTCATATGAGGCTTGGAGTGTGTAAGATTTTCTGCTGTGCTGA 2173
QY 841 ACTTGCTGAACAGAGCTCTTAACATGATCTCTGTTTGGAGGTTCTGTGGGCTCAT 900
DB 2174 ACTTGCTGAACAGAGCTCTTAACATGATCTCTGTTTGGAGGTTCTGTGGGCTCAT 2233
QY 901 CCGCAGCAAGTAACTGTGAGAAATTAAGAGAGTTCAAGTGGAAATTTGAAGAGCTTT 960
DB 2234 CCGCAGCAAGTAACTGTGAGAAATTAAGAGAGTTCAAGTGGAAATTTGAAGAGCTTT 2293
QY 961 TGAATCTGTGAGAGCTGTTGATCTTGTGATCTGGTCAACAGGCTTTTCCAG 1020
DB 2294 TGAATCTGTGAGAGCTGTTGATCTTGTGATCTGGTCAACAGGCTTTTCCAG 2353
QY 1021 AGAAGTCATCAAGACTTTGATTTTTCACACCGGGCGGCTGCGCTGTGCTT 1080
DB 2354 AGAAGTCATCAAGACTTTGATTTTTCACACCGGGCGGCTGCGCTGTGCTT 2413
QY 1081 TTTTGAAGTTTAAAGATTAATGAGCGGAAGAACCATCTGAGCGGGGGTAACTGTC 1140
DB 2414 TTTTGAAGTTTAAAGATTAATGAGCGGAAGAACCATCTGAGCGGGGGTAACTGTC 2473
QY 1141 TGGATTTTCTGCGCATGCTGTGAGAGCGGTTGTGAGACAAAGATGCGCTGTAC 1200
DB 2474 TGGATTTTCTGCGCATGCTGTGAGAGCGGTTGTGAGACAAAGATGCGCTGTAC 2533
QY 1201 TGTGTCTTCCGTCGCGCCGCGCATTAATACGAGAGAGACGAGACGAGAGAGG 1260
DB 2534 TGTGTCTTCCGTCGCGCCGCGCATTAATACGAGAGAGACGAGAGAGG 2593
QY 1261 AAGCCAGCGCGCGGAG 1320
DB 2594 AAGCCAGCGCGCGGAG 2653
QY 1321 GGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
DB 2654 GGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2713
QY 1381 TACAGAGATGAGGAGGAGGCTTAAAGGGGTAAGAGGAGCGGGGGGCTTGTGAGGCTAC 1440
DB 2714 TACAGAGATGAGGAGGAGGCTTAAAGGGGTAAGAGGAGCGGGGGGCTTGTGAGGCTAC 2773
QY 1441 AGAGAGGCTAGGAATCTAGCTTTAGCTTATATGACAGACACCGTCTGAGTGTATAC 1500
DB 2774 AGAGAGGCTAGGAATCTAGCTTTAGCTTATATGACAGACACCGTCTGAGTGTATAC 2833
QY 1501 TTTTCAACAGATCAAGATTAATTTGCGCTAATGAGCTTATCTGTGCGCAAGATATTC 1560

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Db      2893  TTTTCAAGATCAAGATAATTGGCTAATGAGCTTATCTGCGCCGCAAGTATTC 2893
Qy      1561  CATGAGAGCTGACCACTTACTGGCTGACCCAGGGGATGATTTTGAAGGCTATTAG 1620
Db      2894  CATAGAGAGCTGACCACTTACTGGCTGACCCAGGGGATGATTTTGAAGGCTATTAG 2953
Qy      1621  GGTATATGCAAAAGGTGGCACTTAGGCCAGATTGCAAGTACAAGATCAGCAAACTTGTAAA 1680
Db      2954  GGTATATGCAAAAGGTGGCACTTAGGCCAGATTGCAAGTACAAGATCAGCAAACTTGTAAA 3013
Qy      1681  TATCAGGAATTGTTGCTACATTTCTGGGAACGGGGCCAGGTGAGATAGATAGAGAGGA 1740
Db      3014  TATCAGGAATTGTTGCTACATTTCTGGGAACGGGGCCAGGTGAGATAGATAGAGAGGA 3073
Qy      1741  TAGGGTGGCCTTTAGATGTAGCATGATTAATATGTGGCCGGGGGTGCTTGGCATGGAACGG 1800
Db      3074  TAGGGTGGCCTTTAGATGTAGCATGATTAATATGTGGCCGGGGGTGCTTGGCATGGAACGG 3133
Qy      1801  GGTGGTTATTAATGAATGAATGAATGCTGAGCCCAATTTTACGGGTACGGTTTCTTGGC 1860
Db      3134  GGTGGTTATTAATGAATGAATGAATGCTGAGCCCAATTTTACGGGTACGGTTTCTTGGC 3193
Qy      1861  CAATACCAACCTTATCTTACACGGGTGAAGCTTCTATGGGTTTAACAATACCTGTGTGA 1920
Db      3194  CAATACCAACCTTATCTTACACGGGTGAAGCTTCTATGGGTTTAACAATACCTGTGTGA 3253
Qy      1921  AGCTTGACCGATGTAAAGGTTTCGGGGCTGTGCTTTTACTGCTGTGGAAGGGGGTGTGT 1980
Db      3254  AGCTTGACCGATGTAAAGGTTTCGGGGCTGTGCTTTTACTGCTGTGGAAGGGGGTGTGT 3313
Qy      1981  GTGTGGCCCCCAAAAGCAAGGGCTTCAATTAAGAAATGCTCTTTTAAAGGTGTACTTGGG 2040
Db      3314  GTGTGGCCCCCAAAAGCAAGGGCTTCAATTAAGAAATGCTCTTTTAAAGGTGTACTTGGG 3373
Qy      2041  TATCTGTCTGAGGGTAACTCAAGGGTGGCCCAATGATGGGCTCCGACTGTGGTGTCTT 2100
Db      3374  TATCTGTCTGAGGGTAACTCAAGGGTGGCCCAATGATGGGCTCCGACTGTGGTGTCTT 3433
Qy      2101  CATGCTAAGTAAAGCGTGGCTGTGATTAAGCATTAAGATGATGTGGCAACCTGCGAGA 2160
Db      3434  CATGCTAAGTAAAGCGTGGCTGTGATTAAGCATTAAGATGATGTGGCAACCTGCGAGA 3493
Qy      2161  CAGGGGCTCTCAAGTGTGACCTGCTGGACGGGAATGTCACTGCTGTAAGACATTTCA 2220
Db      3494  CAGGGGCTCTCAAGTGTGACCTGCTGGACGGGAATGTCACTGCTGTAAGACATTTCA 3553
Qy      2221  CGTAGCCAGCCACTCTGCAAGGCTGGCCAGTGTGAGCATTAACATCTGACCCGCTG 2280
Db      3554  CGTAGCCAGCCACTCTGCAAGGCTGGCCAGTGTGAGCATTAACATCTGACCCGCTG 3613
Qy      2281  TTCCTTGCAATTTGGGTAAAGAGAGGGGGGTTCCTTACCTTACCAATGCAATTTGACTCA 2340
Db      3614  TTCCTTGCAATTTGGGTAAAGAGAGGGGGGTTCCTTACCTTACCAATGCAATTTGACTCA 3673
Qy      2341  CACTAAGATTTTCTTGAGGCCAGAGACATCTCCAAAGTGAACCTGAAACGGGGTGTGGA 2400
Db      3674  CACTAAGATTTTCTTGAGGCCAGAGACATCTCCAAAGTGAACCTGAAACGGGGTGTGGA 3733
Qy      2401  CATGACCATGAAGATCTGAAGGTGCTGAGGTAGCATGAGAACCCGACCAAGGTGACAGAC 2460
Db      3734  CATGACCATGAAGATCTGAAGGTGCTGAGGTAGCATGAGAACCCGACCAAGGTGACAGAC 3793
Qy      2461  CTGCGAGTGTGGCGGTAAACATATTAGAAACAGCCTGTGATGCTGATGTGAACCGAGA 2520
Db      3794  CTGCGAGTGTGGCGGTAAACATATTAGAAACAGCCTGTGATGCTGATGTGAACCGAGA 3853
Qy      2521  GCTGAGGCCGATCACTTGGTGTGGCTGACACCCGGGCTGAGTTGGCTTACCGATGA 2580
Db      3854  GCTGAGGCCGATCACTTGGTGTGGCTGACACCCGGGCTGAGTTGGCTTACCGATGA 3913
Qy      2581  AGATACAGATTGAG 2594
Db      3914  AGATACAGATTGAG 3927

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RESULT 8
AAV32373
ID AAV32373 standard; DNA; 11152 BP.
XX
AC AAV32373;
XX
DT 25-MAR-2003 (revised)
DT 29-SEP-1998 (first entry)
XX
DE Complete sequence of the pDEX/E1 plasmid.
XX
KW Circular; adenovirus type 5; pMAM plasmid; structural protein;
KW complementation; fiber protein; gene therapy; HIV; tumour; AD5;
KW Huntington's disease; Tay-Sachs disease; early gene; sickle cell disease;
KW E1 regulatory protein; MMTV; mouse mammary tumour virus promoter; ds.
XX
OS Synthetic.
XX
FH Key
FT misc_feature
FT /tag= a
FT /note= "pMAM backbone"
FT misc_feature
FT /tag= b
FT /note= "AD5 E1 regulatory gene consisting of a MMTV LTR
FT promoter at 5' end of this gene"
FT /tag= c
FT /note= "pMAM backbone"
XX
PN W09813499-A2.
XX
PD 02-Apr-1998.
XX
PF 24-SEP-1997; 97MO-EP005251.
XX
PR 25-SEP-1996; 96US-00719806.
XX
PA (NOVS ) NOVARTIS AG.
PA (SCRI ) SCRIPPS RES INST.
XX
PI Nemerow GR, Von Seggern DJ;
XX
DR WPI; 1998-230709/20.
XX
PT Adenoviral vectors - which lack DNA encoding for structural protein or
PT fibre protein used particularly for gene therapy.
XX
PS Example 1; Page 97-111; 170pp; English.
XX
CC The present sequence is that of a pDEX/E1 plasmid used in the method of
CC the invention. The plasmid contains an adenovirus type 5 (AD5) E1
CC regulatory gene controlled by a mouse mammary tumour virus (MMTV)
CC promoter. The invention provides adenoviral vectors having deletions of
CC all or part of various gene sequences encoding adenoviral structural
CC proteins and/or early region proteins. Deletions in these proteins would
CC allow a reduced risk of wild-type virus contamination and would also
CC allow packaging of foreign DNA in such vectors for a variety of
CC diagnostic and therapeutic applications. The adenoviral vectors having
CC deletions in the structural and/or early gene regions are produced by
CC cellular complementation of these adenoviral genes. Therefore, the
CC pDEX/E1 plasmid was used as a complementation plasmid which was
CC introduced into a host cell line where parts of the E1 gene region would
CC be stably inserted into the host cell chromosomes. The resulting E1 gene
CC deficient plasmid can be used as a gene delivery vector. The vectors can
CC be used for diagnosis or gene therapy, e.g. for treating conditions
CC characterised by hyper-proliferative cells (e.g. tumours), genetic
CC diseases (e.g. Huntington's disease, Tay-Sachs disease, or sickle cell
CC disease), or infections (e.g. HIV infection). They can also be used for
CC in vitro production of biologically active proteins. (Updated on 25-MAR-
CC 2003 to correct PI field.)

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XX	Sequence	11152 BP; 2877 A; 2520 C; 2729 G; 3026 T; 0 U; 0 Other;	
SQL	Query Match	100.0%; Score 2594; DB 2; Length 11152;	
	Best Local Similarity	100.0%; Pred. No. 0;	
	Matches 2594; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	ATCGATCTTAACCTGCGACGAGCGTGGCTTTCCACCCAGTGAACGACGAGATGAAAGGGT	60
DB	1825	ATCGATCTTAACCTGCGACGAGCGTGGCTTTCCACCCAGTGAACGACGAGATGAAAGGGT	1884
QY	61	GAGAGTTTGTGTAAATTAATGTGAGACACCCCGGACGCTTTCAGTCTTGTCAATAT	120
DB	1885	GAGAGTTTGTGTAAATTAATGTGAGACACCCCGGACGCTTTCAGTCTTGTCAATAT	1944
QY	121	CACCGGAGAAATACGGGGGACCCAGATTTATGTGTCCGTTTGCTATATAGAGACCTGT	180
DB	1945	CACCGGAGAAATACGGGGGACCCAGATTTATGTGTCCGTTTGCTATATAGAGACCTGT	2004
QY	181	GGCATGTTTGTCTACAGTAAGTAAATTAATGGCAGTGGGTGATAGTGTGGTTTG	240
DB	2005	GGCATGTTTGTCTACAGTAAGTAAATTAATGGCAGTGGGTGATAGTGTGGTTTG	2064
QY	241	GTGTGTAATTTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT	300
DB	2065	GTGTGTAATTTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT	2124
QY	301	TTTTTTTAAAGTCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCGAAACCGGAGCTG	360
DB	2125	TTTTTTTAAAGTCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCGAAACCGGAGCTG	2184
QY	361	CAAGACCTACCCGCGTCTTAAATTTGCGCTGATCTTGAAGCCGCGCATCACTG	420
DB	2185	CAAGACCTACCCGCGTCTTAAATTTGCGCTGATCTTGAAGCCGCGCATCACTG	2244
QY	421	TGTCTAGAGATGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	480
DB	2245	TGTCTAGAGATGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	2304
QY	481	CTGAGATACACCCGCGTGTCTGACCTGAGCCTGAGCCCGAGCCGAAACCGGAGCTG	540
DB	2305	CTGAGATACACCCGCGTGTCTGACCTGAGCCTGAGCCCGAGCCGAAACCGGAGCTG	2364
QY	541	GGCGTGGCAGGCTGTGATATGATGAGGAGCTTGTCTTAAAGAGCTGGGCACTTTGG	600
DB	2365	GGCGTGGCAGGCTGTGATATGATGAGGAGCTTGTCTTAAAGAGCTGGGCACTTTGG	2424
QY	601	ACTGAGCTGTAAACGCCCCAGGCCATTAAGGTGAACCTGTGATTGCTGTGTGTTAA	660
DB	2425	ACTGAGCTGTAAACGCCCCAGGCCATTAAGGTGAACCTGTGATTGCTGTGTGTTAA	2484
QY	661	CGCCTTTTGTGCTGAATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	720
DB	2485	CGCCTTTTGTGCTGAATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	2544
QY	721	TGCATGGCGGTAAATGAGGCGGCTTAAAGGATTAATTAATTAATTAATTAATTAAT	780
DB	2545	TGCATGGCGGTAAATGAGGCGGCTTAAAGGATTAATTAATTAATTAATTAATTAAT	2604
QY	781	TGGTAAATCTGACCTGAGAGGCTTGGAGTGTGGAAGATTTTTCCTGTGTGCTAA	840
DB	2605	TGGTAAATCTGACCTGAGAGGCTTGGAGTGTGGAAGATTTTTCCTGTGTGCTAA	2664
QY	841	ACTTGTGGAACAGAGCTTAAACAGTAACCTTGTGTTTGGAGTTTCTGTGGGGCTCAT	900
DB	2665	ACTTGTGGAACAGAGCTTAAACAGTAACCTTGTGTTTGGAGTTTCTGTGGGGCTCAT	2724
QY	901	CCGAGGCAAGTTAGTCTGCAAGATTAAGAGAGATTAACAAGTGGGATTTGAAGACTTT	960
DB	2725	CCGAGGCAAGTTAGTCTGCAAGATTAAGAGAGATTAACAAGTGGGATTTGAAGACTTT	2784
QY	961	TGAATCTGTGTGAGCTGTGTTGATCTTTGATCTGGGTCAACAGGCGCTTTTCAAG	1020

DB	2785	TGAATCTGTGTGAGCTGTGTTGATCTTTGATCTGGGTCAACAGGCGCTTTTCAAG	2844
QY	1021	AGAGGTCAATCAAGCTTTTGATTTTTCACACCGGGGCGGCTGCTGTGTTGCTT	1080
DB	2845	AGAGGTCAATCAAGCTTTTGATTTTTCACACCGGGGCGGCTGCTGTGTTGCTT	2904
QY	1081	TTTTAGTTTAAAGATTAATGAGAGGAAACCATGTGAGCGGGGTACTCTGC	1140
DB	2905	TTTTAGTTTAAAGATTAATGAGAGGAAACCATGTGAGCGGGGTACTCTGC	2964
QY	1141	TGGAATTTCTGGCAATGATCTGTGAGAGCGGTGTGAGACACAAGATTCCTGCTAC	1200
DB	2965	TGGAATTTCTGGCAATGATCTGTGAGAGCGGTGTGAGACACAAGATTCCTGCTAC	3024
QY	1201	TGTTGTCTTCCGTCGCGCGGGAATTAATCCGACGGAAGAGACGACGACAGAGAG	1260
DB	3025	TGTTGTCTTCCGTCGCGCGGGAATTAATCCGACGGAAGAGACGACGACAGAGAG	3084
QY	1261	AGCCGAGGGGGGGGGGAGAGACAGCCCATGGAACCCGAGAGCCGGCTTGACCTTC	1320
DB	3085	AGCCGAGGGGGGGGGGAGAGACAGCCCATGGAACCCGAGAGCCGGCTTGACCTTC	3144
QY	1321	GGGAATGAATGTGTACAGGTGGCTGAACCTGATTCAGAACTGAGACGATTTGACAA	1380
DB	3145	GGGAATGAATGTGTACAGGTGGCTGAACCTGATTCAGAACTGAGACGATTTGACAA	3204
QY	1381	TACAGAGATGGCGAGGCTTAAAGGGGTTAAAGAGAGCGGGGGGCTGTGAGGCTAC	1440
DB	3205	TACAGAGATGGCGAGGCTTAAAGGGGTTAAAGAGAGCGGGGGGCTGTGAGGCTAC	3264
QY	1441	AGAGAGGCTGAGAAATCTAGCTTTTAACTTAATGACACAGACACGCTCTGATATTAC	1500
DB	3265	AGAGAGGCTGAGAAATCTAGCTTTTAACTTAATGACACAGACACGCTCTGATATTAC	3324
QY	1501	TTTTCAACAGATCAAGATTAATTCGCTAATGATGATCTGTGCGCGCAAGTATTC	1560
DB	3325	TTTTCAACAGATCAAGATTAATTCGCTAATGATGATCTGTGCGCGCAAGTATTC	3384
QY	1561	CATAGACAGCTGACCACTTAATGCTGTGACGACGAGGAGATTTTGAAGGCTAATTAG	1620
DB	3385	CATAGACAGCTGACCACTTAATGCTGTGACGACGAGGAGATTTTGAAGGCTAATTAG	3444
QY	1621	GGTATATGCAAGGTGGCACTTAGGCGCAGATTGCAATGACAAATCAAGATCACTTGTAA	1680
DB	3445	GGTATATGCAAGGTGGCACTTAGGCGCAGATTGCAATGACAAATCAAGATCACTTGTAA	3504
QY	1681	TATCAGAAATTTGCTACATTTTGTGGAAACGGGCGGAGGTGAGATATTAAGAGGA	1740
DB	3505	TATCAGAAATTTGCTACATTTTGTGGAAACGGGCGGAGGTGAGATATTAAGAGGA	3564
QY	1741	TAGGTTGCTTTTGAATGTAGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1800
DB	3565	TAGGTTGCTTTTGAATGTAGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	3624
QY	1801	GGTGTATTAATGAATGATGATTAATGAGCCCAATTTTAAAGCGGTATCTGTGC	1860
DB	3625	GGTGTATTAATGAATGATGATTAATGAGCCCAATTTTAAAGCGGTATCTGTGC	3684
QY	1861	CAATACCAACCTTAATCTTACACGCTGAAGCTTCTAGGGTTTAAACAATCTCTGTGGA	1920
DB	3685	CAATACCAACCTTAATCTTACACGCTGAAGCTTCTATAGGGTTTAAACAATCTCTGTGGA	3744
QY	1921	AGCTTGACCGATTAAGGTTTCGGGGCTGTGCTTTTAACTGCTGTGGAAGGGGGTGT	1980
DB	3745	AGCTTGACCGATTAAGGTTTCGGGGCTGTGCTTTTAACTGCTGTGGAAGGGGGTGT	3804
QY	1981	GTGTGCGCCCAAAACAGAGGCTTCAATTAAGAAATGCTCTTTTGAAGGTGATCTTGGG	2040
DB	3805	GTGTGCGCCCAAAACAGAGGCTTCAATTAAGAAATGCTCTTTTGAAGGTGATCTTGGG	3864
QY	2041	TATCTGTCTGAGGTAATCTCCAGGGTGGCCACAATGTGGCTTCGACTGTGTGCTT	2100
DB	3865	TATCTGTCTGAGGTAATCTCCAGGGTGGCCACAATGTGGCTTCGACTGTGTGCTT	3924

Qy	210.	CATGCTGTGTAAAAAGGTGGCTGTGATTTAAAGCAATPAACAATGGTATGTGGCACTGCGAGA	2160
Db	3925	CATGCTGTGTAAAAAGGTGGCTGTGATTTAAAGCAATPAACAATGGTATGTGGCACTGCGAGA	3984
Qy	2161	CAGGGCTCTCAATGTGTGAACCTGCTCGGACCGGCAACTGTCACTGCTGAAAGACATTTCA	2220
Db	3985	CAGGGCTCTCAATGTGTGAACCTGCTCGGACCGGCAACTGTCACTGCTGAAAGACATTTCA	4044
Qy	2221	CGTAGCAGCAACTCTGCGAAGGCTGGCCAGTGTGAGATTAACATATCACTGAACCCGTG	2280
Db	4045	CGTAGCAGCAACTCTGCGAAGGCTGGCCAGTGTGAGATTAACATATCACTGAACCCGTG	4104
Qy	2281	TTGCTTGCAATTTGGGTAAACAGAGGGGGGTGTTCCTACTTACCAATGCAATTTGAGTCA	2340
Db	4105	TTGCTTGCAATTTGGGTAAACAGAGGGGGGTGTTCCTACTTACCAATGCAATTTGAGTCA	4164
Qy	2341	CACATAAGATTTGTGCTTAGCCCGAGACATGTCCAAAGTGAACCTGAACCGGGGTGTTTGA	2400
Db	4165	CACATAAGATTTGTGCTTAGCCCGAGACATGTCCAAAGTGAACCTGAACCGGGGTGTTTGA	4224
Qy	2401	CATGACCATTGAAGATCTGGAAGGTGCTGAGGTACGATGAGACCCGCAACAGGTGCAGACC	2460
Db	4225	CATGACCATTGAAGATCTGGAAGGTGCTGAGGTACGATGAGACCCGCAACAGGTGCAGACC	4284
Qy	2461	CTGCGAGTGTGGCGGTAAACATATTAGGAACCAAGCTGTGATGCTGATGTGAATGCCAGGA	2520
Db	4285	CTGCGAGTGTGGCGGTAAACATATTAGGAACCAAGCTGTGATGCTGATGTGAATGCCAGGA	4344
Qy	2521	GCTGAGGCCCGCATCACTGGTGTCTGGGCTGCAACCGGCGCTGAGTTGGCTCTAGCAGTGA	2580
Db	4345	GCTGAGGCCCGCATCACTGGTGTCTGGGCTGCAACCGGCGCTGAGTTGGCTCTAGCAGTGA	4404
Qy	2581	AGATTACGATTTGAG	2594
Db	4405	AGATTACGATTTGAG	4418

RESULT	9
AAAS9047	
ID	AAAS9047 standard; DNA; 11152 BP.
AC	AAAS9047;
XX	
DT	07-NOV-2000 (first entry)
XX	
DE	Nucleotide sequence of B1-expressing plasmid pDEX/B1.
XX	
KW	Adenovirus; tripartite leader; adenovirus vector particle; gene delivery;
XX	B1 gene; ss.
OS	Synthetic.
OS	Mastadenovirus.
XX	
PN	MO200042208-A1.
PD	20-JUL-2000.
XX	
PF	14-JAN-2000; 2000WO-EP000265.
XX	
PR	14-JAN-1999; 99US-0115920P.
XX	
PA	(NONS) NOVARTIS AG.
PA	(NONS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
EA	(SCRI) SCRIPPS RES INST.
XX	
PI	Nemerow GR, Von Seggern DJ, Hallenbeck PL, Stevenson SC;
XX	Skripchenko Y,
DR	WPI; 2000-476068/41.
XX	
PT	New nucleic acid comprising an adenovirus tripartite leader nucleotide for producing high-capacity and targeted vectors for adenovirus-based

PT	gene therapy.
XX	
P8	Example 1, Page 156-159; 212pp; English.
XX	
CC	The specification describes a nucleic acid molecule comprising an
CC	adenovirus (AV) tripartite leader (T _{PL}) nucleotide with a sequence
CC	comprising two different T _{PL} exons or three same or different T _{PL} exons.
CC	The nucleic acid is used to produce an adenovirus vector particle,
CC	deliver an exogenous gene to a target cell, pseudotype recombinant viral
CC	vectors, target an adenovirus vector to a cell, produce a modified
CC	adenovirus, deliver a heterologous gene to an animal and produce a
CC	gates adenoviral vector particle. The present sequence represents an E1
CC	-expressing plasmid, which is used for complementation of E1-gene deleted
CC	adenoviruses
XX	
SQ	Sequence 11152 BP; 2877 A; 2520 C; 2729 G; 3026 T; 0 U; 0 Other;
Query Match:	100.0%; Score 2594; DB 3; Length 11152;
Best Local Similarity:	100.0%; Pred. No. 0;
Matches 2594;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY	1	ATCATCTTACCTGCAACGAGGCTGGCTTTCCACCGAGTGCAGACGAGTAAGAGGGT	60
Dp	1825	ATCATCTTACCTGCAACGAGGCTGGCTTTCCACCGAGTGCAGACGAGTAAGAGGGT	1888
OY	61	GAGGAGTTTGTGTAGATTATATGTGAGACACCCGGGACGGTTGCAGTCTTGTCATTAT	120
Dp	1885	GAGGAGTTTGTGTAGATTATATGTGAGACACCCGGGACGGTTGCAGTCTTGTCATTAT	1944
OY	121	CACCGAGGAATACGGGGGACCCAGATATATGTGTTGCTTGCATATAGAGACCTGT	180
Dp	1945	CACCGAGGAATACGGGGGACCCAGATATATGTGTTGCTTGCATATAGAGACCTGT	2004
OY	181	GGCATGTTTGTCTACAGTAAGTGAATTTATGGGCAGTGGGTGATAGAGTGGGTTTG	240
Dp	2005	GGCATGTTTGTCTACAGTAAGTGAATTTATGGGCAGTGGGTGATAGAGTGGGTTTG	2064
OY	241	GTCGTATATTTTTTTTTTAAATTTTACAGTTTGTGGTTTAAAGAAATTTGTATTTGGA	300
Dp	2065	GTCGTATATTTTTTTTTTAAATTTTACAGTTTGTGGTTTAAAGAAATTTGTATTTGGA	2124
OY	301	TTTTTTTTTAAAGGTCTGTGTCTGACCTGAGCCTGAGCCCGACGAACCGAGCCTG	360
Dp	2125	TTTTTTTTTAAAGGTCTGTGTCTGACCTGAGCCTGAGCCCGACGAACCGAGCCTG	2184
OY	361	CAAGACCTACCCGCGCTCTAAAATGGGGCTGTATCTGAGAGCGCCGACATCACCTG	420
Dp	2185	CAAGACCTACCCGCGCTCTAAAATGGGGCTGTATCTGAGAGCGCCGACATCACCTG	2244
OY	421	TGTTTAAAGATGCATATGATATGTAACGATAGCTGTGACTCCGGTCTTCTTAACACACTC	480
Dp	2245	TGTTTAAAGATGCATATGATATGTAACGATAGCTGTGACTCCGGTCTTCTTAACACACTC	2304
OY	481	CTGAGATACACCCGGTGGTCCCGCTGTGCCCATTAACACAGTTGCCGTGAGAGTTGGTG	540
Dp	2305	CTGAGATACACCCGGTGGTCCCGCTGTGCCCATTAACACAGTTGCCGTGAGAGTTGGTG	2364
OY	541	GGCGTCCGCAAGCGCTGTGGAATGATTCGAGGACTTGTCTTAAAGAGCTGGGGCAACTTTTG	600
Dp	2365	GGCGTCCGCAAGCGCTGTGGAATGATTCGAGGACTTGTCTTAAAGAGCTGGGGCAACTTTTG	2424
OY	601	ACTTGAAGCTGTAAACGCCCGAGGCAATAAGGTGTAAACCTGTGATTCGTGTGGTTAA	660
Dp	2425	ACTTGAAGCTGTAAACGCCCGAGGCAATAAGGTGTAAACCTGTGATTCGTGTGGTTAA	2484
OY	661	CGCCTTGTGTGCTGAATGAGTTGATGTAAATTTAATAAGGTGAGATATGTTTAACT	720
Dp	2485	CGCCTTGTGTGCTGAATGAGTTGATGTAAATTTAATAAGGTGAGATATGTTTAACT	2544
OY	721	TGCAATGCGGTAAATATGGGGCGGGCTTAAAGGGTATATATATCCGCGTGGCTATATCT	780
Dp	2545	TGCAATGCGGTAAATATGGGGCGGGCTTAAAGGGTATATATATCCGCGTGGCTATATCT	2604

QY 781 TGGTTACATCTGACCTCATGAGAGCTTGGAGTGTGGAGATTTTCTGCTGTGCGTA 840
DB 2605 TGGTTACATCTGACCTCATGAGAGCTTGGAGTGTGGAGATTTTCTGCTGTGCGTA 2664
QY 841 ACTTGTGGAACAGAGCTCTAACAGTACCTCTTGTGTTTGGAGCTTCTGTGGGCTCAT 900
DB 2665 ACTTGTGGAACAGAGCTCTAACAGTACCTCTTGTGTTTGGAGCTTCTGTGGGCTCAT 2724
QY 901 CCCAGCGAAAGTTAAGTCTGAGAAATTAAGGAGATTAAGTGGGAAATTTGAAGACTT 960
DB 2725 CCCAGCGAAAGTTAAGTCTGAGAAATTAAGGAGATTAAGTGGGAAATTTGAAGACTT 2784
QY 961 TGAATCTGTGGTGAAGCTTGTGATCTTGTGAATCTGGTCAACAGACGCTTTTCCAG 1020
DB 2785 TGAATCTGTGGTGAAGCTTGTGATCTTGTGAATCTGGTCAACAGACGCTTTTCCAG 2844
QY 1021 AGAAGGTCAATCAGACCTTGGATTTTTCACACCGGGGCGCGCTGCGGCTGTGCTT 1080
DB 2845 AGAAGGTCAATCAGACCTTGGATTTTTCACACCGGGGCGCGCTGCGGCTGTGCTT 2904
QY 1081 TTTTGAAGTTTATTAAGATTAATGAGCGAAGAACCCATCTGAGCGGGGGTAACTGC 1140
DB 2905 TTTTGAAGTTTATTAAGATTAATGAGCGAAGAACCCATCTGAGCGGGGGTAACTGC 2964
QY 1141 TGGATTTTCTGGCCATGCTGTGAGAGCGGTTGTGAGACACAGAAATGCGCTGTAC 1200
DB 2965 TGGATTTTCTGGCCATGCTGTGAGAGCGGTTGTGAGACACAGAAATGCGCTGTAC 3024
QY 1201 TGTGTCTTCGTCGCCCGGCGATTAATCCGAGGAGAGACACAGAGAGAGAG 1260
DB 3025 TGTGTCTTCGTCGCCCGGCGATTAATCCGAGGAGAGACACAGAGAGAGAGAG 3084
QY 1261 AAGGACGCGCGCGGAGAGAGACCCATGGAACCCGAGAGCGGCTTGACCTC 1320
DB 3085 AAGGACGCGCGCGGAGAGAGACCCATGGAACCCGAGAGCGGCTTGACCTC 3144
QY 1321 GGAATGATTTGTGACAGTGTGCTGAATCTGATCCAGAACTGAGACGATTTTGACAT 1380
DB 3145 GGAATGATTTGTGACAGTGTGCTGAATCTGATCCAGAACTGAGACGATTTTGACAT 3204
QY 1381 TACAGAGATGAGGCGGCTAAAGGGGGTAAAGGGAGCGGGGGGCTTGTGAGGCTAC 1440
DB 3205 TACAGAGATGAGGCGGCTAAAGGGGGTAAAGGGAGCGGGGGGCTTGTGAGGCTAC 3264
QY 1441 AGAGAGGCTTGAAGTCTTAAAGCTTAAATGACAGACCGTCTCCAGTGAATTAC 1500
DB 3265 AGAGAGGCTTGAAGTCTTAAAGCTTAAATGACAGACCGTCTCCAGTGAATTAC 3324
QY 1501 TTTTCAACAGATCAAGATTAATTTGCGCTAATGAGCTTGAATCTGCGCGAGAGTATTC 1560
DB 3325 TTTTCAACAGATCAAGATTAATTTGCGCTAATGAGCTTGAATCTGCGCGAGAGTATTC 3384
QY 1561 CATAGAGCAGCTGACCACTTAATCTGCTGAGACCAAGGGATGATTTTGAAGGAGCTATTAG 1620
DB 3385 CATAGAGCAGCTGACCACTTAATCTGCTGAGACCAAGGGATGATTTTGAAGGAGCTATTAG 3444
QY 1621 GGTATATGCAAAAGTGGACCTTAAGGCAGATTGCAAGTACAGATCAGCAAACTGTAAA 1680
DB 3445 GGTATATGCAAAAGTGGACCTTAAGGCAGATTGCAAGTACAGATCAGCAAACTGTAAA 3504
QY 1681 TATCAGGAATTTGTGCTACATTTCTGGGAAACGGGGCGAGGTGAGATAGATACGAGAGA 1740
DB 3505 TATCAGGAATTTGTGCTACATTTCTGGGAAACGGGGCGAGGTGAGATAGATACGAGAGA 3564
QY 1741 TAGGGTGCCCTTAAATGATGATTAATATATGTCGGCGGGGGTCTTGGCATGGAACG 1800
DB 3565 TAGGGTGCCCTTAAATGATGATTAATATATGTCGGCGGGGGTCTTGGCATGGAACG 3624
QY 1801 GGTGTTATTAAGATGATGATTAAGTTTCTGAGCCCAATTTTAAAGGATACGGTCTTCTGAG 1860
DB 3625 GGTGTTATTAAGATGATGATTAAGTTTCTGAGCCCAATTTTAAAGGATACGGTCTTCTGAG 3684
QY 1861 CAATACCAACTTATCTCAACGGGTAAAGCTTCTATGAGTTTAAACAATACCTGTGTGA 1920

DB 3685 CAATACCAACTTATCTCAACGGGTAAAGCTTCTATGAGTTTAAACAATACCTGTGTGA 3744
QY 1921 AGCTTGACCGATGTAAGGTTTCGGGGCTGTGCTTTTAACTGCTGTGGAAGGGGTGCT 1980
DB 3745 AGCTTGACCGATGTAAGGTTTCGGGGCTGTGCTTTTAACTGCTGTGGAAGGGGTGCT 3804
QY 1981 GTGTGCCCCCAAAAGCAGGGCTTCAATTAAAGAAATGCTCTTTGAAAGGTACCTTGGG 2040
DB 3805 GTGTGCCCCCAAAAGCAGGGCTTCAATTAAAGAAATGCTCTTTGAAAGGTACCTTGGG 3864
QY 2041 TATCCTGTGAGGGTAACTCCAGGGTGGCCCAATGTGCTCCGACTGTGTTGCTT 2100
DB 3865 TATCCTGTGAGGGTAACTCCAGGGTGGCCCAATGTGCTCCGACTGTGTTGCTT 3924
QY 2101 CATGCTAGTAAAGCGTGTGATTAAGATTAACATGATATGTGGAACAATGCGAGGA 2160
DB 3925 CATGCTAGTAAAGCGTGTGATTAAGATTAACATGATATGTGGAACAATGCGAGGA 3984
QY 2161 CAGGGCTCTCAGATGTGACCTGTGGAACGGCAACTGTCACTGTGGAAGCAATTCA 2220
DB 3985 CAGGGCTCTCAGATGTGACCTGTGGAACGGCAACTGTCACTGTGGAAGCAATTCA 4044
QY 2221 CGTAGCCAGCCTCTCCGCAAGGCTGGCCAGTGTGAGCATTAACATTAAGTGAACCCGCTG 2280
DB 4045 CGTAGCCAGCCTCTCCGCAAGGCTGGCCAGTGTGAGCATTAACATTAAGTGAACCCGCTG 4104
QY 2281 TTCCTTGATTTGGGTAAACAGAGGGGGTGTCTTAACCTTAACATATGCAATTTGAATCA 2340
DB 4105 TTCCTTGATTTGGGTAAACAGAGGGGGTGTCTTAACCTTAACATATGCAATTTGAATCA 4164
QY 2341 CACTAAGATTTTGTGAGGCCCCAGAGCATGTCCAAAGTGAACCTGAACGGGGTGTGGA 2400
DB 4165 CACTAAGATTTTGTGAGGCCCCAGAGCATGTCCAAAGTGAACCTGAACGGGGTGTGGA 4224
QY 2401 CATGACCATGAAGATCTGGAAGGTGTGAGGTACGATGAGACCCGCAACAGGTGCAAGC 2460
DB 4225 CATGACCATGAAGATCTGGAAGGTGTGAGGTACGATGAGACCCGCAACAGGTGCAAGC 4284
QY 2461 CTGCGAGTGTGCGGTAAACATATTAGGAACACAGCTGTGATGCTGATGTGACCGGAGA 2520
DB 4285 CTGCGAGTGTGCGGTAAACATATTAGGAACACAGCTGTGATGCTGATGTGACCGGAGA 4344
QY 2521 GCTGAGGCCCGATCACTTGTGTGCTGCGCTGCAACCGGCTGAGTTTGGCTTAAGCGATGA 2580
DB 4345 GCTGAGGCCCGATCACTTGTGTGCTGCGCTGCAACCGGCTGAGTTTGGCTTAAGCGATGA 4404
QY 2581 AGATACAGATTGAG 2594
DB 4405 AGATACAGATTGAG 4418

RESULT 10
ABA94256
ID ABA94256 standard; DNA; 11152 BP.
XX ABA94256;
XX
XX 13-MAR-2002 (first entry)
XX
DE Nucleotide sequence of expression plasmid pDEX/E1.
XX
XX Adenovirus; Invertebr terminal repeat sequence; ITRs; ocular disease;
KW fiber protein; photoreceptor; rhodopsin; strabismic disease gene; SMDG1;
KW optical; inflammatory; antidiabetic; cytostatic;
XX gene therapy; ss.
XX
XX Synthetic.
XX
XX WO200183729-A2.
XX
XX 08-NOV-2001.
XX

PF 30-APR-2001 / 2001WO-EP004863.
 XX 01-MAY-2000 / 2000US-00562934.
 XX (NOVS) NOVARTIS AG.
 PA (SCRI) SCRIPPS RES INST.
 PA (NEME) NEMEROW G R.
 PA (VSEG/) VON SEGGERN D J.
 PA (FRIE/) FRIEDLANDER M.
 PI Nemerow GR, Von Seggern DJ, Friedlander M;
 DR WPI, 2002-082846/11.
 XX Polynucleotide for making vectors, useful for treating ocular diseases,
 PT e.g., retinitis pigmentosa, comprises adenovirus inverter terminal repeat
 XX sequences, packaging signal and photoreceptor-specific promoter.
 XX
 XX Example 1, Page 110-113; 149pp; English.
 CC The invention provides an isolated polynucleotide comprising adenovirus
 CC (AV) inverter terminal repeat sequences (ITRS), AV packaging signal
 CC operatively linked to ITRS and a photoreceptor-specific promoter. A
 CC recombinant AV vector (AVV) comprising the polynucleotide is useful for
 CC targeted delivery of a gene product to the eye (especially to the
 CC vitreous cavity), for treating an ocular disease, e.g., retinal
 CC degenerative disease, retinitis pigmentosa, Stargardt's disease, diabetic
 CC retinopathies, retinal vascularizations, and retinoblastoma, of a mammal
 CC preferably human. The AAV comprises a fiber protein that specifically or
 CC selectively binds to receptors that are expressed on cells (preferably
 CC photoreceptors in the eye). Preferably, the recombinant virus comprises a
 CC fiber protein from an adenovirus type D subgroup or is a chimeric protein
 CC containing a portion of the N-terminus of an adenovirus type 2 or type 5
 CC penton, and the therapeutic product is a trophic factor, an anti-
 CC apoptotic factor, gene encoding a rhodopsin protein, a wild-type
 CC Stargardt disease gene (STGD1), an anti-cancer agent and a protein that
 CC regulates expression of a photoreceptor specific gene product. The viral
 CC nucleic acid of AAV comprises ITRS and packaging signal derived from AAV
 CC subgroup B or C, especially an AV type 2 or type 5. AAV is also useful
 CC for targeted gene therapy, where the vector comprises an AV type 37 fiber
 CC protein or its portion, and selectively transduces photoreceptors and
 CC delivers a gene product encoded by AAV. The present sequence represents
 CC an expression plasmid pDex/BI containing the adenovirus BI gene
 XX
 XX Sequence 11152 BP, 2877 A; 2520 C; 2729 G; 3026 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 2594; DB 6; Length 11152;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGATCTTACCTGCAAGAGGCTGCTTTCACCCAGTGAACAAGAGAGAGT 60
 DB 1825 ATGATCTTACCTGCAAGAGGCTGCTTTCACCCAGTGAACAAGAGAGT 1884
 QY 61 GAGAGTTTGTGTAAGTATGAGACACCCCGGAGACGGTTCAGTCTTGTCAATTAT 120
 DB 1885 GAGAGTTTGTGTAAGTATGAGACACCCCGGAGACGGTTCAGTCTTGTCAATTAT 1944
 QY 121 CACCGAGAAATACGGGGGACCCAGATATTATGTTCCGCTTTCATATAGAGACCTGT 180
 DB 1945 CACCGAGAAATACGGGGGACCCAGATATTATGTTCCGCTTTCATATAGAGACCTGT 2004
 QY 181 GGCATGTTTGTCTACATTAAGTAAATTAAGGACATGAGTATAGAGTGTGGGTTTG 240
 DB 2005 GGCATGTTTGTCTACATTAAGTAAATTAAGGACATGAGTATAGAGTGTGGGTTTG 2064
 QY 241 GTGAGGTAATTTTTTTTAAATTTTACAGTTTGTGTTAAAGATTTTGTATTTGTA 300
 DB 2065 GTGAGGTAATTTTTTTTAAATTTTACAGTTTGTGTTAAAGATTTTGTATTTGTA 2124
 QY 301 TTTTAAAAAGGCTCTGTCTGAACCTGAGCTGAGCCGAGACCAAGAGGCTG 360
 DB 2125 TTTTAAAAAGGCTCTGTCTGAACCTGAGCTGAGCCGAGACCAAGAGGCTG 2184

QY 361 CAAGACCTACCCGCGCTCTAAAAATGCGCCTGCTATCTGAGACGCGCGACATCACTCG 420
 DB 2185 CAAGACCTACCCGCGCTCTAAAAATGCGCCTGCTATCTGAGACGCGCGACATCACTCG 2244
 QY 421 TGTCTTAAGAAATGCAATATGTAATGTAACGATAGCTGTGACTCGGTCCTTTTACACACTC 480
 DB 2245 TGTCTTAAGAAATGCAATATGTAATGTAACGATAGCTGTGACTCGGTCCTTTTACACACTC 2304
 QY 481 CTGAGATACACCCCGGTGTCCTGCTGATTTAAACAGTTGCGGTGAGAGTGGTG 540
 DB 2305 CTGAGATACACCCCGGTGTCCTGCTGATTTAAACAGTTGCGGTGAGAGTGGTG 2364
 QY 541 GCGCTGCGCAGGCTGTGAAATGTAATGAGACCTTCTTAAAGACCTGCGCAACTTTGG 600
 DB 2365 GCGCTGCGCAGGCTGTGAAATGTAATGAGACCTTCTTAAAGACCTGCGCAACTTTGG 2424
 QY 601 ACTTGAGCTGTAAACGCGCCAGGCGCATTAAGGTGTAACCTGTGATTTGCTGTGTTAA 660
 DB 2425 ACTTGAGCTGTAAACGCGCCAGGCGCATTAAGGTGTAACCTGTGATTTGCTGTGTTAA 2484
 QY 661 CGCCTTGTGTTGCTGATGATGATGATTAATTAAGGGTGAATTAATGTTTAAT 720
 DB 2485 CGCCTTGTGTTGCTGATGATGATGATTAATTAAGGGTGAATTAATGTTTAAT 2544
 QY 721 TGCATGCGGTGTAATGAGGCGGCGCTTAAAGGTAATTAATGCGCGTGGGCTAAATCT 780
 DB 2545 TGCATGCGGTGTAATGAGGCGGCGCTTAAAGGTAATTAATGCGCGTGGGCTAAATCT 2604
 QY 781 TGTGTAATCTGACCTGATGAGAGCTTGGAGAGTCTTGGAAAGATTTTCTGCTGTGCTA 840
 DB 2605 TGTGTAATCTGACCTGATGAGAGCTTGGAGAGTCTTGGAAAGATTTTCTGCTGTGCTA 2664
 QY 841 ACTTGCTGAACAGAGCTCTAACAGTACTCTTGTTTGAAGGTTCTGTGGGCTCAT 900
 DB 2665 ACTTGCTGAACAGAGCTCTAACAGTACTCTTGTTTGAAGGTTCTGTGGGCTCAT 2724
 QY 901 CCCAGCAAAAGTTATGCTGCAAAATTAAGAGATTAACAATGGGAATTTGAAGAGCTTT 960
 DB 2725 CCCAGCAAAAGTTATGCTGCAAAATTAAGAGATTAACAATGGGAATTTGAAGAGCTTT 2784
 QY 961 TGAATTCCTGTGAGAGCTGTTGATTTTGAATCTGAGTCAACAGGCGCTTTCCAG 1020
 DB 2785 TGAATTCCTGTGAGAGCTGTTGATTTTGAATCTGAGTCAACAGGCGCTTTCCAG 2844
 QY 1021 AGAAGGTCATCAAGACTTTGATTTTTCACACCGGGGCGGCTGCGGCTGTGCTT 1080
 DB 2845 AGAAGGTCATCAAGACTTTGATTTTTCACACCGGGGCGGCTGCGGCTGTGCTT 2904
 QY 1081 TTTTGAATTTTAAAGATTAATGAGCGAAGAAACCAATCTGAGCGGGGGTACTGTC 1140
 DB 2905 TTTTGAATTTTAAAGATTAATGAGCGAAGAAACCAATCTGAGCGGGGGTACTGTC 2964
 QY 1141 TGAATTTTCTGGCAGTCACTGTGAGAGCGGTTGTGAACACCAAGATTCGCTGCTAC 1200
 DB 2965 TGAATTTTCTGGCAGTCACTGTGAGAGCGGTTGTGAACACCAAGATTCGCTGCTAC 3024
 QY 1201 TGTGTCTTCCTGCGCGCGCGCATTAATACGACGAGAGACAGACAGACAGAGAGG 1260
 DB 3025 TGTGTCTTCCTGCGCGCGCGCATTAATACGACGAGAGACAGACAGACAGAGAGG 3084
 QY 1261 AAGCCAGGCGGCGCGCGCAGAGACAGAGCCCATGAAACCCGAGAGCGGCTGGAACCTC 1320
 DB 3085 AAGCCAGGCGGCGCGCGCAGAGACAGAGCCCATGAAACCCGAGAGCGGCTGGAACCTC 3144
 QY 1321 GGGAAATGAATGTTGTAAGGTGTGCTGAATCTGTAATCCAGAACTGAGACGCAATTTTGA 1380
 DB 3145 GGGAAATGAATGTTGTAAGGTGTGCTGAATCTGTAATCCAGAACTGAGACGCAATTTTGA 3204
 QY 1381 TACAGAGATAGGCGAGGCGCTAAAGGAGGCTAAAGAGGAGCGGAGGCTTGTGAGGCTAC 1440
 DB 3205 TACAGAGATAGGCGAGGCGCTAAAGGAGGCTAAAGAGGAGCGGAGGCTTGTGAGGCTAC 3264

1441 AGAGAGGCTAGGAATCTAGCTTTAGCTTAATGACCAAGACACCGTCTGAGTATTAAC 1500
1501 TTTTCAACAGATCAAGATTAATTCGGCTAATGAGCTTTGATCTCTGGCCGACAAAGTATTC 1560
1561 CATAGAGAGCTACCACTTACCTGCGTGCAGCGAGGGAGATTTTGAAGAGGCTATTAG 1620
1621 GGTATATGCAAGAGGTGACCTTAGGCGCAGATTGCAAGTACAAATCGCAAACTTGTAAA 1680
1681 TATCAGGAATTTGTTGCTACATTTCTGGGAAACGGGGCCGAGGTGAGATTAATACGAGGA 1740
1741 TAGGGTGGCTTTTAGATAGTACATGAATTAATGATGGCCGGGGGCTTGGCATGAGACGG 1800
1801 GGTGTTATTATGAATGTAAGGTTTACTGCGCCCAATTTTACCGGTACGGTTTCTGGC 1860
1861 CAATACCAACCTTATCTTACACCGGTGTAAGCTTTATGAGGTTTAACAATACCTGTGGA 1920
1921 AGCTTGACCCGATTAAGGGTTCGGGGGCTGACCTTTTACTGCTGCGGAGGGGTGGT 1980
1981 GTGTGCGCCCAAAACAGAGGGCTTCAATTAGAATATGCTCTTTGAAGGTGATCCTTGGG 2040
2041 TATCTGTCTGAGGTTAACTCCAGGGTCCGCCAATGTGGCTCCGACTGCTGTTGGTTC 2100
2101 CATGCTAGTGAAGAGCTGGGCTGTGATTAAAGCATTAATGATGATGCAACTGCGAGGA 2160
2161 CAGGCGCTCTCAGATGCTGACCTGCTCGGACGGCAATGTCTCACTGCTGAGAACCAATTCA 2220
2221 CGTAGCCAGCACTCTCCGAAAGGCTGGCCAGTGTGTTGAGCATTAATCATACCCGGCTG 2280
2281 TTCCTTGCATTTGGGTTAAGAGAGGGGGGTGTTCTCACTTACCAATGCAATTTGAGTCA 2340
2341 CACTAAGATATTGCTTGAAGCCGAGAGCATGTCCAAAGGTGAACCTGAACGGGGTGTTTGA 2400
2401 CATGACCATGAGATCTGGAAGGTCTGAGGTGCAATGAGACCCCGACCAAGGTGAGAC 2460
2461 CTGCGAGTGTGGGTTAAATATTTAGGAACGAGCTGTGATCTGGATGTGACCGAGGA 2520
2521 GCTGAGGCCCGATCACTGTGTGCTGACCCGCGCTGAGTTGGCTTACGAGTGA 2580

4345 GCTGAGGCCGATCACTGTGCTGCTGCGCCCTGACACCGCGCTGAGTTGGCTTACGATGA 4404
2581 AGATACAGATTGAG 2594
4405 AGATACAGATTGAG 4418
RESULT 11
ADB75153
ID ADB75153 standard; DNA; 11152 BP.
XX
AC ADB75153;
XX
DT 04-DEC-2003 (first entry)
XX
DE Plasmid pDEX/E1 DNA sequence.
KW ophthalmological; antiinflammatory; antidiabetic; gene therapy;
KW adenovirus inverted terminal repeat sequence;
KW adenovirus packaging signal; photoreceptor-specific promoter;
KW adenovirus type 37; adenovirus type D serotype; adenovirus type 2;
KW adenovirus type 5; photoreceptor; trophic factor; anti-apoptotic factor;
KW rhodopsin; wild-type Stargardt disease gene; STDB1; anti-cancer agent;
KW retinal degenerative disease; retinitis pigmentosa; Stargardt's disease;
KW diabetic retinopathy; retinal vascularisation; choroideraemia;
KW gyrate atrophy; macular dystrophy; retinoblastoma;
KW photoreceptor-restricted transgene expression;
KW recombinant adenovirus vector; adenovirus type 5; E1a; E1b; pDEX/E1;
KW plasmid; cyclic; circular; db.
XX
XX Synthetic.
OS Human adenovirus type 6.
XX
XX US2002193327-A1.
XX
XX 19-DEC-2002.
XX
XX 01-MAY-2001; 2001US-00847101.
XX
XX 01-MAY-2000; 2000US-00562934.
XX
XX (SCRI) SCRIPPS RES INST.
XX
XX Nemerow GR, Von Seggern DJ, Friedlander M;
XX
XX MPI; 2003-657234/62.
XX
XX Novel nucleic acids comprising adenovirus inverted terminal repeat
XX sequences, adenovirus packaging signals operatively linked to the
XX PT sequences and photoreceptor-specific promoters, useful for treating
XX PT retinitis pigmentosa.
XX
XX Example 1; Page 45-50; 106pp; English.
XX
XX The invention describes an isolated nucleic acid (I) comprising
XX CC adenovirus inverted terminal repeat sequence, an adenovirus packaging
XX CC signal operatively linked to the sequence, and a photoreceptor-specific
XX CC promoter. A Recombinant adenovirus vector (II) comprising (I) is useful
XX CC for targeted delivery of a gene product to the eye of a mammal which
XX CC involves administering (II) that comprises heterogeneous DNA encoding the
XX CC gene product or resulting in expression of the gene product, where the
XX CC recombinant virus comprises a fibre protein that specifically or
XX CC selectively binds to receptors that are expressed on cells which are
XX CC photoreceptors, in the eye. The recombinant virus comprises a fibre
XX CC protein which is an adenovirus type 37, from an adenovirus type D
XX CC serotype. The fibre is a chimeric protein containing a sufficient portion
XX CC of the N-terminus of an adenovirus type 2 or type 5 penton, and a sufficient
XX CC interaction with an adenovirus type 2 or type 5 penton, and a sufficient
XX CC portion of an adenovirus serotype D knob portion of the fiber for
XX CC selective binding to photoreceptors in the eye of a mammal. The
XX CC encapsulated nucleic acid comprises a photoreceptor-specific promoter
XX CC operatively linked to a nucleic acid comprising the therapeutic product


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DB      3625 GGTGTTATTGAAATGTAAGTTTAACTGCGCCCAATTTTACGGTCTTCTGCGC 3684
      |||
OY      1861 CAATAACAACCTTATCTTACACGGTGTAAAGCTTTATGCGTTTAAACAATCTGTGTGA 1920
      |||
DB      3685 CAATACCAACCTTATCTTACACGGTGTAAAGCTTTATGCGTTTAAACAATCTGTGTGA 3744
      |||
OY      1921 AGCCTGACCCGATGTAAGGTTTGGGGCTGTGCTTTTATCTGCTGTGGAAGGGGGTGT 1980
      |||
DB      3745 AGCCTGACCCGATGTAAGGTTTGGGGCTGTGCTTTTATCTGCTGTGGAAGGGGGTGT 3804
      |||
OY      1981 GTGTGCCCCCAAAAGACGGCTTCAATTAAGAAATGCTCTTTTGAAGGTGTACCTTGGG 2040
      |||
DB      3805 GTGTGCCCCCAAAAGACGGCTTCAATTAAGAAATGCTCTTTTGAAGGTGTACCTTGGG 3864
      |||
OY      2041 TATCTGTCTGAGGGTAACTCAAGGGTGGCCCAATGTGGCTCCGACTGTGTGTTGCTT 2100
      |||
DB      3865 TATCTGTCTGAGGGTAACTCAAGGGTGGCCCAATGTGGCTCCGACTGTGTGTTGCTT 3924
      |||
OY      2101 CATGCTAAGTAAAGCTGGCTGTGATTAAGCATTAACATGTATGTGGCACTGGGAGGA 2160
      |||
DB      3925 CATGCTAAGTAAAGCTGGCTGTGATTAAGCATTAACATGTATGTGGCACTGGGAGGA 3984
      |||
OY      2161 CAGGCGCTCTCAGATGCTGACCTGTGCGACGGCAACTGTCACTGTGTAAGACCAATTCA 2220
      |||
DB      3985 CAGGCGCTCTCAGATGCTGACCTGTGCGACGGCAACTGTCACTGTGTAAGACCAATTCA 4044
      |||
OY      2221 CGTAGCCACCACTCTCGCAAGGCTGTGCGCAAGTGTGTAAGCATATCTGACCCGCTG 2280
      |||
DB      4045 CGTAGCCACCACTCTCGCAAGGCTGTGCGCAAGTGTGTAAGCATATCTGACCCGCTG 4104
      |||
OY      2281 TTCCTTGCAATTTGGGTAACAAGAGGGGGGTGTTCCACTTCCAAATGCAATTTGAGTCA 2340
      |||
DB      4105 TTCCTTGCAATTTGGGTAACAAGAGGGGGGTGTTCCACTTCCAAATGCAATTTGAGTCA 4164
      |||
OY      2341 CACTAAGATATTTGCTTGAGCCCGAGAGCATGTTCAAAGTGAACCTGAAACGGGGTGTTTGA 2400
      |||
DB      4165 CACTAAGATATTTGCTTGAGCCCGAGAGCATGTTCAAAGTGAACCTGAAACGGGGTGTTTGA 4224
      |||
OY      2401 CATGACCATGAAGATGTGAAGGTGTGTAAGTTCAGATGAGACCCCGACCAAGTGCAGACC 2460
      |||
DB      4225 CATGACCATGAAGATGTGAAGGTGTGTAAGTTCAGATGAGACCCCGACCAAGTGCAGACC 4284
      |||
OY      2461 CCGCAGTGTGGCGGTAAACATTTATGGAACCAAGCCTGTGATGCTGGATGTGACCGAAGGA 2520
      |||
DB      4285 CCGCAGTGTGGCGGTAAACATTTATGGAACCAAGCCTGTGATGCTGGATGTGACCGAAGGA 4344
      |||
OY      2521 GCTGAGGCCCGATCACTTGTGTGCTGCTGCAACCCGCGCTGAGTTTGCTTACGATGA 2580
      |||
DB      4345 GCTGAGGCCCGATCACTTGTGTGCTGCTGCAACCCGCGCTGAGTTTGCTTACGATGA 4404
      |||
OY      2581 AGATACAGATTGAG 2594
      |||
DB      4405 AGATACAGATTGAG 4418
      |||

RESULT 12
ADF48798 standard; DNA; 11152 BP.
ID      ADF48798
AC      ADF48798;
XX      12-FEB-2004 (first entry)
DT      XX
XX      E1 expressing plasmid pB4/Hygro.
DE      cytosolic; anti-HIV; gene therapy; HIV gene expression inhibitor;
XX      HIV gene expression activation; adenovirus tripartite leader; TPL;
XX      gutless adenoviral vector particle;
XX      helper-independent fiberless recombinant adenovirus vector;
XX      packaging cell line; pseudotyping; adenovirus vector; gene therapy;
XX      hereditary disorder; tumour; HIV infection; E1 transcription unit;
XX      E1-gene-deleted adenoviruses; hygromycin resistance; ds; circular;

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KM      cyclic.
XX
OS      Synthetic.
OS      Human adenovirus type 5.
XX
XX      US2003157688-A1.
XX
XX      21-AUG-2003.
XX
XX      14-JAN-2000; 2000US-00482682.
XX
XX      14-JAN-1999; 99US-0115920P.
XX      PR      26-JUN-2000; 2000US-00423783.
XX
XX      (VSEB/) VON SEGGERN D J.
XX      (NEMER/) NEMEROW G R.
XX      (HALL/) HALLENBECK P.
XX      (STEV/) STEVENSON S.
XX      (SKRI/) SKRIPCHENKO Y.
XX
XX      Von Seggern DJ, Nemerow GR, Hallenbeck P, Stevenson S;
PI      Skripchenko Y;
XX
XX      WPI; 2003-843463/78.
XX
XX      Novel isolated nucleic acid molecule useful for delivering heterologous
PT      gene to human or any animal, or for producing gutless adenoviral vector
PT      particle.
XX
XX      Example 1; SEQ ID NO 12; 157bp; English.
XX
XX      The invention describes an isolated nucleic acid molecule (I) comprising
CC      an adenovirus tripartite leader (TPL) nucleotide, the TPL nucleotide
CC      sequence comprising a first and second different TPL exons or first,
CC      second and third same or different TPL exons, the TPL exons chosen from
CC      CC complete or partial TPL exon 1, complete TPL exon 2 and complete TPL exon
CC      3. (I) is useful for delivering a heterologous gene to a human or any
CC      animal, or for producing a gutless adenoviral vector particle. A
CC      recombinant adenovirus particle (II) is useful for delivery of an
CC      exogenous gene to a target cell which involves contacting the cell with
CC      an amount of (II) sufficient to infect the cell. A helper-independent
CC      CC fiberless recombinant adenovirus vector genome (III) is useful for
CC      producing an adenovirus vector particle containing (III) which involves
CC      providing a packaging cell line which complements replication and
CC      packaging of the genome and (III) which is deficient in expressing
CC      sufficient functional fiber protein to support assembly of fiber
CC      containing particles and harvesting the particle produced by the cell
CC      CC line. (III) is useful for pseudotyping recombinant viral vectors which
CC      involves complementing a missing fiber gene of (III) or helper-dependent
CC      CC fiberless recombinant adenovirus vector genome by expressing in packaging
CC      cells a fiber gene from a different adenoviral serotype than the
CC      recombinant adenovirus vector. (III) is also useful for specifically
CC      targeting an adenovirus vector to a cell of choice. (I) is useful for
CC      gene therapy. (II) is useful for treating diseases such as hereditary
CC      disorder, and for reducing proliferation of tumour cells in a subject, or
CC      to disrupt HIV infection. This sequence represents the pBEX/E1 plasmid,
CC      an adenovirus E1 expressing plasmid containing a hygromycin resistance
CC      gene for complementation of E1-gene-deleted adenoviruses.
XX
XX      Sequence 11152 BP; 2877 A; 2520 C; 2729 G; 3026 T; 0 U; 0 Other;
SQ

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Query Match      100.0%; Score 2594; DB 10; Length 11152;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY      1 ATCGATCTTACCTGCCACGAGGCTGGCTTTCACCCAGTGAAGAGATGAAGAGGT 60
      |||
DB      1825 ATCGATCTTACCTGCCACGAGGCTGGCTTTCACCCAGTGAAGAGATGAAGAGGT 1884
      |||
OY      61 GAGGAGTTTGTGTTGATTAATGTGAAGCAACCCGGGACAGGTTGCAAGTCTGTCAATTAT 120
      |||
DB      1885 GAGGAGTTTGTGTTGATTAATGTGAAGCAACCCGGGACAGGTTGCAAGTCTGTCAATTAT 1944
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QY 121 CACGGAGGAATAGGGGACCCAGATATTATGTTGCTTGTCTATATGAGACCTGT 180
DB 1945 CACGGAGGAATAGGGGAGCCAGATATTATGTTGCTTGTCTATATGAGACCTGT 2004
QY 181 GGCATGTTTGTCTACAGTAAAGTAAATTTATGGCAGTGGTGATAGTGGTGGTTTG 240
DB 2005 GGCATGTTTGTCTACAGTAAAGTAAATTTATGGCAGTGGTGATAGTGGTGGTTTG 2084
QY 241 GTGGGTAAATTTTTTTTTTAATTTTAAAGTTTGTGGTTTAAAGATTGTGATGGA 300
DB 2065 GTGGGTAAATTTTTTTTTTAATTTTAAAGTTTGTGGTTTAAAGATTGTGATGGA 2124
QY 301 TTTTTTAAAGGTCCTGTGTCTGAACCTGAGCCCTGAGCCCGAAGAACCGGAGCTTG 360
DB 2125 TTTTTTAAAGGTCCTGTGTCTGAACCTGAGCCCTGAGCCCGAAGAACCGGAGCTTG 2184
QY 361 CAAGACCTAACCCGCTGCTTAAATGGCGCTGCTATCTGAGACGCCGACATCACTTG 420
DB 2185 CAAGACCTAACCCGCTGCTTAAATGGCGCTGCTATCTGAGACGCCGACATCACTTG 2244
QY 421 TGTCTAGAGAAATGCMAATAGTATGTAAGGATAGCTGTGACTCCGCTCTTAAACAACCTC 480
DB 2245 TGTCTAGAGAAATGCMAATAGTATGTAAGGATAGCTGTGACTCCGCTCTTAAACAACCTC 2304
QY 481 CTGAGATACACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
DB 2305 CTGAGATACACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2364
QY 541 GGCCTGCCAGGCTGTGGAATGTATCGAGACTTGTCTTAAAGACCTGGGCAACCTTTGG 600
DB 2365 GGCCTGCCAGGCTGTGGAATGTATCGAGACTTGTCTTAAAGACCTGGGCAACCTTTGG 2424
QY 601 ACTTGAAGCTGTAAAGCCGCCAGCCATTAAGGTGTAAACCTGTGATGTGGTGTGTAA 660
DB 2425 ACTTGAAGCTGTAAAGCCGCCAGCCATTAAGGTGTAAACCTGTGATGTGGTGTGTAA 2484
QY 661 CGCCTTGTGTGTGCTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 720
DB 2485 CGCCTTGTGTGTGCTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 2544
QY 721 TGCATGCGTGTAAATGGGCGGGGCTTAAAGGCTATTAATGCGCGTGGGCTAAATCT 780
DB 2545 TGCATGCGTGTAAATGGGCGGGGCTTAAAGGCTATTAATGCGCGTGGGCTAAATCT 2604
QY 781 TGGTTACATCTGACCTTCAAGAGGCTTGGAGTGTGGAGTGTGGAGTGTGGTGTGGA 840
DB 2605 TGGTTACATCTGACCTTCAAGAGGCTTGGAGTGTGGAGTGTGGAGTGTGGTGTGGA 2664
QY 841 ACTTGTCTGGAACAGAGCTCTTAACAGTACCTTGTGTTTGGAGTGTCTGTGGGCTCAT 900
DB 2665 ACTTGTCTGGAACAGAGCTCTTAACAGTACCTTGTGTTTGGAGTGTCTGTGGGCTCAT 2724
QY 901 CCCAGGCAAAAGTTAGTGTGACAGATTAAGAGATTAAGAGTGGGAATTTGAAGAGCTTT 960
DB 2725 CCCAGGCAAAAGTTAGTGTGACAGATTAAGAGATTAAGAGTGGGAATTTGAAGAGCTTT 2784
QY 961 TGAATCTGTGTGAGCTGTTGATTTCTTGAATCTGTGGTCAACAGGCGCTTTTCCAG 1020
DB 2785 TGAATCTGTGTGAGCTGTTGATTTCTTGAATCTGTGGTCAACAGGCGCTTTTCCAG 2844
QY 1021 AGAAGGTCATCAAGACTTTTGGATTTTTCACACCGGGGCGGCTGCGCTGTGCTT 1080
DB 2845 AGAAGGTCATCAAGACTTTTGGATTTTTCACACCGGGGCGGCTGCGCTGTGCTT 2904
QY 1081 TTTTGAATTTTAAAGATTAATGAGCGAAGAAACCATCTGAGCGGGGGGTAACTGTC 1140
DB 2905 TTTTGAATTTTAAAGATTAATGAGCGAAGAAACCATCTGAGCGGGGGGTAACTGTC 2964
QY 1141 TGAATTTTCTGGCCATCATCTGTGAGAGCGGTTGTGAGACACAAGAAATGCTGTCTAC 1200
DB 2965 TGAATTTTCTGGCCATCATCTGTGAGAGCGGTTGTGAGACACAAGAAATGCTGTCTAC 3024
QY 1201 TGTGTCTTCCGTCCGCCCGGCGATTAATACGAGAGGAGACAGACAGACAGAGAGG 1260

DB 3025 TGTGTCTTCCGTCCGCCCGGCGATTAATCCGAGGAGAGACAGACAGACAGAGAGG 3084
QY 1261 AAGCCAGCGCGCGCGCAGAGCAGAGCCCATGGAACCCGAGAGCCGCTGAGACCTTC 1320
DB 3085 AAGCCAGCGCGCGCGCAGAGCAGAGCCCATGGAACCCGAGAGCCGCTGAGACCTTC 3144
QY 1321 GGGATGAAATGTTGTACAGTGGCTGAACTGTATCCGAACCTGAGACGCATTTGACAT 1380
DB 3145 GGGATGAAATGTTGTACAGTGGCTGAACTGTATCCGAACCTGAGACGCATTTGACAT 3204
QY 1381 TACAGAGATGGGCGGCGTAAAGGGGGTAAAGAGGAGCGGGGCTGTGAGGCTAC 1440
DB 3205 TACAGAGATGGGCGGCGTAAAGGGGGTAAAGAGGAGCGGGGCTGTGAGGCTAC 3264
QY 1441 AGAGAGGCTAGAGATCTAGCTTTTAACTTAATGACAGACACCGCTCGAGTAAATTA 1500
DB 3265 AGAGAGGCTAGAGATCTAGCTTTTAACTTAATGACAGACACCGCTCGAGTAAATTA 3324
QY 1501 TTTTCAACAGTCAAGATTAATTCGCTTAATGACTTGTATGCTGCGCAGAAATATTC 1560
DB 3325 TTTTCAACAGTCAAGATTAATTCGCTTAATGACTTGTATGCTGCGCAGAAATATTC 3384
QY 1561 CATAGAGAGCTGACCACTTACTGCTGACGCGCAGCGGAGTGAATTTGAGAGGCTATTAG 1620
DB 3385 CATAGAGAGCTGACCACTTACTGCTGACGCGCAGCGGAGTGAATTTGAGAGGCTATTAG 3444
QY 1621 GGTATATGCAAGGTGACACTTAGGCGCAGATTGCAATGATCAAGATCAAGAACTTTGAA 1680
DB 3445 GGTATATGCAAGGTGACACTTAGGCGCAGATTGCAATGATCAAGATCAAGAACTTTGAA 3504
QY 1681 TATCAGGAATTTGTTCTACATTTCTGGAAACGGGCGGAGGTGAGATAGATACGAGGA 1740
DB 3505 TATCAGGAATTTGTTCTACATTTCTGGAAACGGGCGGAGGTGAGATAGATACGAGGA 3564
QY 1741 TAGGTTGCTTTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1800
DB 3565 TAGGTTGCTTTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3624
QY 1801 GGTGTTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1860
DB 3625 GGTGTTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3684
QY 1861 CAATACCAACCTTAATCTTAACAGGTGTAAGCTTATGCTTAAACATACCTGTGGA 1920
DB 3685 CAATACCAACCTTAATCTTAACAGGTGTAAGCTTATGCTTAAACATACCTGTGGA 3744
QY 1921 AGCCTGGAACGAGTGTAGGGTGGGCTGCTGCTTTTACCTGCTGCGAAGGGGCTGCT 1980
DB 3745 AGCCTGGAACGAGTGTAGGGTGGGCTGCTGCTTTTACCTGCTGCGAAGGGGCTGCT 3804
QY 1981 GTGTGCGCCCAAAAGCAGGGCTTCAATTAAGAAATGCTCTTTGAAAGGTGATCACTTGG 2040
DB 3805 GTGTGCGCCCAAAAGCAGGGCTTCAATTAAGAAATGCTCTTTGAAAGGTGATCACTTGG 3864
QY 2041 TATCTGTCTGAGGGTAACTTCAAGGCTGCGCACATGTGGCTCCGACTGTGTGCTT 2100
DB 3865 TATCTGTCTGAGGGTAACTTCAAGGCTGCGCACATGTGGCTCCGACTGTGTGCTT 3924
QY 2101 CATGCTAGTAAAGACGTGCTGCTGATTAAGCATTAATGATGATGATGATGATGATG 2160
DB 3925 CATGCTAGTAAAGACGTGCTGCTGATTAAGCATTAATGATGATGATGATGATGATG 3984
QY 2161 CAGGGCTCTCAGATGTGACTGCTGCTGCAAGGCACTGTCACTGCTGGAAGACATTTCA 2220
DB 3985 CAGGGCTCTCAGATGTGACTGCTGCTGCAAGGCACTGTCACTGCTGGAAGACATTTCA 4044
QY 2221 CGTAGCCAGCACTCTGCAAGGCTGCGCAAGGCTGTTGAGCATTAATCTGACCCGCTG 2280
DB 4045 CGTAGCCAGCACTCTGCAAGGCTGCGCAAGGCTGTTGAGCATTAATCTGACCCGCTG 4104
QY 2281 TTGCTTGATTTGGGTAAAGAGGGGGGTGTTCTTACCTTAACCAATTTGAGTCA 2340

Qy 721 TGCATGCGGTGTAAATGCGCGGCGCTTAAAGGTATATATGCGCGGTAACT 780
Db 2545 TGCATGCGGTGTAAATGCGCGGCGCTTAAAGGTATATATGCGCGGTAACT 2604
Qy 781 TGTATACATCTGACCTCATGAGGCTTGGAGTGTGGAAGATTTTCTGTGCGTA 840
Db 2605 TGTATACATCTGACCTCATGAGGCTTGGAGTGTGGAAGATTTTCTGTGCGTA 2664
Qy 841 ACTTGTGGAACAGAGCTCTAACAGTACCTTGTGTTTGGAGGTTTCTGTGCGTCA 900
Db 2665 ACTTGTGGAACAGAGCTCTAACAGTACCTTGTGTTTGGAGGTTTCTGTGCGTCA 2724
Qy 901 CCGAGGCAAGTGTGTGCAAGATTAAGAGAGATTAAGTGGGAATTTGAAGCTTT 960
Db 2725 CCGAGGCAAGTGTGTGCAAGATTAAGAGAGATTAAGTGGGAATTTGAAGCTTT 2784
Qy 961 TGAATCCTGTGTGAGCTGTTTGAATCTTGAATCTGGTCAACAGGCGCTTTCCAG 1020
Db 2785 TGAATCCTGTGTGAGCTGTTTGAATCTTGAATCTGGTCAACAGGCGCTTTCCAG 2844
Qy 1021 AGAAGTCAATCAAGACTTTGGATTTTTCACACCGGGCGCGCTGCGCTGTGCTT 1080
Db 2845 AGAAGTCAATCAAGACTTTGGATTTTTCACACCGGGCGCGCTGCGCTGTGCTT 2904
Qy 1081 TTTTGAAGTTTATTAAGATTAATGAGAGCAAGAAACCATCTGAGCGGGGGTAACTGC 1140
Db 2905 TTTTGAAGTTTATTAAGATTAATGAGAGCAAGAAACCATCTGAGCGGGGGTAACTGC 2964
Qy 1141 TGGATTTTCTGCGCATCTGTGAGAGCGGTTGTGAGACACAGAAATGCGCTGTAC 1200
Db 2965 TGGATTTTCTGCGCATCTGTGAGAGCGGTTGTGAGACACAGAAATGCGCTGTAC 3024
Qy 1201 TGTGTCTTCCGTCGCGCGCGCGGCAATATACCGACGAGAGCAGCAGCAGCAGAG 1260
Db 3025 TGTGTCTTCCGTCGCGCGCGCGGCAATATACCGACGAGAGCAGCAGCAGCAGAG 3084
Qy 1261 AAGCAGGCGCGCGCGCGAGAGAGAGAGCCCATGGAACCCGAGCGCGCTGTGACCTC 1320
Db 3085 AAGCAGGCGCGCGCGCGAGAGAGAGAGCCCATGGAACCCGAGCGCGCTGTGACCTC 3144
Qy 1321 GGGAAATGATTTGTTACAGTGTGCTGAACTGTATTCAGAACTGAGACGATTTTGA 1380
Db 3145 GGGAAATGATTTGTTACAGTGTGCTGAACTGTATTCAGAACTGAGACGATTTTGA 3204
Qy 1381 TACAGAGATGAGGAGCGGCTTAAAGGCGTAAAGAGAGCGGCGGCTTGTAGGCTAC 1440
Db 3205 TACAGAGATGAGGAGCGGCTTAAAGGCGGCTTAAAGAGAGCGGCGGCTTGTAGGCTAC 3264
Qy 1441 AGAGAGGCTTAAAGATTAAGTGTGTTAATGACCAAGACACCGTCTGTAGTGTATAC 1500
Db 3265 AGAGAGGCTTAAAGATTAAGTGTGTTAATGACCAAGACACCGTCTGTAGTGTATAC 3324
Qy 1501 TTTTCAACAGATCAAGATTAATGCGCTTAATGAGCTTGTGCTGCGCGAGAGTATTC 1560
Db 3325 TTTTCAACAGATCAAGATTAATGCGCTTAATGAGCTTGTGCTGCGCGAGAGTATTC 3384
Qy 1561 CATAGACAGCTGACCACTTAAGTGTGCAAGCAGCGGAGTATTTTGAAGAGCTATTAG 1620
Db 3385 CATAGACAGCTGACCACTTAAGTGTGCAAGCAGCGGAGTATTTTGAAGAGCTATTAG 3444
Qy 1621 GGTATATGCAAAAGGTGCACTTAAGCCAGATTTGAGAGTAAAGATCAAGTAACTTTG 1680
Db 3445 GGTATATGCAAAAGGTGCACTTAAGCCAGATTTGAGAGTAAAGATCAAGTAACTTTG 3504
Qy 1681 TATCAGGAATTTGTTGCTAATTTTGGGAAAGCGGAGCCAGGTGAGATAGATAGAGAGA 1740
Db 3505 TATCAGGAATTTGTTGCTAATTTTGGGAAAGCGGAGCCAGGTGAGATAGATAGAGAGA 3564
Qy 1741 TAGGGTGGCTTTAGATGATGATGATTAATATATGTGCGCGGCGGCTTGTGCAATGACG 1800
Db 3565 TAGGGTGGCTTTAGATGATGATGATTAATATATGTGCGCGGCGGCTTGTGCAATGACG 3624
Qy 1801 GGTGGTTATTAATGAATGAAGTTTACGCGCCCAATTTTGAAGCGGTACGGTTTCTGCGC 1860

Db 3625 GGTGGTTATTAATGAATGAAGTTTACGCGCCCAATTTTGAAGCGGTACGGTTTCTGCGC 3684
Qy 1861 CAATACCAACCTTATCTTACACGCGTGAAGCTTCTATGAGGTTTAAACATATCTGTGGA 1920
Db 3685 CAATACCAACCTTATCTTACACGCGTGAAGCTTCTATGAGGTTTAAACATATCTGTGGA 3744
Qy 1921 AGCTGGAACGATGAAGGTTGCGGCGTGTGCTTTTACCTGTGCTGGAAGGCGGTGCT 1980
Db 3745 AGCTGGAACGATGAAGGTTGCGGCGTGTGCTTTTACCTGTGCTGGAAGGCGGTGCT 3804
Qy 1981 GTGTGCGCCCAAAAGCAGGCGCTTCAATTAAGAAATGCTCTTGAAGGTATACCTTGG 2040
Db 3805 GTGTGCGCCCAAAAGCAGGCGCTTCAATTAAGAAATGCTCTTGAAGGTATACCTTGG 3864
Qy 2041 TATCTGTCTGAGGGTAACTCAGAGGTGCGCACAATGTGCGCTCGACTGTGTGCTT 2100
Db 3865 TATCTGTCTGAGGGTAACTCAGAGGTGCGCACAATGTGCGCTCGACTGTGTGCTT 3924
Qy 2101 CATGCTAGTGAAGACGTGCTGTGATTTAGCATTAATGTGATGTGCAACTGCGAGGA 2160
Db 3925 CATGCTAGTGAAGACGTGCTGTGATTTAGCATTAATGTGATGTGCAACTGCGAGGA 3984
Qy 2161 CAGGCGCTTCAAGTGTGCACTGTGCTGAGAGGCACTGTGCACTGTGAGAGACATTCA 2220
Db 3985 CAGGCGCTTCAAGTGTGCACTGTGCTGAGAGGCACTGTGCACTGTGAGAGACATTCA 4044
Qy 2221 CGTAGCAGACCACTCTGCAAGGCTGCGCAAGTGTGAGCATTAATCTGACCCGCTG 2280
Db 4045 CGTAGCAGACCACTCTGCAAGGCTGCGCAAGTGTGAGCATTAATCTGACCCGCTG 4104
Qy 2281 TTCTTGTGATTTGGGTAAACAGAGGCGGCTTCTTACCTTACCAATGCAATTTGATCA 2340
Db 4105 TTCTTGTGATTTGGGTAAACAGAGGCGGCTTCTTACCTTACCAATGCAATTTGATCA 4164
Qy 2341 CACTAAGATTTGTGTAAGCCCGAGACATGTCCAAGGTGAACCTGAACGCGGGTGTGA 2400
Db 4165 CACTAAGATTTGTGTAAGCCCGAGACATGTCCAAGGTGAACCTGAACGCGGGTGTGA 4224
Qy 2401 CATGACCATGAAGATCTGGAAGTGTGAGGATGATGAGATGAGATGAGATGAGATGAG 2460
Db 4225 CATGACCATGAAGATCTGGAAGTGTGAGGATGATGAGATGAGATGAGATGAGATGAG 4284
Qy 2461 CTGCGAGTGTGCGGTAAACATATTAGGAACCAAGCTGTGATGCTGATGATGATGAG 2520
Db 4285 CTGCGAGTGTGCGGTAAACATATTAGGAACCAAGCTGTGATGCTGATGATGATGAG 4344
Qy 2521 GCTGAGGCGCGATCACTTGTGCTGCGCTGCAACCGCGCTGAGTTGCTTACGATGA 2580
Db 4345 GCTGAGGCGCGATCACTTGTGCTGCGCTGCAACCGCGCTGAGTTGCTTACGATGA 4404
Qy 2581 AGATACAGATTGAG 2594
Db 4405 AGATACAGATTGAG 4418

RESULT 14
ID AAA59050
AAA59050 standard; DNA, 14455 BP.
XX
AC AAA59050;
XX
DT 07-NOV-2000 (first entry)
XX
Nucleotide sequence of the EI/fiber-expressing plasmid pEI/fiber.
DE Adenovirus; tripartite leader; adenovirus vector particle; gene delivery;
KW EI gene; fiber gene; se.
XX
OS Synthetic.
XX Human adenovirus type 5.
XX
PN W0200042208-A1.

XX 20-JUL-2000.
PD 14-JAN-2000; 2000MO-EP000265.
XX 14-JAN-1999; 99US-0115920P.
XX (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERN GES MBH.
PA (SCRI) SCRIPBS RES INST.
XX Nemerow GR, Von Seggern DJ, Hallenbeck PL, Stevenson SC,
PI Skripchenko Y;
XX WPI; 2000-476068/41.
XX New nucleic acid comprising an adenovirus tripartite leader nucleotide
PT for producing high-capacity and targeted vectors for adenovirus-based
PT gene therapy.

PS Example 1; Page 160-164; 212pp; English.

XX The specification describes a nucleic acid molecule comprising an
CC adenovirus (AV) tripartite leader (TPL) nucleotide with a sequence
CC comprising two different TPL exons or three same or different TPL exons.
CC The nucleic acid is used to produce an adenovirus vector particle,
CC deliver an exogenous gene to a target cell, pseudotype recombinant viral
CC vectors, target an adenovirus vector to a cell, produce a modified
CC adenovirus, deliver a heterologous gene to an animal and produce a
CC E1/fiber-expressing plasmid, which was used for complementation of
CC E1/fiber-gene deleted adenoviruses

XX Sequence 14455 BP; 3698 A; 3271 C; 3565 G; 3921 T; 0 U; 0 Other;

Query Match 100.0%; Score 2594; DB 3; Length 14455;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCATCTTACCTCCACGAGGCTGGCTTTCACCCCACTGACGAGAGTGAAGAGGT 60
DB 1825 ATGCATCTTACCTCCACGAGGCTGGCTTTCACCCCACTGACGAGAGTGAAGAGGT 1884
QY 61 GAGGAGTTTGTGTAGATTATGTGAGACACCGGAGCGGTTGCAAGTCTTGTCAATTAT 120
DB 1885 GAGGAGTTTGTGTAGATTATGTGAGACACCGGAGCGGTTGCAAGTCTTGTCAATTAT 1944
QY 121 CACCGAGAGAAATACGGGGGACCCAGATATTATGTGTGCTTTGCTATATGAGACCTGT 180
DB 1945 CACCGAGAGAAATACGGGGGACCCAGATATTATGTGTGCTTTGCTATATGAGACCTGT 2004
QY 181 GGCATTTTGTGCTACAGTAAGTGAATAATTATGGCAGTGGGTATAGTGTGGGTTTG 240
DB 2005 GGCATTTTGTGCTACAGTAAGTGAATAATTATGGCAGTGGGTATAGTGTGGGTTTG 2064
QY 241 GTGTGTAATTTTATTTTATTTTATTTTACAGTTTGTGTGTTTAAAGATTTTGTATTGGA 300
DB 2065 GTGTGTAATTTTATTTTATTTTATTTTACAGTTTGTGTGTTTAAAGATTTTGTATTGGA 2124
QY 301 TTTTAAAAAGTCTGTGTCTGAACCTGAGCCCTGAGCCCGAGCCAGAACCGAGCCTG 360
DB 2125 TTTTAAAAAGTCTGTGTCTGAACCTGAGCCCTGAGCCCGAGCCAGAACCGAGCCTG 2184
QY 361 CAAGACCTACCCGCGCTCTTAAATGAGCGCTGCTATCTTGAAGCGCCGACATCACTG 420
DB 2185 CAAGACCTACCCGCGCTCTTAAATGAGCGCGCTGCTATCTTGAAGCGCCGACATCACTG 2244
QY 421 TGTCTAGAGATGCAATAGTAGTAGAGATAGTAGTCTCGGCTCTTCAACACCTC 480
DB 2245 TGTCTAGAGATGCAATAGTAGTAGAGATAGTAGTCTCGGCTCTTCAACACCTC 2304
QY 481 CTGAGATACACCCGGGTGCTCCGCTGTGCCCCATTAAACAGTTGCCGTGAGAGTTGTTG 540

DB 2305 CTGAGATACACCCGGGTGCTCCGCTGTGCCCATTAACAGTTGCCGTGAGAGTTGTTG 2364
QY 541 GCGTCGCCAGGCTGTGGAATGTATGAGGACTTGCTTAACAGCCCTGGGCAACTTTGG 600
DB 2365 GCGTCGCCAGGCTGTGGAATGTATGAGGACTTGCTTAACAGCCCTGGGCAACTTTGG 2424
QY 601 ACTTGAGCTGTAAACGCCCGGACCATTAAGTGTAAACCTGTGATTCGTGTGTTAA 660
DB 2425 ACTTGAGCTGTAAACGCCCGGACCATTAAGTGTAAACCTGTGATTCGTGTGTTAA 2484
QY 661 GCGCTTTGTTGCTGAAATGATGTATGTTAATTAAAGCGTGAGATTAATTTAACT 720
DB 2485 GCGCTTTGTTGCTGAAATGATGTATGTTAATTAAAGCGTGAGATTAATTTAACT 2544
QY 721 TGCAATGCGTAAATGAGGCGGCGCTTAAAGGATATATATGCGCGGTGCTAAATCT 780
DB 2545 TGCAATGCGTAAATGAGGCGGCGCTTAAAGGATATATATGCGCGGTGCTAAATCT 2604
QY 781 TGGTTACATCTGACCTTCATGAGGCTTGGAGTGTGTAAGATTTTCTGTGCGTA 840
DB 2605 TGGTTACATCTGACCTTCATGAGGCTTGGAGTGTGTAAGATTTTCTGTGCGTA 2664
QY 841 ACTTGCTGAAACAGAGCTCTTAACATACCTCTTGTGTTGAGGTTCTGTGGGCTCAT 900
DB 2665 ACTTGCTGAAACAGAGCTCTTAACATACCTCTTGTGTTGAGGTTCTGTGGGCTCAT 2724
QY 901 CCCAGGCAAGTTAGTGTGAGAAATTAAAGAGATTACAATGAGGAATTTGAAGAGCTTT 960
DB 2725 CCCAGGCAAGTTAGTGTGAGAAATTAAAGAGATTACAATGAGGAATTTGAAGAGCTTT 2784
QY 961 TGAATCTGTGTGAGCTGTTGATTTCTTGAATCTGTGTACAGAGCTTTTCCAG 1020
DB 2785 TGAATCTGTGTGAGCTGTTGATTTCTTGAATCTGTGTACAGAGCTTTTCCAG 2844
QY 1021 AGAAGTCTATCAAGACTTTGATTTTCCACACCGGGCGCGCTGCGCTCTTGTGTT 1080
DB 2845 AGAAGTCTATCAAGACTTTGATTTTCCACACCGGGCGCGCTGCGCTCTTGTGTT 2904
QY 1081 TTTTGAATTTTAAAGATTAATGAGGAGAAACCATCTGAGCGGGGGTACCTGC 1140
DB 2905 TTTTGAATTTTAAAGATTAATGAGGAGAAACCATCTGAGCGGGGGTACCTGC 2964
QY 1141 TGGATTTTCTGCGCATCATCTGTGAGAGCGGTTGTGAACACAAAGATTCCTGTAC 1200
DB 2965 TGGATTTTCTGCGCATCATCTGTGAGAGCGGTTGTGAACACAAAGATTCCTGTAC 3024
QY 1201 TGTGTCTTCCTGCGCGCGCGCATTAATCCGACGAGAGACAGACAGACAGAGG 1260
DB 3025 TGTGTCTTCCTGCGCGCGCGCATTAATCCGACGAGAGACAGACAGACAGAGG 3084
QY 1261 AAGCCAGGCGGCGGCGAGAGAGCCCATGGAACCCGAGAGCGGCTGAGACCTC 1320
DB 3085 AAGCCAGGCGGCGGCGAGAGAGCCCATGGAACCCGAGAGCGGCTGAGACCTC 3144
QY 1321 GGGAAATGATTTGTATACAGGTGCTGAACGTATCCAGAACTGAGACGCAATTTTGACAT 1380
DB 3145 GGGAAATGATTTGTATACAGGTGCTGAACGTATCCAGAACTGAGACGCAATTTTGACAT 3204
QY 1381 TACAGAGATGCGGAGGCGCTAAAGGGGCTAAAGGAGAGCGGGGCTTGTGAGGCTAC 1440
DB 3205 TACAGAGATGCGGAGGCGCTAAAGGGGCTAAAGGAGAGCGGGGCTTGTGAGGCTAC 3264
QY 1441 AGAGAGGCTAGGAATAGCTTTAGCTTAATGACAGACACCGCTGAGTGTATTAC 1500
DB 3265 AGAGAGGCTAGGAATAGCTTTAGCTTAATGACAGACACCGCTGAGTGTATTAC 3324
QY 1501 TTTTCAACAGATCAAGATTAATGCGCTAAATGAGCTTGTATCTGTGCGCAGAAATATTC 1560
DB 3325 TTTTCAACAGATCAAGATTAATGCGCTAAATGAGCTTGTATCTGTGCGCAGAAATATTC 3384
QY 1561 CATAGAGAGCTGACCACTTAATCTGTGACAGCCAGGGAGTATTTTGAAGGCTATTAG 1620
DB 3385 CATAGAGAGCTGACCACTTAATCTGTGACAGCCAGGGAGTATTTTGAAGGCTATTAG 3444

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OY 1621 GGTATATGCAAAAGGTGGCACTTAAGCCGATTTGCAAGTACAGCAAACTTGTAAA 1680
DB 3445 GGTATATGCAAAAGGTGGCACTTAAGCCGATTTGCAAGTACAGCAAACTTGTAAA 3504
OY 1681 TATCAGGAATTGTTGCTCATTTTCTGGGAACGGGGCCGAGGTGGAGATAGATAGCAAGGA 1740
DB 3505 TATCAGGAATTGTTGCTCATTTTCTGGGAACGGGGCCGAGGTGGAGATAGATAGCAAGGA 3564
OY 1741 TAGGGTGGCTTTAGATGTAGCATGATTAATATATGTGGCCGGGGGGTCTTGGCATGAGACG 1800
DB 3565 TAGGGTGGCTTTAGATGTAGCATGATTAATATATGTGGCCGGGGGGTCTTGGCATGAGACG 3624
OY 1801 GGTGGTATTTATGATGATTAAGGTTTACTGGCCCAATTTTACGGGTACGGTTTCTGGC 1860
DB 3625 GGTGGTATTTATGATGATTAAGGTTTACTGGCCCAATTTTACGGGTACGGTTTCTGGC 3684
OY 1861 CAATACCAACCTTTATCTTACACGGGTAAAGCTTCTATGGGTTTAAACAATACCTGTGGA 1920
DB 3685 CAATACCAACCTTTATCTTACACGGGTAAAGCTTCTATGGGTTTAAACAATACCTGTGGA 3744
OY 1921 AGCTGGAACCGATGTAAAGGTTTCGGGGCTGTGCTTTTACTGTGCTGGAAGGGGGTGGT 1980
DB 3745 AGCTGGAACCGATGTAAAGGTTTCGGGGCTGTGCTTTTACTGTGCTGGAAGGGGGTGGT 3804
OY 1981 GTGTGCGCCCAAAAGCAGGGCTTCAATTAAGAATGCTCTTTGAAAGGTACCTTGGG 2040
DB 3805 GTGTGCGCCCAAAAGCAGGGCTTCAATTAAGAATGCTCTTTGAAAGGTACCTTGGG 3864
OY 2041 TATCTGTCTGAGGGGTAACTCAAGGGTGGCCCAAAATGTGGCTTCCGACTGGTGTGTT 2100
DB 3865 TATCTGTCTGAGGGGTAACTCAAGGGTGGCCCAAAATGTGGCTTCCGACTGGTGTGTT 3924
OY 2101 CATCTAGTGAAGAAAGCGTGTGTGATTTAGCATTAACAATGATGTGGCACTGCAAGGA 2160
DB 3925 CATCTAGTGAAGAAAGCGTGTGTGATTTAGCATTAACAATGATGTGGCACTGCAAGGA 3984
OY 2161 CAGGGCTCTCAAGTACTGACCTGTGTGCAAGCGCACTGTCACTGTGTAAGACCATTC 2220
DB 3985 CAGGGCTCTCAAGTACTGACCTGTGTGCAAGCGCACTGTCACTGTGTAAGACCATTC 4044
OY 2221 CGTAGCAGCACTCTGCAAGGCTGGCCAGTGTGAGATTAACATACCTGACCCGCTG 2280
DB 4045 CGTAGCAGCACTCTGCAAGGCTGGCCAGTGTGAGATTAACATACCTGACCCGCTG 4104
OY 2281 TTCTTTCATTTGGGTAAACAGAGAGGGGGTGTCTTCACTTACCAATGCAATTTGAGTCA 2340
DB 4105 TTCTTTCATTTGGGTAAACAGAGAGGGGGTGTCTTCACTTACCAATGCAATTTGAGTCA 4164
OY 2341 CACTTAAGATTTGCTTGAAGCCCGAGAGCATATCCAGGTGAACCTGAAACGGGGTGTGGA 2400
DB 4165 CACTTAAGATTTGCTTGAAGCCCGAGAGCATATCCAGGTGAACCTGAAACGGGGTGTGGA 4224
OY 2401 CATGACCATGAAGATCTGGAAGGTGTGAGGTAGAGTGAAGCCGACAGGTGCAAGCC 2460
DB 4225 CATGACCATGAAGATCTGGAAGGTGTGAGGTAGAGTGAAGCCGACAGGTGCAAGCC 4284
OY 2461 CTGCGAGTGTGGCCGTAAACATATTAAGAACACAGCTGTGATGTGATGTGACCGAGGA 2520
DB 4285 CTGCGAGTGTGGCCGTAAACATATTAAGAACACAGCTGTGATGTGATGTGACCGAGGA 4344
OY 2521 GCTGAGGCGCGATCACTTGTGTGCTGCGCTGCAACCGCGCTGAGTTTGTCTTACCGATGA 2580
DB 4345 GCTGAGGCGCGATCACTTGTGTGCTGCGCTGCAACCGCGCTGAGTTTGTCTTACCGATGA 4404
OY 2581 AGATACAGATTGAG 2594
DB 4405 AGATACAGATTGAG 4418
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RESULT 15
ABA94259
ID ABA94259 standard; DNA; 14455 BP.

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XX AC ABA94259;
XX DT 13-MAR-2002 (first entry)
XX DE Nucleotide sequence of expression plasmid pEL/Fiber.
XX KW Adenovirus; Inverter terminal repeat sequence; ITRS; ocular disease;
XX KW fiber protein; photoreceptor; rhodopsin; stargardt disease gene; STDG1;
XX KW opthalmological; antiinflammatory; antidiabetic; cyostatic;
XX KW gene therapy; ss.
XX OS Synthetic.
XX PN W0200183729-A2.
XX PD 08-NOV-2001.
XX PF 30-APR-2001; 2001WO-EP004863.
XX PR 01-MAY-2000; 2000US-00562934.
XX PA (NOVS ) NOVARTIS AG.
XX PA (SCRI ) SCRIPS RES INST.
XX PA (NEME/) NEMEROW G R.
XX PA (VSEG/) VON SEGGERN D J.
XX PA (FRIE/) FRIEDLANDER M.
XX PI Nemerow GR, Von Seggern DJ, Friedlander M;
XX WP: 2002-082846/11.
XX DR
XX PT Polynucleotide for making vectors, useful for treating ocular diseases,
XX PT e.g., retinitis pigmentosa, comprises adenovirus inverter terminal repeat
XX PT sequences, packaging signal and photoreceptor-specific promoter.
XX PS Example 1, Page 114-118; 149pp; English.
XX XX
XX CC The invention provides an isolated polynucleotide comprising adenovirus
XX CC (AV) inverter terminal repeat sequences (ITRS), AV packaging signal
XX CC operatively linked to ITRS and a photoreceptor-specific promoter. A
XX CC recombinant AV vector (AVV) comprising the polynucleotide is useful for
XX CC targeted delivery of a gene product to the eye (especially to the
XX CC vitreous cavity), for treating an ocular disease, e.g., retinal
XX CC degenerative disease, retinitis pigmentosa, Stargardt's disease, diabetic
XX CC retinopathies, retinal vascularizations, and retinoblastoma, of a mammal
XX CC preferably human. The AVV comprises a fiber protein that specifically or
XX CC selectively binds to receptors that are expressed on cells (preferably
XX CC photoreceptors in the eye). Preferably, the recombinant virus comprise
XX CC a fiber protein from an adenovirus type D subgroup or is a chimeric protein
XX CC containing a portion of the N-terminus of an adenovirus type 2 or type 5
XX CC penton, and the therapeutic product is a trophic factor, an anti-
XX CC apoptotic factor, gene encoding a rhodopsin protein, a wild-type
XX CC stargardt disease gene (STDG1), an anti-cancer agent and a protein that
XX CC regulates expression of a photoreceptor specific gene product. The viral
XX CC nucleic acid of AVV comprises ITRS and packaging signal derived from AVV
XX CC subgroup B or C, especially an AV type 2 or type 5. AVV is also useful
XX CC for targeted gene therapy, where the vector comprises an AV type 37 fiber
XX CC protein or its portion, and selectively transduces photoreceptors and
XX CC delivers a gene product encoded by AVV. The present sequence represents
XX CC an expression plasmid pEL/Fiber containing the adenovirus EI and Fiber
XX CC gene
XX SQ Sequence 14455 BP; 3698 A; 3271 C; 3565 G; 3921 T; 0 U; 0 Other;
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OY 1 ATCGATCTTACCTGCAAGAGGCTGCTTCCACCCAGTACGACGAGATGAAGAGGCT 60
DB 1825 ATCGATCTTACCTGCAAGAGGCTGCTTCCACCCAGTACGACGAGATGAAGAGGCT 1884

Query Match 100.0%; Score 2594; DB 6; Length 14455;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY	121	CACCGAGAAATACGGGGGAGCCACAGATTTATATGTGTTGCTTTGCTATATAGAGACCTGT	180
Db	1945	CACCGAGAAATACGGGGGAGCCACAGATTTATATGTGTTGCTTTGCTATATAGAGACCTGT	2004
QY	181	GGCATGTTGTCTACAGTAAGTGAATAATATGAGCATGTGGGTGATATAGTGTGGGTTTG	240
Db	2005	GGCATGTTGTCTACAGTAAGTGAATAATATGAGCATGTGGGTGATATAGTGTGGGTTTG	2064
QY	241	GTGTGCTAATTTTTTTTTTAATTTTACAATTTTGTGCTTTAAAGAAATTTTGTATTTGTGA	300
Db	2065	GTGTGCTAATTTTTTTTTTAATTTTACAATTTTGTGCTTTAAAGAAATTTTGTATTTGTGA	2124
QY	301	TTTTTTTAAAGAGTCTGTGTCTGAACCTGAGCCGAGCCGAGCCAGAACCCGAGCGTG	360
Db	2125	TTTTTTTAAAGAGTCTGTGTCTGAACCTGAGCCGAGCCGAGCCAGAACCCGAGCGTG	2184
QY	361	CAAGACCTACCGCGCGTCTTAAATATGAGCGCTGTATCTGTAGAAGCCCGACATCACCTG	420
Db	2185	CAAGACCTACCGCGCGTCTTAAATATGAGCGCGTGTATCTGTAGAAGCCCGACATCACCTG	2244
QY	421	TGTCATAGAAATGCATATGTAGTACGATATAGCTGTGACTCCGGTCTTTTAAACAACCTC	480
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QY	481	CTGAAATACACCCGGTGGTCCCGCGTGTGCCCATTTAAACAGTTGGCGGTGAGATTTGTG	540
Db	2305	CTGAAATACACCCGGTGGTCCCGCGTGTGCCCATTTAAACAGTTGGCGGTGAGATTTGTG	2364
QY	541	GCGCTGCGCAGGCTGTGATATGTATCGAGACTTGTCTTAAAGAGCTTGGCAACCTTTTG	600
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Db	2845	AGAAAGTCAATCAAGCTTTTGAATTTTTCACAACCGGGGCGCGCTGTGCTGTGCTT	2904
QY	1081	TTTTAGTTTTTAAAGATTAATGAGAGAAACCATCTGAGCGGGGGTAACTGCG	1140
Db	2905	TTTTAGTTTTTAAAGATTAATGAGAGAAACCATCTGAGCGGGGGTAACTGCG	2964
QY	1141	TGGAATTTTCTGGCATGTACTGTGTGAGAGCGGTGTGTGAGACACAGAATGCGCTGTCA	1200

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Db	3025	TGTTGCTTCCGTCGCCGCCGAGTAATAACGACGAGACAGACAGCAGAGAGG	3084
Qy	1261	AAGCCAGCCGCGCGCGCAGAGACAGACCCGAGACCCGAGACCCGCTGACCTC	1320
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Qy	1321	GGGAATGAATGTTGTACAGGTGGCTGAACCTGTATCCAGAACTGAGAGCAATTTGACAA	1380
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Qy	1381	TACAGAGATGCGCAGGGGCTAAAGGGGCTAAAGAGGAGACGGGGGCTTGTGAGCTAC	1440
Db	3205	TACAGAGATGCGCAGGGGCTAAAGGGGCTAAAGAGGAGACGGGGGCTTGTGAGCTAC	3264
Qy	1441	AGAGAGGCTTAGAATCTAGCTTTTACCTTAAATGACACACCGTCTTAGATATAC	1500
Db	3265	AGAGAGGCTTAGAATCTAGCTTTTACCTTAAATGACACACCGTCTTAGATATAC	3324
Qy	1501	TTTTCAACATATCAAGATATATGGCGTAAATGAGCTTGAATCTGCGCGCAAGATATTC	1560
Db	3325	TTTTCAACATATCAAGATATATGGCGTAAATGAGCTTGAATCTGCGCGCAAGATATTC	3384
Qy	1561	CATAGACAGCTGACCACTTAATGCTGCTGACACGAGGAGATGATTTTATAGAGCTATATAG	1620
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Qy	1741	TAGGGTGGCCCTTATGATGTAGATGATATAATATGTGCGCCGGGGGTCTTGGCATGACGCG	1800
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Qy	1861	CAATACCAACCTTATCTTACACGGTGTAACTTATAGGGTTTAAACAATCCTGTGTGGA	1920
Db	3685	CAATACCAACCTTATCTTACACGGTGTAACTTATAGGGTTTAAACAATCCTGTGTGGA	3744
Qy	1921	AGCCGTGACGATGTAAAGGGTTCGGGGCTGTGCTTTTACGTGCTGAGAAAGGGGGTGT	1980
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Qy	1981	GTGTGCGCCCAAAAGCAGGGCTTCAATTAAGAAATGCTCTTTGAAAGGTGTACCTTGGG	2040
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Qy	2041	TATCTGTCTGAGGGTAACTTCAGGGGTGCGCACAAATGTGGCTTCGACCTGTGGTTGCTT	2100
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Qy	2101	CATCTATGTGAAAAGCGGTGCTGATTAAGCATTAACATGGTATGTGGCAACTGCGAGGA	2160
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Qy	2161	CAGGGCCCTTCAGATGCTGACCTGTGCGACCGCAACTGTACCTGTGTAAGACCAATTC	2220
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Qy	2221	CGTACCAAGCACTCTGCGCAAGGCTTGGCCAGTGTTTGAGCATTAATCTGACCCGCTG	2280

Db	4045	CGTAGCCAGCCACTCTGCGAAGGCTGSCAGTGTTCGACATAACATCTGACCCGCTG	4104
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Db	4105	TTCTTGCAATTTGGGTAAACAGAGAGGGGTGTTCCTACCTTACCAATGCAATTTGAGTCA	4164
QY	2341	CACCTAAGATATTGCTTGAGCCCGAGAGCATGTCCAAAGTGAACCTGAAACGGGGTGTGGA	2400
Db	4165	CACCTAAGATATTGCTTGAGCCCGAGAGCATGTCCAAAGTGAACCTGAAACGGGGTGTGGA	4224
QY	2401	CATGACCATGAAGATCTGGAAGTGTCTGAGGTAGATGAGACCCGACACAGGTGCAGACC	2460
Db	4225	CATGACCATGAAGATCTGGAAGTGTCTGAGGTAGATGAGACCCGACACAGGTGCAGACC	4284
QY	2461	CTGCGAGTGTGGCGGTAAACATATTAGGAACCAAGCTGTGATGCTGATGTGACCGAGGA	2520
Db	4285	CTGCGAGTGTGGCGGTAAACATATTAGGAACCAAGCTGTGATGCTGATGTGACCGAGGA	4344
QY	2521	GCTGAGGCCCGATCACTTGTGTGCTGTGCAACCCGCGCTGAGTTGGCTCTAGCGATGA	2580
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QY	2581	AGATACAGATTGAG	2594
Db	4405	AGATACAGATTGAG	4418

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Job time : 1364 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 30, 2005, 18:47:03 ; Search time 8240 Seconds
(without alignments)
11982.854 Million cell updates/sec

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:
1: gb_eest1.*
2: gb_eest2.*
3: gb_hic.*
4: gb_eest3.*
5: gb_eest4.*
6: gb_eest5.*
7: gb_eest6.*
8: gb_gsest1.*
9: gb_gsest2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	615.8	23.7	648	4	BM655780 170006873
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3	476	18.4	726	6	CA307899 UI-H-FT1-
4	476	18.4	750	6	CD370352 UI-H-FT1-
5	476	18.4	766	6	CD742927 UI-H-FT1-
6	469.4	18.1	743	6	CA306892 UI-H-FT1-
7	460	17.7	602	6	CD370856 UI-H-FT1-
8	335.4	12.9	337	2	BM591710 170006873
9	249.8	9.6	347	2	BF915148 IL3-UT011
10	224.2	8.6	321	2	BF914577 IL3-UT011
11	223.8	8.6	321	2	BF915126 IL3-UT011
12	223.8	8.6	741	6	CD366021 UI-H-FT1-
13	173.6	6.7	667	6	CD742922 UI-H-FT1-
14	167	6.4	661	6	CD365243 UI-H-FT2-
15	162	6.2	173	4	BM600614 170006870
16	131.8	5.1	229	2	BF915892 IL3-UT011
17	100.8	3.9	198	2	BF914321 IL3-UT011
18	50.2	1.9	884	9	CNS006500
19	48.6	1.9	942	9	CNS00601
20	48.2	1.9	940	9	CNS03004
21	47.6	1.8	1101	9	CNS00100
22	47.2	1.8	732	7	CK305430 SB02029B1
23	46.8	1.8	1220	6	CD504965
24	46.6	1.8	1032	9	CL505993 SAIL_759_

25	46.4	1.8	519	4	BM439574
26	46.2	1.8	1101	9	CNS017M2
27	46	1.8	670	9	CNS04K72
28	46	1.8	807	9	CNS0128R
29	46	1.8	1511	9	CG753350
30	45.8	1.8	662	5	BU303489
31	45.8	1.8	891	5	BU842949
32	45.6	1.8	536	9	CR36545
33	45.6	1.8	1003	9	CNS017UQ
34	45.6	1.8	1042	9	CNS0039B
35	45.4	1.8	922	9	CNS0073W
36	45.4	1.8	1101	9	CNS00LT2
37	45	1.7	861	9	CNS0075A
38	45	1.7	1098	9	CNS015EM
39	45	1.7	1101	9	CNS000D1
40	44.8	1.7	564	9	CNS00711
41	44.8	1.7	768	7	CK306519
42	44.6	1.7	455	2	BE208710
43	44.6	1.7	713	9	AG506778
44	44.6	1.7	939	9	CNS00CNG
45	44.6	1.7	1101	9	CNS0100X

ALIGNMENTS

RESULT 1
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LOCUS 17000687386917 A.Gam.ad.cdNA1 Anopheles gambiae cDNA clone
DEFINITION 19600449669374 5', mRNA sequence.
ACCESSION BM655780
VERSION BM655780.1 GI:18955291
KEYWORDS EST.
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae
Neoptera; Metazoa; Arthropoda; Hexapoda; Insecta; Preygota;
Bukaryota; Enderoperygota; Diptera; Nematocera; Culicoidae;
Anopheles.
REFERENCE 1 (bases 1 to 648)
Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L.,
Charlab,R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
Celera Anopheles gambiae EST project
Unpublished (2002)
CONTACT: Holt R.A.
Celera Genomics
45 W. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
Fax: 2404534580
Email: HoltR@celera.com
Plate: ND010049S row: M column: 20
Seq primer: M13 Reverse.

FEATURES

1..648
Location/Qualifiers
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strat="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"
/db_xref="taxon:7165"
/clone="19600449669374"
/dev_stage="Adult"
/lab_host="DH10B"
/clone_lib="A.Gam.ad.cdNA1"
/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."

ORIGIN

Query Match 23.7%; Score 615.8; DB 4; Length 648;
Best Local Similarity 97.7%; Pred. No. 8.7e-156;

Matches	636;	Conservative	0;	Mismatches	12;	Indels	3;	Gaps	1;
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Db	61	CGTGTAAATGAGGCGGCTTAAAGGATATATATGCGCGTGGCTAATCTTGATAC		120					
Qy	788	ATTCGACCTCATGAGGCTTGGAGTGTGGAGATTTTTCTGCTGTGCTTAATCTT		847					
Db	121	ATTCGACCTCATGAGGCTTGGAGTGTGGAGATTTTTCTGCTGTGCTTAATCTT		180					
Qy	848	GGAACAGGCTCTTAACATTAATCTTGGTGTGGAGGTTTCTGTGGGCTCATCCAGC		907					
Db	181	GGAACAGGCTCTTAACATTAATCTTGGTGTGGAGGTTTCTGTGGGCTCATCCAGC		240					
Qy	908	AAAGTTAATCTGCAAGATTAAGAGAGATTTACAAGTGGAAATTTGAAGCTTTGAATC		967					
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Qy	1028	CATCAAGCTTTGATTTTTTCCACACCGGGCGCGCTGCTGTGCTTTTGTAG		1087					
Db	361	CATCAAGCTTTGATTTTTTCCACACCGGGCGCGCTGCTGTGCTTTTGTAG		420					
Qy	1088	TTTTTAATGAATTAATGAGAGAGAAACCATCTGAGCGGGGTACTGCTGATTT		1147					
Db	421	TTTTTAATGAATTAATGAGAGAGAAACCATCTGAGCGGGGTACTGCTGATTT		480					
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Db	481	TCTGCGCATGCACTGTGAGAGCGGTTGTGAGAGACACAAGAACTGCTTACTGTTTC		540					
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Qy	1268	GCGGCGGCGGAG		1318					
Db	598	GCGGCGGCGGAG		648					
RESULT 2	CK624194	625 bp	mRNA	linear	EST 26-JAN-2004				
LOCUS	m18c08.v1	Mouse RPE/choroid, unamplified: ml/mj	Mus musculus cDNA						
DEFINITION	clone m18c08 5', mRNA sequence.								
ACCESSION	CK624194								
VERSION	CK624194.1	GI:41345080							
KEYWORDS	EST.								
SOURCE	Mus musculus (house mouse)								
ORGANISM	Mus musculus								
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.								
AUTHORS	1 (bases 1 to 625) Ida,H., Boylan,S., Weigel,A., Smit-McBride,Z., Chao,A., Gao,J., Buchhoff,P., Wistow,G. and Hjeltnelund,L. Expressed sequence tag analysis of mouse RPE/choroid								
TITLE	Unpublished (2004)								
JOURNAL	Comment: M18c08								
COMMENT	Contact: M18c08 Section on Molecular Structure and Function National Eye Institute 6/331, NIH, Bethesda, MD 20892-2740, USA Tel: 301 402 3452 Fax: 301 496 0078 Email: g18c08@h18c08.nih.gov Plate: 18 row: C column: 08 Seq primer: M18c08 reverse primer (ABI).								

FEATURES	location/Qualifiers
SOURCE	1..625 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="m18c08" /sex="Male" /issue_type="RPE/choroid" /dev_stage="Adult" /lab_host="EMD10B" /clone_id="Mouse RPE/choroid, unamplified: ml/mj" /note="Organ: Eye; Vector: pSPORT1; 64ug total RNA was extracted from 200 adult male mouse RPE/choroids. A directionally cloned cDNA library in the pSPORT1 vector (Life Technologies) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the Superscript plasmid System full details of which are contained in the manufacturer's instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adaptor [5'-pGACTGTTTGAATGCAAGGCGGCGGCT(15-3')]. cDNA was cloned in Not I/Sal I sites. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."
ORIGIN	Query Match 22.9%; Score 592.8; DB 7; Length 625; Best Local Similarity 97.6%; Pred. No. 1.6e-149; Matches 613; Conservative 0; Mismatches 12; Indels 3; Gaps 1;
Qy	669 TTTCCTGAATGAGTGTGATGTTAATTAAGGCTGAGATAATGTTAACTTGCAATG
Db	1 TTTCCTGAATGAGTGTGATGTTAATTAAGGCTGAGATAATGTTAACTTGCAATG
Qy	729 GTGTTAAATGAGGCGGCTTAAAGGATATATATGCGCGCTTAATCTTGATTA
Db	61 GTGTTAAATGAGGCGGCTTAAAGGATATATATGCGCGCTTAATCTTGATTA
Qy	789 TCTGACCTCATGAGGCTTGGAGATGTTTGAAGATTTTCTGTGGCTTAATCTG
Db	121 TCTGACCTCATGAGGCTTGGAGATGTTTGAAGATTTTCTGTGGCTTAATCTG
Qy	849 GAACAGAGCTTAACAGTACTCTTGGTTTGAAGTTTCTGTGGGCTCATCCAGGCA
Db	181 GAACAGAGCTTAACAGTACTCTTGGTTTGAAGTTTCTGTGGGCTCATCCAGGCA
Qy	909 AAGTTAGCTGCAATTAAGAGAGATTAACAGTGGAAATTTGAAGCTTTGAATCC
Db	241 AAGTTAGCTGCAATTAAGAGAGATTAACAGTGGAAATTTGAAGCTTTGAATCC
Qy	969 TGTGTGAGCTGTTGATCTTTGAATCTGGGTCAACAGGCGCTTTCCAGAGAGTC
Db	301 TGTGTGAGCTGTTGATCTTTGAATCTGGGTCAACAGGCGCTTTCCAGAGAGTC
Qy	1029 ATCAAGACTTTGATTTTCCACACCGGCGGCTGCGCTGCTGTTTGTAGT
Db	361 ATCAAGACTTTGATTTTCCACACCGGCGGCTGCGCTGCTGTTTGTAGT
Qy	1089 TTTTAATGAATTAATGAGAGAGAAACCATCTGAGCGGGGATCTGCTGATTTT
Db	421 TTTTAATGAATTAATGAGAGAGAAACCATCTGAGCGGGGATCTGCTGATTTT
Qy	1149 CTGCGCATGCACTGTGAGAGCGGTTGTGAGACAAAGATTCGCTGCTGCTGCT
Db	481 CTGCGCATGCACTGTGAGAGCGGTTGTGAGACAAAGATTCGCTGCTGCTGCT
Qy	1209 TCCGTCCGCGCGGATTAATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
Db	541 TCCGTCCGCGCGGATTAATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
Qy	1269 GCGGCGGCGGAG

RESULT 3
CA307899/c

LOCUS CA307899 726 bp mRNA linear EST 05-AUG-2004

DEFINITION UI-H-FrT1-b1-b-a-23-0-UI.61 NCI CGAP_FrT1 Homo sapiens cDNA clone

ACCESSION UI-H-FrT1-b1-b-a-23-0-UI 3', mRNA sequence.

VERSION CA307899

KEYWORDS CA307899.1 GI:24470953

SOURCE EST.

ORGANISM Homo sapiens (human)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 726)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)

COMMENT
Contact: Robert Strunberg, Ph.D.
Email: cgaps-remail.nih.gov.
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-21, >AT-rich#low_complexity (matched complement)
Seq primer: M13 FORWARD
POLYA=yes.

location/Qualifiers
1. 726
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-PT1-b1-a-23-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP P11"
/note="Organ: Lung; Vector: pT73-Pec (Pharmacia) with a modified polylinker; Site,1: EcoR I; Site,2: Not I; NCI CGAP P11 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/mL, 3 hours; LPS 100 ng/mL, 24 hours; PMA 10 ng/mL, 3 hours; PMA 10 ng/mL, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV EGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV EGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pec vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GCGATGCGC. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

ORIGIN TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-PT1
TAG_SEQ=GGCCAGCCG"

Query Match	18.4%	Score	476;	DB	6;	Length	726;
Best Local Similarity	83.8%	Pred.	No.	9.7e-118;			
Matches	602;	Conservative	0;	Mismatches	0;	Indels	116;
						Gaps	1;

Oy	1	ATCATCTTACCTCCACGAGGCTGGCTTTCCACCCAGTGAACGAGATGAAGAGGT	60
Db	618	ATCATCTTACCTCCACGAGGCTGGCTTTCCACCCAGTGAACGAGATGAAGAGGT	559
Oy	61	GAGGAGTTTGTTAGATTATGTGAGAACCCCGGGACAGGGTTGCAGGTCTTGTCAATTAT	120
Db	558	GAGGAGTTTGTTAGATTATGTGAGAACCCCGGGACAGGGTTGCAGGTCTTGTCAATTAT	499
Oy	121	CACGGAGGAATACGGGGGAGCCGAGATATTATGTGCTTGCTCTPATGAGGACCTGT	180
Db	498	CACGGAGGAATACGGGGGAGCCGAGATATTATGTGCTTGCTCTPATGAGGACCTGT	439
Oy	181	GGCATGTTTGTCTACAGTAAGTGAATAATTATGGCAGTGGGTGATAGAGTGTTGG	240
Db	438	GGCATGTTTGTCTACA-----	423
Oy	241	GTGTGATATTTTTTTTATTTTACAGTTTGTGTGTTTAAGAAATTTGTATTTGTGA	300
Db	422	-----	423
Oy	301	TTTTTTTAAAGTCTGTGTCTGAACCTGAGCCGAGCCGAGAACCGGAGCCTG	360
Db	422	-----GTCTGTGTCTGAACCTGAGCCGAGCCGAGAACCGGAGCCTG	375
Oy	361	CAAGACTTACCCCGCTCTTAAATGGCGCTGTATCTCTGAAGCGCCCGACATCACTG	420
Db	374	CAAGACTTACCCCGCTCTTAAATGGCGCTGTATCTCTGAAGCGCCCGACATCACTG	315
Oy	421	TGTTAGAGATGCAATGATAGTACGAGTATGCTGTGACTCGGTCCTTCTTACAACACTC	480
Db	314	TGTTAGAGATGCAATGATAGTACGAGTATGCTGTGACTCGGTCCTTCTTACAACACTC	255
Oy	481	CTGAGATACACCCGCTGTGCCGTGTGCCCTGTATCTCTGAAGCGCCCGACATCACTG	540
Db	254	CTGAGATACACCCGCTGTGCCGTGTGCCCTGTATCTCTGAAGCGCCCGACATCACTG	195
Oy	541	GGCGTCCCAAGGCTGTGGAATGTATCAGGACTGTATACGAGCTGTGGCAACTCTTGG	600
Db	194	GGCGTCCCAAGGCTGTGGAATGTATCAGGACTGTATACGAGCTGTGGCAACTCTTGG	135
Oy	601	ACTTGAGCTGTAAACGCCCAAGGCATTAAGTGTAAACCTGTGATTGCGTGTGTGTAA	660
Db	134	ACTTGAGCTGTAAACGCCCAAGGCATTAAGTGTAAACCTGTGATTGCGTGTGTGTAA	75
Oy	661	CGCCTTGTGTGCTGAATGAGTGAATGAATGAATTAATGAAGGGAGATATATGTTAA	718
Db	74	CGCCTTGTGTGCTGAATGAGTGAATGAATGAATTAATGAAGGGAGATATATGTTAA	17

[illegible]

JOURNAL
COMMENT

Tumor Gene Index
Unpublished (1997)
Contact: Robert Stransberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Gary W. Humminghake, U of I
cDNA library preparation: Dr. M. Bento Soares, University of Iowa
cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cgap.html>
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

source

Location/Qualifiers
1..750
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bkb-j-17-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_id="NCI_CGAP_FTI"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP FTI is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ads CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ads CMV eGFP), moi 500, 24 hours; Adenovirus moi 500, 3 hours; Adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; Adenovirus + LPS 3 hours; Adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCATGCCG. The tissue was provided by Dr. Gary W. Humminghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCATGCCG"

ORIGIN

Query Match 18.4%; Score 476; DB 6; Length 750;
Best Local Similarity 83.8%; Pred. No. 9.8e-115;
Matches 602; Conservative 0; Mismatches 0; Indels 116; Gaps 1;

QY 1 ATCCATCTTACTCGCAGAGGCTGGCTTCCACCCAGTACGAGAGGAGTGAAGAGGCT 60
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QY 61 GAGAGATTGTGTTAGATTATGTGAGACACCCGGGACGGTTGCGAGGCTTGTCTATTAT 120
Db 558 GAGAGATTGTGTTAGATTATGTGAGACACCCGGGACGGTTGCGAGGCTTGTCTATTAT 499
QY 121 CACCGAGAGATACCGGGGAGCCAGATATATATGTGCTTGGCTTATATGAGACCTGT 180
Db 498 CACCGAGAGATACCGGGGAGCCAGATATATATGTGCTTGGCTTATATGAGACCTGT 439

QY 181 GGCATGTTGTTCTACAGTAAGTAAATTAATGCGCACTGGGTGATAGAGTGTGGGTTTG 240
Db 438 GGCATGTTGTTCTACAGTAAGTAAATTAATGCGCACTGGGTGATAGAGTGTGGGTTTG 423
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Db 374 CAAGACCTACCCGCGCTTAAATGAGCGCTGCTATCTGAGAGCGCCGACATCACCTG 315
QY 421 TGTTAGAGATGCAATAGTATGATAGATAGCTGTGATCTCGTCTTAAACACACTTC 480
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QY 481 CTGAGATACACCCGGTGTGCTCCGCTGTGCCCATTTAAACCACTTCCGTGAGATTGGTG 540
Db 254 CTGAGATACACCCGGTGTGCTCCGCTGTGCCCATTTAAACCACTTCCGTGAGATTGGTG 195
QY 541 GGCCTCGCAGGCTGTGGAATGTATCGAGGACTTGAACGAGCTGGGCAACTTTTG 600
Db 194 GGCCTCGCAGGCTGTGGAATGTATCGAGGACTTGAACGAGCTGGGCAACTTTTG 135
QY 601 ACTGACCTGTAAAGCCGCCAGCCAGTAACTGTGATTCGTGTGTGTTAA 660
Db 134 ACTGACCTGTAAAGCCGCCAGCCAGTAACTGTGATTCGTGTGTGTTAA 75
QY 661 GGCCTTGTGTTGCTGATAGTATGATGTTAAATTAAGGCTGAGATATGTTTAA 718
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RESULT 5

CD742927/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CD742927 766 bp mRNA linear EST 05-AUG-2004
UI-H-FT1-bka-m-09-0-UI.s1 NCI_CGAP_FTI Homo sapiens cDNA clone
CD742927
CD742927.1 GI:32293777
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 766)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Gary W. Humminghake, U of I
cDNA library preparation: Dr. M. Bento Soares, University of Iowa
cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cgap.html>
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

source

Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

/clone="UI-H-Ftl-bta-m-09-0-UI"
 /tissue_Type="Alveolar Macrophage"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_idb="NCI CGAP Ftl"
 /note="Organ: Lung; Vector: p773-Pac (Pharmacia) with a modified polylinker, Site_1: EcoR I, Site_2: Not I; NCI-CGAP_Ftl is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages; challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella mol 10, 3 hours; Klebsiella mol 10, 24 hours; Staph aureus mol 10, 3 hours; Staph aureus mol 10, 24 hours; Adenoviral vector (Ad5 CMV egfp), mol 500, 3 hours; Adenoviral vector (Ad5 CMV egfp), mol 500, 24 hours; wt adenovirus mol 500, 3 hours; wt adenovirus mol 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (drr)18 tail. The sequence tag for this library is GGCATCGCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
 TAG_TISSUE=Human Lung Alveolar Macrophage
 TAG_LIB=UI-H-Ftl
 TAG_SEQ=GGCATCGCG"

ORIGIN

Query Match	18.4%	Score 476	DB 6	Length 766
Best Local Similarity	83.8%	Pred. No. 9.9e-118		
Matches 602	Conservative 0	Mismatches 0	Indels 116	Gaps 1
QY 1 ATGCATCTTACCTGCGACGAGGCTGGCTTTCACCCAGTAGCGACGAGATGAGAGCGGT	60			
Db 618 ATGCATCTTACCTGCGACGAGGCTGGCTTTCACCCAGTAGCGACGAGATGAGAGCGGT	559			
QY 61 GAGAGATTGTTGTTAAGTATATGTGAGACACCCGGGCACGGTTGACAGTCTTGTCAATTAT	120			
Db 558 GAGAGATTGTTGTTAAGTATATGTGAGACACCCGGGCACGGTTGACAGTCTTGTCAATTAT	499			
QY 121 CACCGGAGGAAATACGGGGGACCCAGATATTATGTGTCGCTTTGCTATATAGGACCTGT	180			
Db 498 CACCGGAGGAAATACGGGGGACCCAGATATTATGTGTCGCTTTGCTATATAGGACCTGT	439			
QY 181 GGCATGTTTGTCTACAGTAAAGTAAATATATGGGCACTGGGTGATGAGTGTGGCTTTG	240			
Db 438 GGCATGTTTGTCTACAGTAAAGTAAATATATGGGCACTGGGTGATGAGTGTGGCTTTG	423			
QY 241 GTGNGTAAATTTTTTTTTTAATTTTACAGTTTGTGCTTTAAAGATTTTGTATTTGTA	300			
Db 422 -	423			
QY 301 TTTTTTAAAAAGTCTGTGTCTGAACTTGAGCCTGAGCCGAGCCAGAAACCGAGGCTG	360			
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QY 361 CAAGACCTACCGGCGGTCTTAAATATGGCGCTGTATCTGAGAGCGCCGACATCACTTG	420			
Db 374 CAAGACCTACCGGCGGTCTTAAATATGGCGCTGTATCTGAGAGCGCCGACATCACTTG	315			

QY	421	TGTCAGAGATGCAATAGTAAGTACGGATAGCTGTGACTCCGCTCTTTCTTAACACACTC	480
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QY	481	CTGAGATACACCCGGTGTGCTCCGCTGTGCCCATTTAAACAGATTGCCGTGAGATTGGTG	540
Db	254	CTGAGATACACCCGGTGTGCTCCGCTGTGCCCATTTAAACAGATTGCCGTGAGATTGGTG	195
QY	541	GCGCTCCGCAAGCTGTGGAATGTATCGAGACCTTGCTTAAACAGCCTGGGCAACTTTGG	600
Db	194	GCGCTCCGCAAGCTGTGGAATGTATCGAGACCTTGCTTAAACAGCCTGGGCAACTTTGG	135
QY	601	ACTTGACCTGTAAACGCCCAAGCCATTAAGTGTAAACCTGTGATTCCGTGTGGTTAA	660
Db	134	ACTTGACCTGTAAACGCCCAAGCCATTAAGTGTAAACCTGTGATTCCGTGTGGTTAA	75
QY	661	GCGCTTTGTTTGCAGATGAGTTGATGTAAATTAAAGGGTGAGATATGTTTAA	718
Db	74	GCGCTTTGTTTGCAGATGAGTTGATGTAAATTAAAGGGTGAGATATGTTTAA	17

FEATURES	LOCATION/Qualifiers
SOURCE	1. .743
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CA306892/c	
LOCUS	
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ACCESSION	UI-H-FT1-bht-p-24-0-UI.81 NCI_CGAP_FTI Homo sapiens cDNA clone
VERSION	UI-H-FT1-bht-p-24-0-UI 3, mRNA sequence.
KEYWORDS	CA306892
SOURCE	CA306892.1 GI:2446946
ORGANISM	EST.
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	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 743)
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL	Tumor Gene Index
COMMENT	Unpublished (1997)
	Contact: Robert Straubeberg, Ph.D.
	Email: cgapsb-remail.nih.gov
	Tissue Procurement: Dr. Gary W. Hunninghake, U of I
	CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
	CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
	DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
	Clone Distribution: Clone distribution information can be obtained
	from Dr. M. Bento Soares, bento-soaresuiowa.edu
	Seq primer: M13 FORWARD
	PolyA=yes.

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-Ft1-bnt-P-24-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_1b="NCI_CGAP_Ft1"
/notes="Organ: lung; Vector: pDT73-Pac (Pharmacia) with a
modified polylinker; Site 1: Ecor I; Site 2: Not I;
NCI CGAP Ft1 is a normalized cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples
were a mixture of these conditions (times refer to
incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of
the conditions, other donor macrophages in different
conditions). The mRNA samples were pooled for library
construction. Control 0 hours; control 3 hours; control 24
hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
mol 10, 3 hours; Klebsiella mol 10, 24 hours; Staph aureus
mol 10, 3 hours; Staph aureus mol 10, 24 hours; Adenoviral

```

vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCATGCCC. The tissue was provided by Dr. Gary W. Hummingake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCATGCCC"

ORIGIN

Query Match 18.1%; Score 469.4; DB 6; Length 743;
Best Local Similarity 83.7%; Pred. No. 6.1e-116;
Matches 607; Conservative 0; Mismatches 1; Indels 117; Gaps 2;

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DB      1 ATCGATCTTACCTGCGACGAGCTGCTTCCACCCAGGACGACGAGAGTGAAGAGGT 60
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DB      625 ATCGATCTTACCTGCGACGAGCTGCTTCCACCCAGGACGACGAGAGTGAAGAGGT 566
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DB      61 GAGGAGTTTGTTAGATTATGTGAGACCCCGGCGACGAGTTGACGCTTGTCTATTAT 120
OY      121 CACCGGAGAGTAATCGGGGAGACCCAGATATATATGTGCTTGTCTATATAGACCTGT 180
DB      121 CACCGGAGAGTAATCGGGGAGACCCAGATATATATGTGCTTGTCTATATAGACCTGT 180
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DB      505 CACCGGAGAGTAATCGGGGAGACCCAGATATATATGTGCTTGTCTATATAGACCTGT 446
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DB      181 GGCATGTTTGTCTACAGTAAGTGAATAATTATGCGAGTGGGATGAGTGGGCTTGG 240
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DB      445 GGCATGTTTGTCTACAGTAAGTGAATAATTATGCGAGTGGGATGAGTGGGCTTGG 430
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DB      241 GTGTGTGTAATTTTTTTTAAATTTTAAAGTTTGTGTTTAAAGATTTGTATGTGA 300
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OY      141 ACTTGAGCTGTAAAGCGCCCGAGCCATTAAGGTGTAACCTGTGATGCGTGTGTGTTAA 82
DB      141 ACTTGAGCTGTAAAGCGCCCGAGCCATTAAGGTGTAACCTGTGATGCGTGTGTGTTAA 82
OY      661 GGCCTTTGTGTTGCTGAATGAGTGTATGTAAGTTTAAATTAAGGAGTGTGTTAAAC 719
DB      661 GGCCTTTGTGTTGCTGAATGAGTGTATGTAAGTTTAAATTAAGGAGTGTGTTAAAC 719
OY      81 GGCCTTTGTGTTGCTGAATGAGTGTATGTAAGTTTAAATTAAGGAGTGTGTTAAAC 22
DB      81 GGCCTTTGTGTTGCTGAATGAGTGTATGTAAGTTTAAATTAAGGAGTGTGTTAAAC 22
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OY 720 TTGCA 724
DB 21 TTGAA 17

RESULT 7

CD370856/c

LOCUS

DEFINITION

UI-H-FT1-bj2-n-11-0-UI 61 NCI CGAP_FTI Homo sapiens cDNA clone

UI-H-FT1-bj2-n-11-0-UI 3', mRNA sequence.

ACCESSION

CD370856

VERSION

CD370856.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE

1 (bases 1 to 602)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgaps-roman1.nih.gov

Tissue Procurement: Dr. Gary W. Hummingake, U of I

cDNA library preparation: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

<http://genome.uiowa.edu/distribution/cgap.html>

Seq primer: M13 FORWARD

POLYA=Yes.

FEATURES

Source

1..602
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bj2-n-11-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_id="NCI CGAP_FTI"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP_FTI is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; wt adenovirus + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCATGCCC. The tissue was provided by Dr. Gary W. Hummingake of the University of Iowa.

ORIGIN

TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

Query Match 17.7%; Score 460; DB 6; Length 602;
Best Local Similarity 83.5%; Pred. No. 2.1e-113; Indels 116; Gaps 1;
Matches 586; Conservative 0; Mismatches 0;

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QY 17 ACGAGGCTGCTTTCCACCAGTGCAGACGAGATGAAGAGGCTGAGAGTTGTGTAG 76
DB 602 ACGAGGCTGCTTTCCACCAGTGCAGACGAGATGAAGAGGCTGAGAGTTGTGTAG 543
DB 77 ATTATGTGACACCCCGGCGACGGTTGCAGCTTGTTCATTATACCGAGAAATACG 136
DB 542 ATTATGTGACACCCCGGCGACGGTTGCAGCTTGTTCATTATACCGAGAAATACG 483
QY 137 GGGACCCGATATTATGTTGCTTGTATATGAGACCTGTGCGATGTTGTCTACA 196
DB 482 GGGACCCGATATTATGTTGCTTGTATATGAGACCTGTGCGATGTTGTCTACA 423
QY 197 GTAAAGTAAATTAATGCGCAGTGGTGAATAGATGGTGGTGGTGTGTAATTTT 256
DB 422 -----
QY 257 TTATATTTTCAAGTTTGTGTTTAAAGAAATTTTGTATTTTAAAAAGTCC 316
DB 422 -----
QY 317 TGTGCTGAACCTGAGCTGAGCCGAGCCAGAACCGAGGCTGACACCTACCCGCG 376
DB 418 TGTGCTGAACCTGAGCTGAGCCGAGCCAGAACCGAGGCTGACACCTACCCGCG 359
QY 377 TCTTAAATGCGCGCTGCTATCTGAGAGCGCCGACATCACCTGTGTCTAGAGATGCA 436
DB 358 TCTTAAATGCGCGCTGCTATCTGAGAGCGCCGACATCACCTGTGTCTAGAGATGCA 299
QY 437 TAGTAGTAGGATAGCTGTACTCGGTCTTCTTAACACCTCTGTGATACACCCGT 496
DB 298 TAGTAGTAGGATAGCTGTACTCGGTCTTCTTAACACCTCTGTGATACACCCGT 239
QY 497 GGTCCCGCTGCGCCATTAAACGATGCGGTGAGATGGTGGGCGTCCGACGGCTGT 556
DB 238 GGTCCCGCTGCGCCATTAAACGATGCGGTGAGATGGTGGGCGTCCGACGGCTGT 179
QY 557 GGAATGTATCGAGACTTGTCTTAAAGAGCTGTGGCACTTTGAGCTTGAAGTAAAG 616
DB 178 GGAATGTATCGAGACTTGTCTTAAAGAGCTGTGGCACTTTGAGCTTGAAGTAAAG 119
QY 617 CCCCAAGCCATTAAGGTGTAACCTGTGTGATGCTGTGTGTTAACGCCCTTTGTGCTGA 676
DB 118 CCCCAAGCCATTAAGGTGTAACCTGTGTGATGCTGTGTGTTAACGCCCTTTGTGCTGA 59
QY 677 ATGAGTTGATGATGATTAATTAAGGCTGAGATTAATGTTAA 718
DB 58 ATGAGTTGATGATGATTAATTAAGGCTGAGATTAATGTTAA 17

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RESULT 8
BMS91710 337 bp mRNA linear EST 25-FEB-2002
LOCUS BMS91710
DEFINITION 1700687388831 A.Gam.ad.cDNA.blood1 Anopheles gambiae cDNA clone
19600449695952 5', mRNA sequence.
ACCESSION BMS91710
VERSION BMS91710.1 GI:18887571
KEYWORDS EST.
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Anopheles.
REFERENCE 1 (bases 1 to 337)
Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L.,

TITLE
JOURNAL
COMMENT

Charlab,R., Colling,F.H., Venter,J.C. and Hoffman,S.L.
Celera Anopheles gambiae EST project
Unpublished (2002)
Contact: Holt R.A.
Celera Genomics
45 W. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
Fax: 2404534580
Email: HoltR@celera.com
Plate: N01004AB8 row: P column: 18
Seq primer: M13 Reverse.

FEATURES

SOURCE

1..337

location/qualifiers

/organism="Anopheles gambiae"

/mol_type="mRNA"

/strain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"

/db_xref="taxon:7165"

/clone="19600449695952"

/dev_stage="Adult"

/lab_host="DHI0b"

/clone_11b="A.Gam.ad.cDNA.blood1"

/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen 24 hours after human blood feeding. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)"

ORIGIN

Query Match 12.9%; Score 335.4; DB 4; Length 337;
Best Local Similarity 99.7%; Pred. No. 1.4e-79;
Matches 336; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 668 GTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 727
DB 1 GTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 60
QY 728 CGTGTAAATGAGGCGGCGCTTAAAGGATATATATGCGCGGTGCTTAATCTTGTTAC 787
DB 61 CGTGTAAATGAGGCGGCGCTTAAAGGATATATATGCGCGGTGCTTAATCTTGTTAC 120
QY 788 ATCTGACCTCATGAGAGCTTGGAGAGTGTGGAAGATTTTCTGCTGCGCTAATCTTCT 847
DB 121 ATCTGACCTCATGAGAGCTTGGAGAGTGTGGAAGATTTTCTGCTGCGCTAATCTTCT 180
QY 848 GGAACAGAGCTCTAAGATCACTCTTGGTTTGAAGGTTTCTGAGGAGCTATCCAGAGC 907
DB 181 GGAACAGAGCTCTAAGATCACTCTTGGTTTGAAGGTTTCTGAGGAGCTATCCAGAGC 240
QY 908 AAAGTTAGTCTGAGATTAAGAGATTAAGAGATTAAGAGATTAAGAGATTAAGAG 967
DB 241 AAAGTTAGTCTGAGATTAAGAGATTAAGAGATTAAGAGATTAAGAGATTAAGAG 300
QY 968 CTGTGAGAGCTGTTGATTTCTTGAATCTGGCTAC 1004
DB 301 CTGTGAGAGCTGTTGATTTCTTGAATCTGGCTAC 337

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RESULT 9
BP915148/c 347 bp mRNA linear EST 18-JAN-2001
LOCUS BP915148
DEFINITION IL3-UT0114-041200-328-H03_1 UT0114 Homo sapiens cDNA, mRNA
sequence.
ACCESSION BP915148
VERSION BP915148.1 GI:12306606
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 347)
Dias Neto,E., Garcia Correa,R., Veijovski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.P., Matsukuma,A., Bata,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
TITLE
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&ct=IL3-UT0114-
041200-328-H03_1&ct3=2000-12-04&ct4=1)
Seq primer: puc 18 forward
High quality sequence stop: 329.
Location/Qualifiers
1. .347
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_1lb="UT0114"
/note="Organ: uterus tumor; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORSTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
ORIGIN
Query Match 9.6%; Score 249.8; DB 2; Length 347;
Best Local Similarity 95.5%; Pred. No. 2.8e-56;
Matches 257; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY CCGACATACCTGCTCTAGAGAAATGCAATGATAGTACGATAGCTCCGGTCT 467
DB CCGACATACCTGCTCTAGAGAAATGCAATGATAGTACGATAGCTCCGGTCT 288
QY TCTTAACACACCTCTGAGATACACCCGGTGTCCCGCTGCCCATTAACCAAGTCC 527
DB TCTTAACACACCTCTGAGATACACCCGGTGTCCCGCTGCCCATTAACCAAGTCC 228
QY 528 GTGAGAGTGTGGGGCGTCCGCAAGCTGTGGAATGATCGAGAACTTCTTAACGAGCT 587
DB 227 GTGAGAGTGTGGGGCGTCCGCAAGCTGTGGAATGATCGAGAACTTCTTAACGAGCT 168
QY 588 GGGCAACCTTTGGAATTGAGCTGTAAAGCCCCGAGCCATTAAGCTGTAAACCTTGATG 647
DB 167 GGGCAACCTTTGGAATTGAGCTGTAAAGCCCCGAGCCATTAAGCTGTGATG 108
QY 648 CGTGTGTGTTAAACGCTTTGTTTCTGA 676
DB 107 CGTGTGTGTTCTTGTATTGCACTTA 79
RESULT 10
BF914577/c 323 bp mRNA linear EST 18-JAN-2001
LOCUS IL3-UT0114-011200-362-G09_1 UT0114 Homo sapiens cDNA, mRNA
DEFINITION
Sequence.
ACCESSION BF914577
VERSION BF914577.1 GI:12306035
KEYWORDS EST.

SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&ct=IL3-UT0114-
011200-362-G09_1&ct3=2000-12-01&ct4=1)
Seq primer: puc 18 forward
High quality sequence stop: 322.
Location/Qualifiers
1. .323
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_1lb="UT0114"
/note="Organ: uterus tumor; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORSTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
ORIGIN
Query Match 8.6%; Score 224.2; DB 2; Length 323;
Best Local Similarity 94.7%; Pred. No. 2.5e-49;
Matches 232; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 432 TGCATATGTATGATAGATGATGATCGGTCCTTCTAACACACCTCGAGTACAC 491
DB 323 TGCATATGTATGATAGATGATGATCGGTCCTTCTAACACACCTCGAGTACAC 264
QY 492 CCGGTGTCCGCTGTCCCATTAACCAAGTTCCGCTGAGAGTTGGTGGCGCCAG 551
DB 263 CCGGTGTCCGCTGTCCCATTAACCAAGTTCCGCTGAGAGTTGGTGGCGCCAG 204
QY 552 GCTGTGAATGATGAGAGACTTCTTAAAGAGCTGGGCAACTTTGAGACTGT 611
DB 203 GCTGTGAATGATGAGAGACTTCTTAAAGAGCTGGGCAACTTTGAGACTGT 144
QY 612 AAAGCCCCGAGCCATTAAGGTAAAGTGGTGTGTTGATTAAGCCTTTGTTT 671
DB 143 AAAGCCCCGAGCCATTAAGGTAAAGTGGTGTGTTGATTAAGCCTTTGTTTGA 84
QY 672 GCTGA 676
DB 83 GCTTA 79
RESULT 11
BF915126/c

LOCUS	BP915126	321 bp	mRNA	linear	EST 18-JAN-2001
DEFINITION	IL3-UT0114-041200-328-A10_1 UT0114	Homo sapiens	cDNA, mRNA		
ACCESSION	BF915126				
VERSION	BF915126.1	GI:12306584			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens (human)				
REFERENCE	Mullalyotla, Netasoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 321)				
AUTHORS	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Britones, M. R., Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F., Goldman, G. H., Carvalho, A. P., Matukuma, A., Bala, G. S., Simpson, D. H., Brunstein, A., deoliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J.				
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)				
MEDLINE	20202863				
PubMed	10737800				
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Tel: +55-11-2707001 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the PAPESP/ILCR Human Cancer Genome Project. This entry can be seen in the following URL http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&ct=IL3-UT0114-041200-328-A10.1&cs=2000-12-04&ca=1 Seq primer: puc 18 forward High quality sequence atpoc 159. Location/Qualifiers 1..321 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /def_features="Adult" /clone_id="UT0114" /note="Organ: uterus; tumor; Vector: puc18; Site: 1: Smal; Site 2: Smal; A mini-library was made by cloning products derived from ORSTS PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."				
FEATURES					
SOURCE					
ORIGIN					
Query Match	8.6%	Score 223.8	DB 2	Length 321	
Best Local Similarity	95.1%	Pred. No. 3.3e-49			
Matches 231	Conservative 0	Mismatches 12	Indels 0	Gaps 0	
QY	434	CAATAGTAGTACGATAGCTGACTCCGGCTCTTCAACACACCTCTGAGATACACC	493		
DB	321	CAATAGTAGTACGATAGCTGACTCCGGCTCTTCAACACACCTCTGAGATACACC	262		
QY	494	GGTGGTCCCGCTGGCCCATTTAAACAGTTGCGGTGAGTTGGTGGGCGTCCGACGC	553		
DB	261	GGTGGTCCCGCTGGCCCATTTAAACAGTTGCGGTGAGTTGGTGGGCGTCCGACGC	202		
QY	554	TGTGGATGTATCGAGGACTTGCTTAAAGACCTGGGCAACCTTGGACTGAGCTGTA	613		
DB	201	TGTGGATGTATCGAGGACTTGCTTAAAGAGCTGGGCAACCTTGGACTGAGCTGTA	142		
QY	614	ACGCCACGAGCATTAAGGTGTAACCTTGATTGGTGTGTTGAAGCCTTGTGTTGC	673		
DB	141	ACGCCACGAGCATTAAGGTGTAACCTTGATTGGTGTGTTGTTGTTTATTGACGC	82		
QY	674	TGA 676			

Db	1	1	741 bp	mRNA	linear	EST 05-AUG-2004
CD366021/c	CD366021	741 bp	mRNA	linear	EST 05-AUG-2004	
LOCUS	UT-H-FT1-bj5-k-22-0-UT	81	NCI_CGAP_FTI	Homo sapiens	CDNA clone	
DEFINITION	UT-H-FT1-bj5-k-22-0-UT 3', mRNA sequence.					
ACCESSION	CD366021					
VERSION	CD366021.1	GI:31150111				
KEYWORDS	EST.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryote, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;					
AUTHORS	Mammalia, Eutheria, Primates, Catarrhini, Homiidae, Homo.					
TITLE	1 (bases 1 to 741)					
JOURNAL	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .					
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index					
FEATURES	Unpublished (1997)					
SOURCE	Contact: Robert Strausberg, Ph.D.					
	Email: cgapsb@omall.nih.gov					
	Tissue Procurement: Dr. Gary W. Hunninghake, U of I					
	CDNA Library preparation: Dr. M. Bento Soares, University of Iowa					
	CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa					
	DNA Sequencing by: Dr. M. Bento Soares, University of Iowa					
	Clone Distribution: Distribution information can be found at					
	http://genome.uiowa.edu/distribution/cgap.html					
	Seq primer: M13 FORWARD					
	POLYA-yes.					
	Location/Qualifiers					
	1..741					
	/organism="Homo sapiens"					
	/mol_type="mRNA"					
	/db_xref="taxon:9606"					
	/clone="UT-H-FT1-bj5-k-22-0-UT"					
	/tissue_type="Alveolar Macrophage"					
	/dev_stage="Adult"					
	/lab_host="DH10B (Life Technologies)"					
	/clone_l1b="NCI CGAP_FTI"					
	/note="Organ: Lung; Vector: pRTT3-Pac (Pharmacia) with a					
	modified polylinker; Site_1: EcoR I; Site_2: Not I.					
	NCI_CGAP_FTI is a normalized CDNA library constructed from					
	a pool of 81 RNA samples from Alveolar Macrophages					
	challenged with different treatments. The mRNA samples					
	were a mixture of these conditions (times refer to					
	incubations following isolation by bronchoalveolar lavage)					
	(some normal donor macrophages were cultured in some of					
	the conditions, other donor macrophages in different					
	conditions). The mRNA samples were pooled for library					
	construction. Control 0 hours; LPS 100 ng/ml, 24 hours;					
	LPS 100 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella					
	PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella					
	moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus					
	moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral					
	vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector					
	(Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500,					
	3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS					
	3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3					
	hours; wt adenovirus + LPS 24 hours. The library was					
	normalized according to Bonaldo, Lennon and Soares, Genome					
	Research, 6:791-806, 1996. First strand CDNA synthesis was					
	primed with an oligo-dT primer containing a Not I site.					
	Double stranded cDNA was ligated to an EcoR I adaptor,					
	digested with Not I, and cloned directionally into					
	pRTT3-Pac vector. The oligonucleotide used to prime the					
	synthesis of first-strand CDNA contains a library tag					
	sequence that is located between the Not I site and the					
	(dr)18 tail. The sequence tag for this library is					
	GCGCAGCCG. The tissue was provided by Dr. Gary W.					
	Hunninghake of the University of Iowa.					
	TAG TISSUE=Human Lung Alveolar Macrophage					

ORIGIN TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

Query Match 8.6%; Score 222.4; DB 6; Length 741;
Best Local Similarity 98.7%; Pred. No. 9.8e-49;
Matches 234; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 2358 AGCCGAGAGCATGTCGCAAGGAGCAACCGGGCTTTGACATGACATGAAGACT 2417
Db AGCCGAGAGCATGTCGCAAGG- AACCTGAACGGGGTGTGACATGACATGAAGACT 672
2418 GGAAGTCTGAGTACGATGAGACCCGACCAAGTGAAGACCTCGCATGTGGCGGTA 2477
QY 671 GGAAGTCTGAGTACGATGAGACCCGACCAAGTGAAGACCTCGCATGTGGCGGTA 612
Db 2478 AACATATTAGGAACCAAGCTGTGATGCTGATGTGACCGAGAGAGTGAAGCCCATCACT 2537
611 AACATATTAGGAACCAAGCTGTGATGCTGATGTGACCGAGAGAGCTGAAGCCCATCACT 552
QY 2538 TGGTGCTGGCCGTCGACCCGCGCTGAGTTGGCTCAGAGATGAAGATACAGATTGAG 2594
Db 551 TGGTGCTGGCCGTCGACCCGCGCTGAGTTGGCTCAGAGATGAAGATACAGATTGAG 495

RESULT 13
LOCUS CD742922 667 bp mRNA linear EST 05-AUG-2004
DEFINITION UI-H-FT1-bka-k-23-0-UI.81 NCI CGAP_F11 Homo sapiens cDNA clone
CD742922
VERSION CD742922.1 GI:32293772
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 667)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NCI
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
<http://genome.uiowa.edu/distribution/cgap.html>
The following repetitive elements were found in this cDNA
sequence: 546-595, >(CAG)n#Simple_repeat (matched complement).
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bka-k-23-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_1lb="NCI CGAP FT1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: Ecor I; Site 2: Not I;
NCI CGAP FT1 is a normalized cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples
were a mixture of these conditions (times refer to

incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of
the conditions, other donor macrophages in different
conditions). The mRNA samples were pooled for library
construction. Control 0 hours; control 3 hours; control 24
hours; LPS 100 ng/mL, 3 hours; LPS 100 ng/mL, 24 hours;
PMA 10 ng/mL, 3 hours; PMA 10 ng/mL, 24 hours; Klebsiella
mol 10, 3 hours; Klebsiella mol 10, 24 hours; Staph aureus
mol 10, 3 hours; Staph aureus mol 10, 24 hours; Adenoviral
vector (Ad5 CMV egfp), mol 500, 3 hours; Adenoviral vector
(Ad5 CMV egfp), mol 500, 24 hours; wt adenovirus mol 500,
3 hours; wt adenovirus mol 500, 24 hours; Ad vector + LPS
3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3
hours; wt adenovirus + LPS 24 hours. The library was
normalized according to Bonaldo, Lennon and Soares, Genome
Research, 6:791-806, 1996. First strand cDNA synthesis was
primed with an oligo-dT primer containing a Not I site.
Double stranded cDNA was ligated to an Ecor I adaptor,
digested with Not I, and cloned directionally into
pT7T3-Pac vector. The oligonucleotide used to prime the
synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
GGCCATGCCG. The tissue was provided by Dr. Gary W.
Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 6.7%; Score 173.6; DB 6; Length 667;
Best Local Similarity 97.8%; Pred. No. 1.8e-35;
Matches 176; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1165 GGAAGGCGGTGTGAGACACAAAGATCGCTCTACTGTTCTCTCCGCGCCGGGGA 1224
Db 667 GGAAGGCGGTGTGTGACACAAAGATCGCTCTACTGTTCTCTCCGCGCCGGGGA 608

QY 1225 TAATACCGACGAGC 1284
Db 607 TAATACCGACGAGC 548

QY 1285 AGAGCCCATGGAACCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 1344
Db 547 AGAGCCCATGGAACCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 488

RESULT 14
LOCUS CD365243 661 bp mRNA linear EST 05-AUG-2004
DEFINITION UI-H-FT2-bj-c-23-0-UI.81 NCI CGAP_F12 Homo sapiens cDNA clone
CD365243
VERSION CD365243.1 GI:31149333
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 661)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
<http://genome.uiowa.edu/distribution/cgap.html>
The following repetitive elements were found in this cDNA
sequence: 546-595, >(CAG)n#Simple_repeat (matched complement).
Seq primer: M13 FORWARD

Location/Qualifiers

Source

ORIGIN

Qy

Qy

Qy

Perin

1
2
3
4
5

SOURCE

AUTHORS Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L.

Charlaby, R., Collins, F. H., Venter, J. C. and Hoffman, S. L.

JOURNAL Unpublished (2002)

COMMENT

Celera Genomics
45 W. Gude Dr., Rockville, MD 20850, USA

Tel: 2404533151
Fax: 2404534580

Email: HolcRA@celera.com
 Plate: NU01004AAI row: J column: 01
 Seq primer: M13 Reverse.

FEATURES

Source

ORIGIN

Query Match	Score	DB	Length
6.28;	162;	4;	173;

Best Local Similarity 99.4%; Pred.NO. 1.8e-32;
Matches 173; Conservative 0; Mismatches 0; Indels 1; Gaps 1.

668 GTTTCGATGAGTGTATTAATAAGGCTGAGATAATGTTTAACTTGCATCG 727

Db 1 GTTGGCTGAATGAGTTGATGTAAGTTTAATAAAGGGTGAGATAATGTTAACTTGCATGG 60

728 CGTGTAAATGGGGGGGCTTAAAGGCTATATAATGCGCCGTGGCTAATCTTGGTTAC 787

Db 61 CGTGTAAATGGGGGGGCTTAAGGCTATATAATCGCGCGTGGCTAATCTTGTTAC 120

788 ATCTGACCTCATGAGGCTTGGAGTGTTCGAAGATTTTCTGCTGTGCGTAA 841

Db 121 ATCTGACCTCATGGAGGCTTGGAGTGTTTGGAGA-TTTTCTGCTGTGCCGTA 173

Search completed: October 31, 2005, 01:09:48
Job time : 8248 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 30, 2005, 19:12:23 ; Search time 429 Seconds
(without alignments)
9893.944 Million cell updates/sec

Title: US-10-790-562-33_COPY_459_3052
Perfect score: 2594
Sequence: 1 atcgatcttaccctgcacga.....cgtagaagatcacagattgag 2594

Scoring table:
IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PTCUS.COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2594	100.0	7090	4	US-09-714-550-18
2	2594	100.0	35935	2	US-08-735-609-1
3	2594	100.0	35935	2	US-08-735-609-1
4	2594	100.0	35935	2	US-08-735-609-1
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6	2594	100.0	35935	2	US-08-735-609-1
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8	2594	100.0	35935	2	US-08-735-609-1
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11	2582	99.5	35871	4	US-09-956-335-2
12	2161	83.3	34303	2	US-08-735-609-4
13	2161	83.3	34303	2	US-08-735-609-4
14	2161	83.3	34303	2	US-08-735-609-4
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16	2161	83.3	34303	2	US-08-735-609-4
17	2161	83.3	34303	2	US-08-735-609-4
18	2161	83.3	34303	2	US-08-735-609-4
19	2161	83.3	34303	2	US-08-735-609-4
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21	2161	83.3	34303	2	US-08-735-609-4
22	2161	83.3	34303	2	US-08-735-609-4
23	2161	83.3	34303	2	US-08-735-609-4
24	2161	83.3	34303	2	US-08-735-609-4
25	2161	83.3	34303	2	US-08-735-609-4
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28	634	24.4	1000	1	US-08-301-316B-1	Sequence 1, Appli
29	634	24.4	1000	1	US-08-301-316B-1	Sequence 3, Appli
30	634	24.4	1000	2	US-08-473-399B-1	Sequence 1, Appli
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38	618.2	23.8	34794	4	US-09-713-678-39	Sequence 39, Appli
39	599.6	23.1	35081	2	US-08-752-760A-1	Sequence 1, Appli
40	546.8	21.1	7507	4	US-08-653-114A-1	Sequence 1, Appli
41	463	17.8	1800	1	US-08-540-077-4	Sequence 4, Appli
42	458.2	17.7	1796	1	US-08-540-077-2	Sequence 1, Appli
43	408.6	11.9	315	3	US-08-945-424-1	Sequence 2, Appli
44	308.6	11.9	315	4	US-09-718-865-1	Sequence 1, Appli
45	183.8	7.1	216	4	US-09-714-550-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1									
US-09-714-550-18									
Sequence 18, Application US/09714550									
Patent No. 6558948									
GENERAL INFORMATION:									
APPLICANT: Kochanek, Stefan									
TITLE OF INVENTION: Permanent amniocytic cell line, its									
TITLE OF INVENTION: Production and use for the production of gene transfer									
FILE REFERENCE: 50125/007002									
CURRENT APPLICATION NUMBER: US/09/714,550									
CURRENT FILING DATE: 2000-11-16									
PRIOR APPLICATION NUMBER: US 60/167,439									
PRIOR FILING DATE: 1999-11-23									
NUMBER OF SEQ ID NOS: 18									
SOFTWARE: FastSeq for Windows Version 4.0									
SEQ ID NO 18									
LENGTH: 7090									
TYPE: DNA									
ORGANISM: Plasmid STK146									
US-09-714-550-18									
Query Match									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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DB	3165	ATCGATCTTACTGCGACGAGGCTGCTTCCACCGATGACGAGATGAAGAGGT	3224						
QY	61	GAGGAGTTTGTTGATTAATATGTCGAGACCCCGGCGACCGTTGCAAGTCTTGCATTAT	120						
DB	3225	GAGGAGTTTGTTGATTAATATGTCGAGACCCCGGCGACCGTTGCAAGTCTTGCATTAT	3284						
QY	121	CACCGAGGAATATACGGGGGACCCGATATTAATGTTGCTTATATGAGACCTGT	180						
DB	3285	CACCGAGGAATATACGGGGGACCCGATATTAATGTTGCTTATATGAGACCTGT	3344						
QY	181	GGCATGTTTGTCTACAGTAAGTAAATTAATGCGCACTGGGTGATAGTGGGTTTG	240						
DB	3345	GGCATGTTTGTCTACAGTAAGTAAATTAATGCGCACTGGGTGATAGTGGGTTTG	3404						
QY	241	GTCGCTGATTTTCTTATTTTATTTTACAGTTTGTGCTTAAAGATTTTGTATTTGA	300						
DB	3405	GTCGCTGATTTTCTTATTTTATTTTACAGTTTGTGCTTAAAGATTTTGTATTTGA	3464						
QY	301	TTTTTTAAAGGCTGTGCTGTAACCTGAGCTGAGCCGAGACCGAGGCTG	360						
DB	3465	TTTTTTAAAGGCTGTGCTGTAACCTGAGCTGAGCCGAGACCGAGGCTG	3524						

Oy 361 CAAGACCTAACCCGCGCTGCTTAAATGCGCGCTGCTATCTGAGAGCGCCGACATCACTG 420
Db 3525 CAAGACCTAACCCGCGCTGCTTAAATGCGCGCTGCTATCTGAGAGCGCCGACATCACTG 3584
Oy 421 TGTCTAGAGAAATGCAATATGATGATCGAATAGCTGATCTCCGCTCTTCTAACAACCTC 480
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Db 3645 CTGAGATACACCCGCGTGTCTCCGCTGTGCCCCATTAAACCAAGTTGCCGTGAGTTGTTG 3704
Oy 541 GCGCTCGCAGGCTGTGGAATGTATCGAGGACTTGCTTAAAGAGCTGCGGCAACTTTGG 600
Db 3705 GCGCTCGCAGGCTGTGGAATGTATCGAGGACTTGCTTAAAGAGCTGCGGCAACTTTGG 3764
Oy 601 ACTTGAAGCTGTAAACGCCCCAGGCCATTAAGGTGTAAACCTGTGATTGCGTGTGTAA 660
Db 3765 ACTTGAAGCTGTAAACGCCCCAGGCCATTAAGGTGTAAACCTGTGATTGCGTGTGTAA 3824
Oy 661 CGCCTTTGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Db 3825 CGCCTTTGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3884
Oy 721 TGCAATGCGGTGTAAATGCGCGCGGCTTAAAGGGATATATGCGCGGCTAACT 780
Db 3885 TGCAATGCGGTGTAAATGCGCGCGGCTTAAAGGGATATATGCGCGGCTAACT 3944
Oy 781 TGGTTACATCTGACCTCAATGAGGCTTGGAGTGTGGAAATTTTCTGCTGTGCTA 840
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Oy 961 TGAATCTGTGTGAGAGCTGTGTTGATCTTTGAATCTGGGTCAACGAGCGCTTTTCCAG 1020
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Db 4185 AGAAGGTATCAAGACTTTTGAATTTTCCACACCGGGGCGGCTGCGCTGTGCTT 4244
Oy 1081 TTTTGAAGTTTATTAAGATTAATGAGAGCAAAACCATCTGAGCGGGGCTTACCTGC 1140
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Oy 1141 TGAATTTTCTGCGCAATGATCTGTGAGAGCGGTTGTGACAACAAGATGCTGTCTAC 1200
Db 4305 TGAATTTTCTGCGCAATGATCTGTGAGAGCGGTTGTGACAACAAGATGCTGTCTAC 4364
Oy 1201 TGTGTCTCTCCGCTCGCGCGCGATTAATACGAGAGAGACAGACAGACAGAGAGG 1260
Db 4365 TGTGTCTCTCCGCTCGCGCGCGATTAATACGAGAGAGACAGACAGACAGAGAGG 4424
Oy 1261 AAGCGAGCGCGCGCGAG 1320
Db 4425 AAGCGAGCGCGCGCGAG 4484
Oy 1321 GGAATGATATGTTGATCAGGTGCTGAATCTGATCAGAACTGAGACGATTTTGACAT 1380
Db 4485 GGAATGATATGTTGATCAGGTGCTGAATCTGATCAGAACTGAGACGATTTTGACAT 4544
Oy 1381 TACGAGAGATGAG 1440
Db 4545 TACGAGAGATGAG 4604

Oy 1441 AGAGAGAGCTAGGAATCTAGCTTTTATGCTTAATGACAGACACCGCTCTGAGTATTAAC 1500
Db 4605 AGAGAGAGCTAGGAATCTAGCTTTTATGCTTAATGACAGACACCGCTCTGAGTATTAAC 4664
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Db 4785 GGTATATGCAAGAGTGGCACTTAGGCGAGATGCGAATGACAGATCAAGATCAAGATTTGAAA 4844
Oy 1681 TATCAGGAATTTGTTGTAATTTCTGGAAACGCGGCGGAGGTGAGATAGTAACGAGAGA 1740
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Db 4905 TAGGGTGGCTTTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4964
Oy 1801 GGTGTATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
Db 4965 GGTGTATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5024
Oy 1861 CAATACCAACCTTATCTTACACGAGTGAAGCTTATGAGGTTTAAACAATCTGTGTGGA 1920
Db 5025 CAATACCAACCTTATCTTACACGAGTGAAGCTTATGAGGTTTAAACAATCTGTGTGGA 5084
Oy 1921 AGCTGAGACGATGATGAGGTTGCGGCGTGTGCTTTATCTGCTGCGAGAGGGGGTGT 1980
Db 5085 AGCTGAGACGATGATGAGGTTGCGGCGTGTGCTTTATCTGCTGCGAGAGGGGGTGT 5144
Oy 1981 GTGTGCGCCCAAAAGCAGGCGCTTCAATTAAGAAATGCTCTTTGAAAGTGTACCTTGG 2040
Db 5145 GTGTGCGCCCAAAAGCAGGCGCTTCAATTAAGAAATGCTCTTTGAAAGTGTACCTTGG 5204
Oy 2041 TATCTGTCTGAGGGTAACTTCCAGAGGTGCGCACATGTGCTTCCGACTGTGCTT 2100
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Oy 2101 CATGCTAGTAAAGCGGTGTGATTAAGCATPAACGTGTATGTGGCAACTGAGAGA 2160
Db 5265 CATGCTAGTAAAGCGGTGTGATTAAGCATPAACGTGTATGTGGCAACTGAGAGA 5324
Oy 2161 CAGGGCTCTCAGATGCTGACCTGCTCGAGCGGCACTGTCACTGTGAGAGACATTTCA 2220
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Oy 2221 CGTAGCCAGCACTCTGCGAAGGCTTGGCAAGTGTGAGCATTAACATGACCCGCTG 2280
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Oy 2281 TTTCTTGCATTTTGGGTAAACAGAGAGGGGGTGTCTTCACTTAAAGCAATTTTGAATCA 2340
Db 5445 TTTCTTGCATTTTGGGTAAACAGAGAGGGGGTGTCTTCACTTAAAGCAATTTTGAATCA 5504
Oy 2341 CACTAAGATATTTGCTTGAAGCCGAGACATGTCCAAAGTGAACCTGAAACGAGGTGTTTGA 2400
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Oy 2401 CATGACATGAAAGTCTGGAAGGTGTGAGGTACGATGAGACCCGCAACAGGTGCAAGCC 2460
Db 5565 CATGACATGAAAGTCTGGAAGGTGTGAGGTACGATGAGACCCGCAACAGGTGCAAGCC 5624
Oy 2461 CTGCGAGTGTGCGGTAAACAATATTAGAAACAGGCTGTGATGCGGATGAGACGAGAGA 2520
Db 5625 CTGCGAGTGTGCGGTAAACAATATTAGAAACAGGCTGTGATGCGGATGAGACGAGAGA 5684
Oy 2521 GCTGAGGCCGATCACTTGTGTGCTGAGCTGTGACCCGCGCTGAGTTTGGCTTACGATGA 2580

Db 5685 GCTAGAGCCCATCATCTTGCTGCTGCTGCAACCGCCTAGTTGGCTCTAGAGATGA 5744
Qy 2581 AGATACAGATTGAG 2594
Db 5745 AGATACAGATTGAG 5758

RESULT 2

US-08-735-609-1

Sequence 1, Application US/08735609

Patent No. 5953360

GENERAL INFORMATION:

APPLICANT: Chamberlain, Jeffrey S.

APPLICANT: Amalfitano, Andrea

APPLICANT: Hauser, Michael A.

APPLICANT: Kumar-Singh, Rajendra

APPLICANT: Hartigan-O'Connor, Dennis J.

TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Medlen & Carroll, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: California

COUNTRY: United States Of America

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/735, 609

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Ingolia, Diane E.

REGISTRATION NUMBER: 40,027

REFERENCE/DOCKET NUMBER: UM-02484

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 35935 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

US-08-735-609-1

Query Match 100.0%; Score 2594; DB 2; Length 35935;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 GAGAGTTTGTGTTAGATTATGTGAGACACCCGCGGACGCTTGCACTTAT 120
Db 977 GAGAGTTTGTGTTAGATTATGTGAGACACCCGCGGACGCTTGCACTTAT 1036
Qy 121 CACCGAGGAATAGGGGAGCCAGATATTATGTTGCTTGCTATAGAACCTGT 180
Db 1037 CACCGAGGAATAGGGGAGCCAGATATTATGTTGCTTGCTATAGAACCTGT 1096
Qy 181 GGCATGTTTGTCTACAGTAAGTGAATAATTATGGCAGTGGGTGATAGAGTGGTGG 240
Db 1097 GGCATGTTTGTCTACAGTAAGTGAATAATTATGGCAGTGGGTGATAGAGTGGTGG 1156

Qy 241 GTGTGTAATTTTTTTTAAATTTTACAGTTTGTGTTAAAGAAATTTGTATGTGA 300
Db 1157 GTGTGTAATTTTTTTTAAATTTTACAGTTTGTGTTAAAGAAATTTGTATGTGA 1216
Qy 301 TTTTAAAAAGTCTGTTGCTGAACCTGAGCCGAGCCGAGACGAGACCTG 360
Db 1217 TTTTAAAAAGTCTGTTGCTGAACCTGAGCCGAGCCGAGACCTG 1276
Qy 361 CAAGACCTACCCGCGCTCTAAATAGGCGCTGTATCTGAGACGCCGACATCACTG 420
Db 1277 CAAGACCTACCCGCGCTCTAAATAGGCGCTGTATCTGAGACGCCGACATCACTG 1336
Qy 421 TGTCTAAGGAATGCAATGTATGATACGATAGCTGTGATCTCCGCTCTTCTAACAACCTC 480
Db 1337 TGTCTAAGGAATGCAATGTATGATACGATAGCTGTGATCTCCGCTCTTCTAACAACCTC 1396
Qy 481 CTGAGATPACACCCGCTGCTCCGCTGTCGCCCATTTAAACAGTTGCGGTGAGTGGTG 540
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Qy 541 GCGCTGCGCAGGCTGTGGAATGTATGAGACCTTGAACGAGCCTGGGCAACCTTTGG 600
Db 1457 GCGCTGCGCAGGCTGTGGAATGTATGAGACCTTGAACGAGCCTGGGCAACCTTTGG 1516
Qy 601 ACTTGAGCTGTAAACGCCGCCATTAAGGTAAACCTGTGATTTGCTGTGTTAA 660
Db 1517 ACTTGAGCTGTAAACGCCGCCATTAAGGTAAACCTGTGATTTGCTGTGTTAA 1576
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Qy 781 TGTGTTAATCTGACCTCATGAGAGCTTGGAGTGTGTTGAAAGATTTTCTGCTGCTGA 840
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Db 1877 TGAATCTGTGTGAGCTGTTGATTTGTAATCTGAGTCAACAGGCGCTTTCCAG 1936
Qy 1021 AGAAGTCAATCAAGCTTTGATTTTCCACAGCGGCGCGCTGCGGCTGCTGCTT 1080
Db 1937 AGAAGTCAATCAAGCTTTGATTTTCCACAGCGGCGCGCTGCGGCTGCTGCTT 1996
Qy 1081 TTTTGAATTTTAAAGATTAATGAGAGCAAGAAACCATCTGAGCGGGGGATACCTGC 1140
Db 1997 TTTTGAATTTTAAAGATTAATGAGAGCAAGAAACCATCTGAGCGGGGGATACCTGC 2056
Qy 1141 TGAATTTTCTGCGCATGATCTGTGAGAGCGGTTTGTGACACAAAGATGCTGTGAC 1200
Db 2057 TGAATTTTCTGCGCATGATCTGTGAGAGCGGTTTGTGACACAAAGATGCTGTGAC 2116
Qy 1201 TGTGCTGCTCGCTCGCGCGCGGATTAATACGAGCGAGGACAGACAGACGAGAGG 1260
Db 2117 TGTGCTGCTCGCTCGCGCGCGGATTAATACGAGCGAGGACAGACAGACGAGAGG 2176
Qy 1261 AAGCAGAGCGCGCGCGCAGAGCAGAGCCCATAGAAACCCGAGAGCGGCTGTGACCTTC 1320
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Qy 1321 GGGAAATGATGTTGTACAGGTGCTGAACGTATCCAGAACTGAGACGCAATTTGACAAT 1380

Db 2237 GGGATGAAATTTCTTCAAGTGGCTGAACTGTATCCAGAACTGAGACGCACTTTTGACAT 2296
Qy 1381 TACAGAGATGGCGAGGGGCTAAAGGGGTAAGAGGAGCGGGGGGCTTGTAGGCTAC 1440
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Qy 1441 AGAGAGAGCTAGAGATCTAGCTTTAGCTTAATGACCAAGACACCGCTCTGAGTATTAAC 1500
Db 2257 AGAGAGAGCTAGAGATCTAGCTTTAGCTTAATGACCAAGACACCGCTCTGAGTATTAAC 2416
Qy 1501 TTTTCAACAGATCAAGATTAATTCGCTAATAGCTTGTGCTGGCGAGAAATATTC 1560
Db 2417 TTTTCAACAGATCAAGATTAATTCGCTAATAGCTTGTGCTGGCGAGAAATATTC 2476
Qy 1561 CATAGAGAGCTGACCACTTACTGCTGACCGAGGAGATATTTTGAAGGCTATTTAG 1620
Db 2477 CATAGAGAGCTGACCACTTACTGCTGACCGAGGAGATATTTTGAAGGCTATTTAG 2536
Qy 1621 GGTATATGCAAAAGGTGGCACTTAAAGCCAGATTGCAAGTACAAATCAAGCAACTTGTAAA 1680
Db 2537 GGTATATGCAAAAGGTGGCACTTAAAGCCAGATTGCAAGTACAAATCAAGCAACTTGTAAA 2596
Qy 1681 TATCAGAAATTTGTTCTACATTTCTGGGAAAGGGGCGAGGTGAGATAGTACGAGGA 1740
Db 2597 TATCAGAAATTTGTTCTACATTTCTGGGAAAGGGGCGAGGTGAGATAGTACGAGGA 2656
Qy 1741 TAGAGTGGCTTTAGATGTAGCATGATTAATATGTGCGCGGGGCTGCTTGCAATGACGG 1800
Db 2657 TAGAGTGGCTTTAGATGTAGCATGATTAATATGTGCGCGGGGCTGCTTGCAATGACGG 2716
Qy 1801 GGTGGTATTATGATGATGAAAGTTTAACTGGCCCAATTTTACGGTAAAGGTTTCTGGCC 1860
Db 2717 GGTGGTATTATGATGATGAAAGTTTAACTGGCCCAATTTTACGGTAAAGGTTTCTGGCC 2776
Qy 1861 CAATACCAACCTTATCTTACACGGGTGTAAGCTTCTATGGGTTTAAACAATACCTGTGGA 1920
Db 2777 CAATACCAACCTTATCTTACACGGGTGTAAGCTTCTATGGGTTTAAACAATACCTGTGGA 2836
Qy 1921 AGCTGAGACCGATGTAAAGGGTTCGGGGCTGCGCTTTTACTGCTGTGGAAGGGGGTGT 1980
Db 2837 AGCTGAGACCGATGTAAAGGGTTCGGGGCTGCGCTTTTACTGCTGTGGAAGGGGGTGT 2896
Qy 1981 GGTGCGCCCCAAAGAGAGGGCTTCAATTAAGAAATGCTCTTTGAAGGTGTAACCTTGGG 2040
Db 2897 GGTGCGCCCCAAAGAGAGGGCTTCAATTAAGAAATGCTCTTTGAAGGTGTAACCTTGGG 2956
Qy 2041 TATCTGTCTGAGGGTAACTCAGGGGTGCGCAAAATGTGCTCCGACTGTGGTGTCTT 2100
Db 2957 TATCTGTCTGAGGGTAACTCAGGGGTGCGCAAAATGTGCTCCGACTGTGGTGTCTT 3016
Qy 2101 CATCTAGTGAAGAGCGTGTGATTAACCATTAACATGTATGTGGCACTGCGAGGA 2160
Db 3017 CATCTAGTGAAGAGCGTGTGATTAACCATTAACATGTATGTGGCACTGCGAGGA 3076
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Db 3077 CAGGGCCCTCAGATGCTGACTGCTCGAGCGCAACTGTCACTGCTGGAAGACATTTCA 3136
Qy 2221 CGTAGCCAGCACTCTCGCAAGGCGCTGGCCAGTGTGTTGAGCAATAATGACCCGCTG 2280
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Qy 2281 TTCTCTGATTTGGGTAAAGAGAGGGGGTGTCTTACTTACCAATGCAATTTGAGTCA 2340
Db 3197 TTCTCTGATTTGGGTAAAGAGAGGGGGTGTCTTACTTACCAATGCAATTTGAGTCA 3256
Qy 2341 CACTAAGATATTTGCTGAGCCGAGAGAGCATGTCAAAGGTGAACCTGAACGGGGTGTGGA 2400
Db 3257 CACTAAGATATTTGCTGAGCCGAGAGAGCATGTCAAAGGTGAACCTGAACGGGGTGTGGA 3316
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Db 3317 CATGACCAATGAAGATCTGGAAGGTGCTGAGGTACGATGAGACCCGCAACAGGTGCAAGC 3376
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Db 3377 CTGGAATGTGGCGGTAAACAATATTAGAAACAGGCTGTATGTGATGTGACCGAGGA 3436
Qy 2521 GCTGAGCCCGATCACTTGTGTGCTGCGCTGACCCGCGCTGAGTTGGCTTACGATGA 2580
Db 3437 GCTGAGCCCGATCACTTGTGTGCTGCGCTGACCCGCGCTGAGTTGGCTTACGATGA 3496
Qy 2581 AGATACAGATTGAG 2594
Db 3497 AGATACAGATTGAG 3510

RESULT 3
US-08-735-609-1
Sequence 1, Application US/08735609
Patent No. 5994132
GENERAL INFORMATION:
APPLICANT: Chamberlain, Jeffrey S.
Amalfitano, Andrea
Hauber, Michael A.
Kumar-Singh, Rajendra
Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/735,609
FILING DATE: 23-Oct-1996
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane B.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-02484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 35935 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-08-735-609-1
Query Match 100.0%; Score 2594; DB 2; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATCGATCTTACTCGCAAGAGGCTGGCTTTCCACCAGTGAAGAGATGAAGAGGCT 60
Db 917 ATCGATCTTACTCGCAAGAGGCTGGCTTTCCACCAGTGAAGAGAGGCT 976
Qy 61 GAGGAGTTTGTGTTAATATATGTGAGACACCCGGGAGACGGTTTCAAGTCTTGTCAATTAT 120
Db 977 GAGGAGTTTGTGTTAATATATGTGAGACACCCGGGAGACGGTTTCAAGTCTTGTCAATTAT 1036

QY	121	CACCGAGAGAAATACGGGGAGACCCAGATATTAATGCTTCGCTTGGCTATATAGAGACCTGT	180
Db	1037	CACCGAGAGAAATACGGGGAGACCCAGATATTAATGCTTCGCTTGGCTATATAGAGACCTGT	1096
QY	181	GGCATGTTTGTCTACATGATGTAATAATTATGCGCAGTGGGTGATAGAGTGGGTGG	240
Db	1097	GGCATGTTTGTCTACATGATGTAATAATTATGCGCAGTGGGTGATAGAGTGGGTGG	1156
QY	241	GTTGTGTAAATTTTTTTTTTAAATTTTAAACAGTTTGTGGTTTAAAGAAATTTTGATTTGTGA	300
Db	1157	GTTGTGTAAATTTTTTTTTTAAATTTTAAACAGTTTGTGGTTTAAAGAAATTTTGATTTGTGA	1216
QY	301	TTTTTTTTAAAGCTCTGTGTCTGAACCTGAGACCTGAGCCGAGCCAGAACCGAGACTG	360
Db	1217	TTTTTTTTAAAGGCTCTGTGTGTCTGAACCTGAGACCTGAGCCGAGCCAGAACCGAGACTG	1276
QY	361	CAAGACCTAACCCGCGCTCTAAATATGGCGCTGCTATCTGAGAGCGCCGACATCACTG	420
Db	1277	CAAGACCTAACCCGCGCTCTAAATATGGCGCTGCTATCTGAGAGCGCCGACATCACTG	1336
QY	421	TGTTAGAGAAATGCATATGATAGTACGATAGCTGTGACTCGGATCTTCTAACACCTC	480
Db	1337	TGTTAGAGAAATGCATATGATAGTACGATAGCTGTGACTCGGATCTTCTAACACCTC	1396
QY	481	CTGAGATACACCCGGTGTCCCCGCTGTGCCCATTAACCACTTGCCTGTGAGTGGT	540
Db	1397	CTGAGATACACCCGGTGTCCCCGCTGTGCCCATTAACCACTTGCCTGTGAGTGGT	1456
QY	541	GGCGTCGCGCAGGCTGTGGAAATGATTCGAGGACTTGTAAAGACCTGAGGCGGACACTTGG	600
Db	1457	GGCGTCGCGCAGGCTGTGGAAATGATTCGAGGACTTGTAAAGACCTGAGGCGGACACTTGG	1516
QY	601	ACTTGAGCTGTAAACGCCCCAGGCGCATAGGCTGTAAACCTGTGATTCGCTGTGTGTTAA	660
Db	1517	ACTTGAGCTGTAAACGCCCCAGGCGCATAGGCTGTAAACCTGTGATTCGCTGTGTGTTAA	1576
QY	661	CGCCTTTGTTTCTGGAATGAGTTGATGTAAGTTATTAAGGCTGAGATATGTTTAATCT	720
Db	1577	CGCCTTTGTTTCTGGAATGAGTTGATGTAAGTTATTAAGGCTGAGATATGTTTAATCT	1636
QY	721	TGCATGGCGGTATAATGGGGCGGGGCTTAAGGTTATATAACGCGCTGGGCTAATCT	780
Db	1637	TGCATGGCGGTATAATGGGGCGGGGCTTAAGGTTATATAATCGCGCTGGGCTAATCT	1696
QY	781	TGTTTACATCTGACCTCAATGAGGCTTGGAGTGTGTAAGATTTTTCTCTGACGTA	840
Db	1697	TGTTTACATCTGACCTCAATGAGGCTTGGAGTGTGTAAGATTTTTCTCTGACGTA	1756
QY	841	ACTTGTGGAACAGAGCTCTAACAGTACTCTTGTGTTTGGAGGTTTCTGTGGGCTCAT	900
Db	1757	ACTTGTGGAACAGAGCTCTAACAGTACTCTTGTGTTTGGAGGTTTCTGTGGGCTCAT	1816
QY	901	CCGAGGCAAAATTAAGTCTGCAGAATTAAGAGGATTTACAATGGGAATTTGAAGCTTT	960
Db	1817	CCGAGGCAAAATTAAGTCTGCAGAATTAAGAGGATTTACAATGGGAATTTGAAGAGCTTT	1876
QY	961	TGAATACCTGTGTGAGGCTGTTTGATCTTTGGAATCTGGGTCACAGGCGCTTTTCCAAG	1020
Db	1877	TGAATACCTGTGTGAGGCTGTTTGATCTTTGGAATCTGGGTCACAGGCGCTTTTCCAAG	1936
QY	1021	AGAAAGTCATCAGAATCTTGGAATTTTTCACACCGGCGCGCTGCGGCTGTGTGCTT	1080
Db	1937	AGAAAGTCATCAGAATCTTGGAATTTTTCACACCGGCGCGCTGCGGCTGTGTGCTT	1996
QY	1081	TTTTGAGTTTATATAAGATATAATGAGACCAAGAAACCATCTGAGCGGGGGGTAACTGC	1140
Db	1997	TTTTGAGTTTATATAAGATATAATGAGACCAAGAAACCATCTGAGCGGGGGGTAACTGC	2056
QY	1141	TGGAATTTTCTGCGCATGTCTGTGAGAGGCGTTGTGAGACACAGAATGCGCTGCTAC	1200
Db	2057	TGGAATTTTCTGCGCATGTCTGTGAGAGGCGTTGTGAGACACAGAATGCGCTGCTAC	2116
QY	1201	TGTTGTCTTCCGTCGCCCGCGCATATAACGACGAGAGAGCAGACGACGACGAGG	1260

[illegible]

Db 3197 TTCCTTGATTTGGGTAAACAGAGAGGGGGTGTCTTACCTTACCAATGCAATTTGAGTCA 3256
Qy 2341 CACTTAAGATATTGCTTTGAGCCCGAGAGCATGTCCAAAGTGAACTGAAACGGGGTGTGGA 2400
Db 3257 CACTTAAGATATTGCTTTGAGCCCGAGAGCATGTCCAAAGTGAACTGAAACGGGGTGTGGA 3316
Qy 2401 CATGACCATGAAGATCTGGAAGGTGCTGAGGATGAGATGAGACCCGACACAGGTGACAGC 2460
Db 3317 CATGACCATGAAGATCTGGAAGGTGCTGAGGATGAGATGAGACCCGACACAGGTGACAGC 3376
Qy 2461 CTGCGAGTGTGGCGGTAAACAATATTAGGAACACAGCTGTGATGCTGATGTGAACCGAGGA 2520
Db 3377 CTGCGAGTGTGGCGGTAAACAATATTAGGAACACAGCTGTGATGCTGATGTGAACCGAGGA 3436
Qy 2521 GCTGAGGCCCGCATCTTTGCTGCTGCTGCTGCAACCCGCGCTGATTTGGCTCTAGCGATGA 2580
Db 3437 GCTGAGGCCCGCATCTTTGCTGCTGCTGCTGCAACCCGCGCTGATTTGGCTCTAGCGATGA 3496
Qy 2581 AGATACAGATTGAG 2594
Db 3497 AGATACAGATTGAG 3510

RESULT 4

US-08-379-452-43
Sequence 43, Application US/08379452
Patent No. 6040174

GENERAL INFORMATION:
APPLICANT: IMLER, Jean-Luc
APPLICANT: MEHTALI, Majid
APPLICANT: PAVIRANI, Andrea
TITLE OF INVENTION: DEFECTIVE ADENOVIRUSES AND CORRESPONDING
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHEIS, L.L.P.
STREET: 1737 King Street, Suite 500
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22314-2756
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,452
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR94/00624
FILING DATE: 27-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93 06482
FILING DATE: 28-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Dadio, Susan M.
REGISTRATION NUMBER: 40,373
REFERENCE/DOCKET NUMBER: 029395-002
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 35935 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-379-452-43

Query Match 100.0%; Score 2594; DB 3; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATCTTACCTGCGACGAGGCGCTTTCCACCCAGTGAACGAGATGAAGAGGT 60
Db 917 ATGATCTTACCTGCGACGAGGCGCTTTCCACCCAGTGAACGAGATGAAGAGGT 976
Qy 61 GAGAGTTTGTGTAGATTATGTGAGACACCCCGGGAACGGTTGACAGTCTTGTCAATTAT 120
Db 977 GAGAGTTTGTGTAGATTATGTGAGACACCCCGGGAACGGTTGACAGTCTTGTCAATTAT 1036
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Db 1037 CACCGAGGAATACGGGGGACCCAGATATTATGTGTTCCGCTTTGCTATATAGAGAACCTGT 1096
Qy 181 GGCATGTTTGTCTACAGTAAAGTAAATTAAGGACAGTGGTGTATAGTGTGGTGTG 240
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Qy 241 GTGTGTAATTTTTTTTTTAATTTTACAGTTTGTGTGTTTAAAGAAATTTGTATTTGTA 300
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Qy 301 TTTTAAAAAGTCTGTGTCTGTAACCTGAGCCTGAGCCCGAGACCGAGACCTG 360
Db 1217 TTTTAAAAAGTCTGTGTCTGTAACCTGAGCCTGAGCCCGAGACCGAGACCTG 1276
Qy 361 CAAGACCTACCCGCGCTCTAAATAGGCGCTGCTATCTGAGACGCGCCGACATCACCTG 420
Db 1277 CAAGACCTACCCGCGCTCTAAATAGGCGCTGCTATCTGAGACGCGCCGACATCACCTG 1336
Qy 421 TGTCTAAGAAATGCAATAGTATGATGAGATAGCTGTGATCTCGGTCTTTACACACCTC 480
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Qy 781 TGTTAATCTGACCTGATGAGGCTTGGAGGTGTTGGAAGATTTTCTGCTGTGCTTA 840
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Qy 841 ACTTGTGGAACAGAGCTCTTAACAGTACCTCTGTTTGGAGTTTCTGTGGGCTCAT 900
Db 1757 ACTTGTGGAACAGAGCTCTTAACAGTACCTCTGTTTGGAGTTTCTGTGGGCTCAT 1816
Qy 901 CCCAGCAAGTTAGTCTGAGATTAAGAGATTAACAATGGAATTTGAAGAGCTTT 960
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Db 1877 TGAATCTGTGTGAGCTGTTGATTTTGAATCTGAGTACCAAGCGGCTTTTCCAG 1936
Qy 1021 AGAAGTCATCAAACTTTGATTTTCCACACGGGGCGGCTGCGGCTGTGTGCTT 1080
Db 1937 AGAAGTCATCAAACTTTGATTTTCCACACGGGGCGGCTGCGGCTGTGTGCTT 1996
Qy 1081 TTTTGAAGTTTATGAAGATTAATGAGCGAAGAAACCATCTGAGCGGGGGTACTGCG 1140

QY 2041 TATCTGTCGAGGCTAATCTCCAGGCTGCGCAATGCTGCTGCTGCTGCT 2100
DB 2957 TATCTGTCGAGGCTAATCTCCAGGCTGCGCAATGCTGCTGCTGCTGCT 3016
QY 2101 CATGCTAGTGAAGAGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2160
DB 3017 CATGCTAGTGAAGAGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3076
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QY 2341 CATTAAGATATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2400
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DB 3317 CATGACCAATGAAGATCTGGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3376
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DB 3437 GCTGAGGCGCCGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3496
QY 2581 AGATACAGATTGAG 2594
DB 3497 AGATACAGATTGAG 3510

RESULT 6
US-09-244-752-1
Sequence 1, Application US/09244752
Patent No. 6063622
GENERAL INFORMATION:
APPLICANT: Chamberlain, Jeffrey S.
APPLICANT: Amalfitano, Andrea
APPLICANT: Hauser, Michael A.
APPLICANT: Kumar-Singh, Rajendra
APPLICANT: Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESS: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,752
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/735,609
FILING DATE:
ATTORNEY/AGENT INFORMATION:

NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-02484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 35935 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-09-244-752-1
Query Match 100.0%; Score 2594; DB 3; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCATCTTACCTGCGCAGAGGCTGCTTCCACCCAGTGAAGAGAGAGAGGCT 60
DB 917 ATGCATCTTACCTGCGCAGAGGCTGCTTCCACCCAGTGAAGAGAGAGGCT 976
QY 61 GAGAGTTTGTGTTAGATTAGTGAAGACCCCGGCGCAGGTTGAGAGGCTTGTATTAT 120
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QY 181 GGCATGTTGTCTACAGTAAGTGAATAATTATGCGCAGTGGGTGATGAGTGGGTTTG 240
DB 1097 GGCATGTTGTCTACAGTAAGTGAATAATTATGCGCAGTGGGTGATGAGTGGGTTTG 1156
QY 241 GTGCTGTAATTTTATTTTATTTTACAGTTTGTGCTTATTAAGATTTTGTATTTGA 300
DB 1157 GTGCTGTAATTTTATTTTATTTTACAGTTTGTGCTTATTAAGATTTTGTATTTGA 1216
QY 301 TTTTATTAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 1217 TTTTATTAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1276
QY 361 CAGAAGCTACCCGCGCTCTAAATGCGGCTGCTATCTGAGACGCCGACATCACCTG 420
DB 1277 CAGAAGCTACCCGCGCTCTAAATGCGGCTGCTATCTGAGACGCCGACATCACCTG 1336
QY 421 TGTCTAGAGATGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
DB 1337 TGTCTAGAGATGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1396
QY 481 CTGAGATACACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 1397 CTGAGATACACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1456
QY 541 GCGCTGCGCAGCTGTGGAATGATGAGAGCTTGTCTTAACGAGCTGGGCAACTTTTG 600
DB 1457 GCGCTGCGCAGCTGTGGAATGATGAGAGCTTGTCTTAACGAGCTGGGCAACTTTTG 1516
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DB 1517 ACTGAGCTGTAAGCGCCGAGGCTTAAGGCTTAAGGCTTAAGGCTTAAGGCTTAAGGCT 1576
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QY 721 TGATGCGGTGTTAATGCGGCGGCTTAAGGCTTAATGATGATGATGATGATGATGAT 780
DB 1637 TGATGCGGTGTTAATGCGGCGGCTTAAGGCTTAATGATGATGATGATGATGATGATGAT 1696
QY 781 TGGTTACATCTGACCTCATGAGGCTTGGAGTGTGTTGAAGATTTTCTGCTGCTGCTA 840

Db 1697 TGGTACATCTGACCTCATGAGAGCTTGGAGTGTGGAAGATTTTCTCTGTCGCTA 1756
Qy 841 ACTTGCTGGAACAGAGCTCTAAACAGTACCTCTTGTTTGGAGTTTCTGCGGCTCAT 900
Db 1757 ACTTGCTGGAACAGAGCTCTAAACAGTACCTCTTGTTTGGAGTTTCTGCGGCTCAT 1816
Qy 901 CCCAGGCAAACTTGTGTCGGAATTAAGAGSATTAACTGGGAATTGAAGCTTT 960
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Db 1877 TGAATCTGTGTGAGCTGTTTGAATCTTGAATCTGCTGACAGGCGCTTTTCCAAAG 1936
Qy 1021 AGAAGGTATCAAGACTTTGGATTTTTCACACCGGGCGGCTGCGCTGCTGCTT 1080
Db 1937 AGAAGGTATCAAGACTTTGGATTTTTCACACCGGGCGGCTGCGCTGCTGCTT 1996
Qy 1081 TTTGAGTTTATAAGGATTAATGAGAGAAACCATCTGAGCGGGGGTTACCTGC 1140
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Qy 1561 CATAGAGAGCTGACCACTTACTGCTGACAGCCAGGGGATGATTTTGAAGGCTATTAG 1620
Db 2477 CATAGAGAGCTGACCACTTACTGCTGACAGCCAGGGGATGATTTTGAAGGCTATTAG 2536
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Qy 1741 TAGGCTGCGCTTTAGATGATGATGATTAATATGTGCGCGGGGGTGTGGCATGAGAGG 1800
Db 2657 TAGGCTGCGCTTTAGATGATGATGATTAATATGTGCGCGGGGGTGTGGCATGAGAGG 2716
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Qy 2041 TATCTGTCTGAGGTTAATCTCAGAGGTGCGCCACAATGTGCGCTCCGACTGTGTGCTT 2100
Db 2957 TATCTGTCTGAGGTTAATCTCAGAGGTGCGCCACAATGTGCGCTCCGACTGTGTGCTT 3016
Qy 2101 CATCTAGTGAAGAGGCTGTGATTTAAGCATTAATGTATGTGGCAACTGCGAGGA 2160
Db 3017 CATCTAGTGAAGAGGCTGTGATTTAAGCATTAATGTATGTGGCAACTGCGAGGA 3076
Qy 2161 CAGGCGCTCTCAGATGCTGACCTGCTGAGACGCGCACTGTCACTGTGAGAGACATTTCA 2220
Db 3077 CAGGCGCTCTCAGATGCTGACCTGCTGAGACGCGCACTGTCACTGTGAGAGACATTTCA 3136
Qy 2221 CGTACAGCCACTCTGCAAGGCTGCGCAGTGTGAGCATTAATCTGACCCGCTG 2280
Db 3137 CGTACAGCCACTCTGCAAGGCTGCGCAGTGTGAGCATTAATCTGACCCGCTG 3196
Qy 2281 TTCTTGTGATTTGGGTAAACAGAGGGGGGTGTTCTTACTTAACTTAACAAATTTGAGTCA 2340
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RESULT 7
US-09-245-497-1
Sequence 1, Application US/09245497
Patent No. 6083750
GENERAL INFORMATION:
Applicant: Chamberlain, Jeffrey S.
Applicant: Amalfitano, Andrea
Applicant: Hauser, Michael A.
Applicant: Kumar-Singh, Rajendra
Applicant: Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/245,497
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/735,609
APPLICATION NUMBER: <8> FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-02484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 35935 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-09-245-497-1

Query Match 100.0%; Score 2594; DB 3; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATCCATCTTACTGCGCAGAGCGCTTTCACCCCATGACGACGAGATGAAAGAGCT 60
917 ATCCATCTTACTGCGCAGAGCGCTTTCACCCCATGACGACGAGATGAAAGAGCT 976
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977 GAGAGTTTGTAGTATGATGATGAGACCCCGGGCAGGTTGAGGCTTGTCAATAT 1036
121 CACCGAGAAATACGGGGGACCCAGATATATGTTGCTTGTATATAGAGACTGT 180
1037 CACCGAGAAATACGGGGGACCCAGATATATGTTGCTTGTATATAGAGACTGT 1096
181 GGCATGTTGCTACAGTAAGTAAGAAATTATGCGAGTGGGATAGAGTGGGTTTG 240
1097 GGCATGTTGCTACAGTAAGTAAGAAATTATGCGAGTGGGATAGAGTGGGTTTG 1156
241 GTGTGTAATTTTATTTTATTTTATTTTACAGTTTGTGGTTTAAAGATTTTGTATTGTA 300
1157 GTGTGTAATTTTATTTTATTTTATTTTACAGTTTGTGGTTTAAAGATTTTGTATTGTA 1216
301 TTTTAAAAAGTCTGTGTCTGAACTGAGCTGAGCCGAGCCGAGACCGAGAGCTTG 360
1217 TTTTAAAAAGTCTGTGTCTGAACTGAGCTGAGCCGAGCCGAGACCGAGAGCTTG 1276
361 CAAGACCTACCCCGCTCTCTAAATGCGGCTGTCTATCTGAGAGCCCGACATCACTG 420
1277 CAAGACCTACCCCGCTCTCTAAATGCGGCTGTCTATCTGAGAGCCCGACATCACTG 1336
421 TGTCTAGAGATGCAATAGTAGTACGATAGCTGTGATCTCCGGTCTCTCTAACACACTTC 480
1337 TGTCTAGAGATGCAATAGTAGTACGATAGCTGTGATCTCCGGTCTCTCTAACACACTTC 1396
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1397 CTGAGATACACCCCGTGTCTCCGCTGTGCCCATTTAAACAAGTTGCGTGAAGTTGTG 1456
541 GCGCGCGCAGGCTGTGAATGTATCGAGAGCTTGCTTAAAGAGCTGGGCAACTTTGG 600
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601 ACTTGAGCTGTAAAGCCCGCAGGCAATAAGGTGTAACTGTGATTTGGGTGTGTTAA 660
1517 ACTTGAGCTGTAAAGCCCGCAGGCAATAAGGTGTAACTGTGATTTGGGTGTGTTAA 1576

661 GCGCTTTGTTCTGGAATGATGATGATGATTTAATAAGGCTGAGATTAATGTTAACT 720
1577 GCGCTTTGTTCTGGAATGATGATGATGATTTAATAAGGCTGAGATTAATGTTAACT 1636
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1637 TGCAATGCGGTGTTAAATGCGGCGGGCTTAAAGGATATATATGCGCGGTGGCTAATCT 1696
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841 ACTTGCTGGAACAAGAGCTCTAACAGTACCTTGTGTTTGAAGTTTCTGTGGGCTCAT 900
1757 ACTTGCTGGAACAAGAGCTCTAACAGTACCTTGTGTTTGAAGTTTCTGTGGGCTCAT 1816
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1817 CCCAGGCAAGTTAGTCTGCAAGATTAAGAGGATTAACAAGTGGGAATTTGAAGAGCTTT 1876
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1877 TGAATCTGTGTGAGCTGTTGATTTCTTGAATCTGAGTCAACAGGCGCTTTTCCAG 1936
1021 AGAAGTTCATCAAGACTTTGGAATTTTCCACACCGGGCGCGCTGCGCTGCTGCTT 1080
1937 AGAAGTTCATCAAGACTTTGGAATTTTCCACACCGGGCGCGCTGCGCTGCTGCTT 1996
1081 TTTTGAAGTTTATTAAGGATTAAGAGCGGAAGAACCCATCTAGCGGGGGGTAACTGCG 1140
1997 TTTTGAAGTTTATTAAGGATTAAGAGCGGAAGAACCCATCTAGCGGGGGGTAACTGCG 2056
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2057 TGAATTTTCTGCGCATGATCTGTGAGAGCGGTTGTGAGACACAAGATGCGCTGTAC 2116
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2117 TGTGTCTTCCGTCGCGCGCGGATTAATCCAGAGAGAGACAGACAGACAGAGAGG 2176
1261 AAGCAGGCGCGCGCGAGAGAGAGCCCATGGAACCCGAGAGCGGCGCTGAGACCTC 1320
2177 AAGCAGGCGCGCGCGAGAGAGAGCCCATGGAACCCGAGAGCGGCGCTGAGACCTC 2236
1321 GGAATGATTTGTTACAGGTGCTGAACTGTATCCAGAACTGAGAGCATTTTGACAT 1380
2237 GGAATGATTTGTTACAGGTGCTGAACTGTATCCAGAACTGAGAGCATTTTGACAT 2296
1381 TACAGAGATGGCAAGGGGCTTAAAGGGGTTAAAGAGGAGCGGGGCTGTGAGGCTAC 1440
2297 TACAGAGATGGCAAGGGGCTTAAAGGGGTTAAAGAGGAGCGGGGCTGTGAGGCTAC 2356
1441 AGAGAGGCTTGAAGATCTAGCTTTTACCTTAATACAGACAGACCGTCTGAGTATTAAC 1500
2357 AGAGAGGCTTGAAGATCTAGCTTTTACCTTAATACAGACAGACCGTCTGAGTATTAAC 2416
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2417 TTTTCAACAGATCAAGATTAATGCGCTAATGAGCTTGATCTGTGCGCAGAGATTAAC 2476
1561 CATAGAGAGCTGACCACTTAATCTGCTGACCGCAGGGGATTAATTTGAGGAGCTAATAG 1620
2477 CATAGAGAGCTGACCACTTAATCTGCTGACCGCAGGGGATTAATTTGAGGAGCTAATAG 2536
1621 GGTATATGCAAAAGGTGCACTTAGGCGCAGATTGCAAGTACAGCAACTTGTAAA 1680
2537 GGTATATGCAAAAGGTGCACTTAGGCGCAGATTGCAAGTACAGCAACTTGTAAA 2596
1681 TATCAGGAATTTGTTGCTACATTTCTGAGAAACGGGCGCAGGTTGAGATTAAGTACGAGGA 1740
2597 TATCAGGAATTTGTTGCTACATTTCTGAGAAACGGGCGCAGGTTGAGATTAAGTACGAGGA 2656

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Db	2657	TAGGGTGGCCCTTTAGATGTAGCAATGATPAAATATGTGGCCGGGGGGTCTGGCAATGACACGG	2716
QY	1801	GGTGGTTATTATGATGTATGAGTTTACTGGCCGCCAATTTTATGCGGTACGGTTTTCTTGAC	1860
Db	2717	GGTGGTTATTATGATGTATGAGTTTACTGGCCGCCAATTTTATGCGGTACGGTTTTCTTGAC	2776
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QY	2101	CATCTGTGTGTAAGAAACCGTGGGTGTGATTAACATPAACTGGTATGTGGCACTCCGAGGA	2160
Db	3017	CATCTGTGTGTAAGAAACCGTGGGTGTGATTAACATPAACTGGTATGTGGCACTCCGAGGA	3076
QY	2161	CAGGGCCCTCTCAGATGCTGACCTGTCTCGGAAGGCACTGTCACTGCTGGAAGACCATTTCA	2220
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QY	2521	GCTGAGGCGCGATCACTTGTGATGCTGGCTGACACCGCGCTGAGTTTGGCTTAGACGATGA	2580
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RESULT 8			
US-09-409-670-43			
Sequence 43, Application US/09409670			
Patent No. 6133028			
GENERAL INFORMATION:			
APPLICANT: IMLER, Jean-Luc			
APPLICANT: MEHTALI, Majid			
APPLICANT: PAVIRANI, Andrea			
TITLE OF INVENTION: DEFECTIVE ADENOVIRUSES AND CORRESPONDING			
TITLE OF INVENTION: COMPLEMENTATION LINES			
NUMBER OF SEQUENCES: 43			
CORRESPONDENCE ADDRESSES:			

	ADDRESSSEE:	BURNS, DOANE, SWECKER & MATTHIS, L.L.P.		
	STREET:	1737 King Street, Suite 500		
	CITY:	Alexandria		
	STATE:	Virginia		
	COUNTRY:	United States		
	ZIP:	22314-2756		
	COMPUTER READABLE FORM:			
	MEDIUM TYPE:	Floppy disk		
	COMPUTER:	IBM PC compatible		
	OPERATING SYSTEM:	PC-DOS/MS-DOS		
	SOFTWARE:	PatentIn Release #1.0, Version #1.30		
	CURRENT APPLICATION DATA:			
	APPLICATION NUMBER:	US/09/409,670		
	FILING DATE:			
	CLASSIFICATION:			
	PRIOR APPLICATION DATA:			
	APPLICATION NUMBER:	US/08/379,452		
	FILING DATE:	26-JAN-1995		
	APPLICATION NUMBER:	WO PCT/FR94/00624		
	FILING DATE:	27-MAY-1994		
	PRIOR APPLICATION DATA:			
	APPLICATION NUMBER:	FR 93 06482		
	FILING DATE:	28-MAY-1993		
	ATTORNEY/AGENT INFORMATION:			
	NAME:	Dadio, Susan M.		
	REGISTRATION NUMBER:	40,373		
	REFERENCE/DOCKET NUMBER:	029395-002		
	INFORMATION FOR SEQ ID NO:	43:		
	SEQUENCE CHARACTERISTICS:			
	LENGTH:	35935 base pairs		
	TYPE:	nucleic acid		
	STRANDEDNESS:	single		
	TOPOLOGY:	linear		
	MOLECULE TYPE:	DNA (genomic)		
	US-09-409-670-43			
Query Match	100.0%;	Score 2594;	DB 3;	Length 35935;
Best Local Similarity	100.0%;	Frid. No. 0;		
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Oy	121 CACCGGAGAAATACGGGGGAGCCGCAATTTATGTGTTGCTTTGCTATATAGAACCTGT	180		
Db	1037 CACCGGAGAAATACGGGGGAGCCGCAATTTATGTGTTGCTTTGCTATATAGAACCTGT	1096		
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Db	1097 GGCAATGTTTGTCTACAGTAAGTAAATTTATGGGCA GTGGGATGTAGAGTGAGGTGGTTTG	1156		
Oy	241 GTGTGTAAATTTTTTTTTTAATTTTACAAGTTTGTGGTTTAAAGAAATTTGTATTTGTGA	300		
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Qy 841 ACTTCTGAAACAGAGCTCTAACAGTACCTTGTGTTTGGAGTTTCTGTGTGCTCAT 900
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Db 1877 TGAATCCTGTGTGTAGCTGTTGATTTCTTGAATCTGGGTCAACAAGGCTTTTCCAG 1936
Qy 1021 AGAAGGTATCAAGACTTGTGATTTTTCACACCGGGGGGCGCTGGCTGTGTGCTT 1080
Db 1937 AGAAGGTATCAAGACTTGTGATTTTTCACACCGGGGGGCGCTGGCTGTGTGCTT 1996
Qy 1081 TTTTGAAGTTTATAAAGATTAATGAGCGAAGAAACCATCTGAGCGGGGGTACTGTC 1140
Db 1997 TTTTGAAGTTTATAAAGATTAATGAGCGAAGAAACCATCTGAGCGGGGGTACTGTC 2056
Qy 1141 TGGATTTTCTGGCCATGCTGTGTGAGAGCGGTTGTGAGACAAAGATGGCTGTCTAC 1200
Db 2057 TGGATTTTCTGGCCATGCTGTGTGAGAGCGGTTGTGAGACAAAGATGGCTGTCTAC 2116
Qy 1201 TGGTGTCTTCGTCGCGCGCGGATTAACGAGCGGAGGAGCAGACGAGCAGAGG 1260
Db 2117 TGGTGTCTTCGTCGCGCGCGGATTAACGAGCGGAGGAGCAGACGAGCAGAGG 2176
Qy 1261 AAGCAGGCGCGCGCGAGAGAGCAGAGCCCATGGAACCCGAGAGCCGCGCTGACCTC 1320
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Qy 1381 TACAGAGATGGGCGGAGGCTTAAAGGGGTTAAAGGGAGCGGGGGCTTTGAGGCTAC 1440
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Qy 1441 AGAGAGGCTAGGAATCTAGCTTTTACCTTAATGACAGACACCGTCTGATGTATTAAC 1500
Db 2357 AGAGAGGCTAGGAATCTAGCTTTTACCTTAATGACAGACACCGTCTGATGTATTAAC 2416
Qy 1501 TTTTCAACAGATCAAGATTAATGGCTTAATGAGCTTTGATCTGTGGCGCAGAAATATTC 1560
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Qy 1561 CATAGAGAGCTGACCACTTAAGCTGCTGAGCAGGGGATGTTTGAAGAGGCTATTAG 1620

Db 2477 CATAGAGAGCTGACCACTTAAGCTGCTGAGCAGGGATGATTTTGAAGGCTATTAG 2536
Qy 1621 GGTATATGCAAAAGGTGGCACTTAGGCCAGATTTGCAAGATCAAGATCAAGCAATTTGTA 1680
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Qy 1681 TATCAGAAATTTGTTCTCAATTTCTGGGAAACGGGGCCAGAGGTGAGATATGATACGAGAA 1740
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Db 2657 TAGGATGAGCTTTAGATGTAGATGATGATTAATATGTGCGGGGGGCTTGGCATGAGAG 2716
Qy 1801 GGTGTATTAATGATGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
Db 2717 GGTGTATTAATGATGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2776
Qy 1861 CAATACCAACCTTATCTTACACGCTGTAAAGCTTCTATGAGTTTAAACATACCTGTGTGA 1920
Db 2777 CAATACCAACCTTATCTTACACGCTGTAAAGCTTCTATGAGTTTAAACATACCTGTGTGA 2836
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RESULT 9
US-09-562-919-1

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1 / Sequence 1, Application US/09562919
2 / Patent No. 6451596
3 / GENERAL INFORMATION:
4 / APPLICANT: Chamberlain, Jeffrey S.
5 /             Amalfitano, Andrea
6 /             Hauser, Michael A.
7 /             Kumar-Singh, Rajendra
8 /             Hartigan-O'Connor, Dennis J.
9 / TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
10 / NUMBER OF SEQUENCES: 15
11 / CORRESPONDENCE ADDRESSES:
12 /     ADDRESSEE: Medlen & Carroll, LLP
13 /     STREET: 220 Montgomery Street, Suite 2200
14 /     CITY: San Francisco
15 /     STATE: California
16 /     COUNTRY: United States Of America
17 /     ZIP: 94104
18 / COMPUTER READABLE FORM:
19 /     MEDIUM TYPE: Floppy disk
20 /     COMPUTER: IBM PC compatible
21 /     OPERATING SYSTEM: PC-DOS/MS-DOS
22 /     SOFTWARE: PatentIn Release #1.0, Version #1.30
23 / CURRENT APPLICATION DATA:
24 /     APPLICATION NUMBER: US/09/562,919
25 /     FILING DATE: 02-May-2000
26 /     CLASSIFICATION: <Unknown>
27 / PRIOR APPLICATION DATA:
28 /     APPLICATION NUMBER: US/08/735,609
29 /     FILING DATE: 23-Oct-1996
30 / ATTORNEY/AGENT INFORMATION:
31 /     NAME: Ingolia, Diane B.
32 /     REGISTRATION NUMBER: 40,027
33 /     REFERENCE/DOCKET NUMBER: UM-02484
34 / TELECOMMUNICATION INFORMATION:
35 /     TELEPHONE: (415) 705-8410
36 /     TELEFAX: (415) 397-8338
37 / INFORMATION FOR SEQ ID NO: 1:
38 /     SEQUENCE CHARACTERISTICS:
39 /         LENGTH: 35935 base pairs
40 /         TYPE: nucleic acid
41 /         STRANDEDNESS: double
42 /         TOPOLOGY: linear
43 /     MOLECULE TYPE: other nucleic acid
44 /     DESCRIPTION: /desc = "DNA"
45 /     SEQUENCE DESCRIPTION: SEQ ID NO: 1:
46 / US-09-562-919-1
47
48 Query Match      100.0%; Score 2594; DB 3; Length 35935;
49 Best Local Similarity 100.0%; Pctd. No. 0;
50 Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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52 QY      1 ATGCATCTTACCTGCGACGAGGCTGGCTTCCACCCAGTACGACGAGATGAAGAGGGT 60
53 Db      917 ATGCATCTTACCTGCGACGAGGCTGGCTTCCACCCAGTACGACGAGATGAAGAGGGT 976
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55 QY      61 GAGAGATTGTGTAGATTATGTGAGAGACCCCGGCGACGAGTTGCAAGTCTTGCATTAT 120
56 Db      977 GAGAGATTGTGTAGATTATGTGAGAGACCCCGGCGACGAGTTGCAAGTCTTGCATTAT 1036
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58 QY      121 CACCGAGGAATACGGGGGACCCAGATTTATGTGTTGCTTTGCTATATGAGACCTGT 180
59 Db      1037 CACCGAGGAATACGGGGGACCCAGATTTATGTGTTGCTTTGCTATATGAGACCTGT 1096
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64 QY      241 GTGCGTAATTTTATTTTATTTTATTTTACAGTTTGTGTTGTTTAAAGAAATTTGTATTGGA 300
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Q	y	421	TGCTCTAAGAAATGCATATGATATGCGATGTCGTGATCTCCGCTCTTTACACACTC	480
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D	b	2177	AAGCAGAGCGGCGCGCAGAGACAGAGCCCATGTGAACCCGAGAGCGGCGCTGACCTC	2236
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RESULT 11
US-09-956-335-2
; Sequence 2, Application US/09956335
; Patent No. 6627190
; GENERAL INFORMATION:
; APPLICANT: WOLD, William
; APPLICANT: TOTH, Karoly

APPLICANT: KUPPASAMI, Mohan
APPLICANT: DORONIN, Konstantin
TITLE OF INVENTION: RECOMBINANT ADENOVIRUS VECTORS THAT ARE
TITLE OF INVENTION: REPLICATION-COMPETENT IN TEXT-EXPRESSING CELLS
FILE REFERENCE: 16153-8394
CURRENT APPLICATION NUMBER: US/09/956,335
CURRENT FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 35871
TYPE: DNA
ORGANISM: Adenovirus
US-09-956-335-2

Query Match 99.5%; Score 2582; DB 4; Length 35871;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/735,609
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Ingolla, Diane E.
: REGISTRATION NUMBER: 40,027
: REFERENCE/DOCKET NUMBER: UM-02484
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 705-8410
: TELEFAX: (415) 397-8338
: INFORMATION FOR SRD ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 34303 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: other nucleic acid
: DESCRIPTION: /desc = "DNA"
:
: US-08-735-609-4

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Query Match	83.3%	Score 2161;	DB 2;	length 34303;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 2161; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY	434	CAATAGTAGAGTACGGATTAAGCTGTACACTCCGGTCTCTTCAACACACCTCTAGATATACACC	499
Db	2853	CAATAGTAGAGTACGGATTAAGCTGTACACTCCGGTCTCTTCAACACACCTCTAGATATACACC	2912
QY	494	GGTGTGTCCCGCTGTGCCCATTTAAACCATTTGGCCGTGAGAGTTGGTGGGGGTGGCCAGGC	553
Db	2913	GGTGTGTCCCGCTGTGCCCATTTAAACCATTTGGCCGTGAGAGTTGGTGGGGGTGGCCAGGC	2972
QY	554	TGTGGAATGTATGAGGACTTGTGCTTAAAGAGCTGTGGCAACTTTGGACTTTGAGCTGTAA	613
Db	2973	TGTGGAATGTATGAGGACTTGTGCTTAAAGAGCTGTGGCAACTTTGGACTTTGAGCTGTAA	3032
QY	614	ACGCCCCAGGCCATTAAGGTGTAAACCTGTGATTGCGTGTGTGTAAACGCTTTGTGTTGC	673
Db	3033	ACGCCCCAGGCCATTAAGGTGTAAACCTGTGATTGCGTGTGTGTAAACGCTTTGTGTTGC	3092
QY	674	TGATATGATGTAGATTAAGTTAATTAAGGGTGAATATGTTTAACTTGGATGGCGGTT	733
Db	3093	TGATATGATGTAGATTAAGTTAATTAAGGGTGAATATGTTTAACTTGGATGGCGGTT	3152
QY	734	AAATGGGGCCGGGCTTTAAAGGATATATATATGCGCCGTGGCTAATCTTGGTTACATCTGA	793
Db	3153	AAATGGGGCCGGGCTTTAAAGGATATATATATGCGCCGTGGCTAATCTTGGTTACATCTGA	3212
QY	794	CCTCATATGAGGCTTTGGGAGTGTTTTGGAAAGTTTTCTGTCTGTGCGTAACTTTGCTGGAAACA	853
Db	3213	CCTCATATGAGGCTTTGGGAGTGTGTGGAAAGTTTTCTGTCTGTGCGTAACTTTGCTGGAAACA	3272
QY	854	GAGCTTAAACAGTACCTCTGTGTTTGGAGGTTTCTGTGGGGCTCATCCAGCGAAAGTT	913
Db	3273	GAGCTTAAACAGTACCTCTGTGTTTGGAGGTTTCTGTGGGGCTCATCCAGCGAAAGTT	3332
QY	914	AGTCTGCAGAATTAAAGAGGATTAACAATGGGAAATTTGAAGAAGCTTTTGAATCTGTGG	973
Db	3333	AGTCTGCAGAATTAAAGAGGATTAACAATGGGAAATTTGAAGAAGCTTTTGAATCTGTGG	3392
QY	974	TGAGCTGTGATTTCTTTTGAATCGGGTCAACAGGGGCTTTTCCAAAGAAAGGTCATCAA	1033
Db	3393	TGAGCTGTGATTTCTTTTGAATCGGGTCAACAGGGGCTTTTCCAAAGAAAGGTCATCAA	3452
QY	1034	GACTTTGATTTTTTCCACACCGGGGCGCGCTGGGCGTCTGTGCTTTTGTGAATTTTAT	1093
Db	3453	GACTTTGATTTTTTCCACACCGGGGCGCGCTGGGCGTCTGTGCTTTTGTGAATTTTAT	3512
QY	1094	AAAGAGTAAATTGAAGCGAAAGAAACCATCTGAGCGGGGGGTTACTGCTGGATTTTCTGGC	1153
Db	3513	AAAGAGTAAATTGAAGCGAAAGAAACCATCTGAGCGGGGGGTTACTGCTGGATTTTCTGGC	3572

Oy	2593	AG	2594
		1	
Db	3404	AG	3405

RESULT 12
US-08-735-609-4
! Sequence 4, Application US/08735609

1 GENERAL INFORMATION:
2 APPLICANT: Chamberlain, Jeffrey S.
3 APPLICANT: Amalfitano, Andrea
4 APPLICANT: Hauser, Michael A.
5 APPLICANT: Kumar-Singh, Rajendra
6 APPLICANT: Hartigan-O'Connor, Dennis J.
7 TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
8
9 NUMBER OF SEQUENCES: 15
10
11 CORRESPONDENCE ADDRESS:

ADDRESSSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

QY	434	CAATAGTAGACGGAATAGCTGACACTCCGGTCTTTCTTAAACAACCTCTAGATATACACC	499
Db	2853	CAATAGTAGACGGAATAGCTGACACTCCGGTCTTTCTTAAACAACCTCTAGATATACACC	2912
QY	494	GGTGTGTCCTGCTGTGCCCATTTAAACAATTGGCCGTGAGAGTTGGTGGGGGTGGCCAGGC	553
Db	2913	GGTGTGTCCTGCTGTGCCCATTTAAACAAGTTGGCGTAGAGTTGGTGGGGGTGGCCAGGC	2972
QY	554	TGTGGAATGTATGAGGACTTGTGCTTAAACGAGCTCGGGCAACTTTGGAATTGAGCTGTAA	613
Db	2973	TGTGGAATGTATGAGGACTTGTGCTTAAACGAGCTCGGGCAACTTTGGAATTGAGCTGTAA	3032
QY	614	ACGCCCCAGGCCATTAAGTGTAAACCTGTGATTGCGTGTGTGTTAACGCCCTTTGTTTGC	673
Db	3033	ACGCCCCAGGCCATTAAGTGTAAACCTGTGATTGCGTGTGTGTTAACGCCCTTTGTTTGC	3092
QY	674	TGAATGAGTTGATGATTAAGTTAATAAAGGTGAGATTAATTATTAATTGATGAGCGTGT	733
Db	3093	TGAATGAGTTGATGATTAAGTTAATAAAGGTGAGATTAATTATTAATTGATGAGCGTGT	3152
QY	734	AAATGGGGCGGGCTTTAAAGGATATATATATATGCGCCGTGGGCTAATCTTGTTATCATCTGA	793
Db	3153	AAATGGGGCGGGCTTTAAAGGATATATATATATGCGCCGTGGGCTAATCTTGTTATCATCTGA	3212
QY	794	CTTCATAGGAGGCTTTGGAGTGTTTTGGAAAGTTTTTCTGCTGTGCGTAACTTTGCTGGAAACA	853
Db	3213	CTTCATAGGAGGCTTTGGAGTGTTTTGGAAAGTTTTTCTGCTGTGCGTAACTTTGCTGGAAACA	3272
QY	854	GAGCTTAAACAGTAACTCTTGTTTTGAGAGTTTCTGTGGGGCTCATCCAGGCAAAATT	913
Db	3273	GAGCTTAAACAGTAACTCTTGTTTTGAGAGTTTCTGTGGGGCTCATCCAGGCAAAATT	3332
QY	914	AGTCTGCAGAATTAAGAGAGATTAACAAGTGGGAATTTGAAGAAGCTTTTGAATTCCTGTGG	973
Db	3333	AGTCTGCAGAATTAAGAGAGATTAACAAGTGGGAATTTGAAGAAGCTTTTGAATTCCTGTGG	3392
QY	974	TGAGCTTTTGATCTTTTGAATCTGGGTCAACAAGGCGCTTTTCCAGAGAGAAGTCATCAA	1033
Db	3393	TGAGCTTTTGATCTTTTGAATCTGGGTCAACAAGGCGCTTTTCCAGAGAGAAGTCATCAA	3452
QY	1034	GACTTTGGATTTTTCCACACCGGGGCGCGCTGCGGCTGTGTCGTTTTTTGAATTTTAT	1093
Db	3453	GACTTTGGATTTTTCCACACCGGGGCGCGCTGCGGCTGTGTCGTTTTTTGAATTTTAT	3512
QY	1094	AAAGGATTAATGAGCGCAAAACCAATCTGAGCGGGGGGTAACCTGCTGATATTTTCTGGC	1153
Db	3513	AAAGGATTAATGAGCGCAAAACCAATCTGAGCGGGGGGTAACCTGCTGATATTTTCTGGC	3572

US-08-735-609-4

Query Match	83.3%	Score 2161	DB 2	Length 34303
Best Local Similarity	100.0%	Pred. No. 0		
Matches 2161	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	434	CAATAGTAGTACGATAGCTGACTCCGGTCTTCTTAACAACACTCTTGATACACCC	493	
Db	2853	CAATAGTAGTACGATAGCTGACTCCGGTCTTCTTAACAACACTCTTGATACACCC	2912	
Qy	494	GGTGGTCCCGCTGTGCCCCATTAAACCAATTGCCGTGAGAGTTGGTGGCCCTCCGACGC	553	
Db	2913	GGTGGTCCCGCTGTGCCCCATTAAACCAATTGCCGTGAGAGTTGGTGGCCCTCCGACGC	2972	
Qy	554	TGTGGAATGTATGAGGACTTGCTTAAGAGCTGGGGAACCTTGGACTGAGCTGTA	613	
Db	2973	TGTGGAATGTATGAGGACTTGCTTAAGAGCTGGGGAACCTTGGACTGAGCTGTA	3032	
Qy	614	ACGCCCCAGGCCATTAAGGTGTAACCTGTGATTGCTGTGTTAACGCCCTTGTGTTGC	673	
Db	3033	ACGCCCCAGGCCATTAAGGTGTAACCTGTGATTGCTGTGTTAACGCCCTTGTGTTGC	3092	
Qy	674	TGAATGAGTGTATGATTAATTAAGGGTGAATTAATTTTAACTTGAATGGCGTGT	733	
Db	3093	TGAATGAGTGTATGATTAATTAAGGGTGAATTAATTTTAACTTGAATGGCGTGT	3152	
Qy	734	AAATGGGGCGGGGCTTAAAGGGTATATATAGCGCGTGGCTAATCTTGATTAACCTGA	793	
Db	3153	AAATGGGGCGGGGCTTAAAGGGTATATATAGCGCGTGGCTAATCTTGATTAACCTGA	3212	
Qy	794	CCTCATGAGGCTTGGAGTGTGGAAGATTTTCTGCTGTGCTTAACCTTGGAACA	853	
Db	3213	CCTCATGAGGCTTGGAGTGTGGAAGATTTTCTGCTGTGCTTAACCTTGGAACA	3272	
Qy	854	GAGCTTAACAGTACTTGTGGTTTGGAGGTTTCTGTGGGCTCATCCGACCAAGTT	913	
Db	3273	GAGCTTAACAGTACTTGTGGTTTGGAGGTTTCTGTGGGCTCATCCGACCAAGTT	3332	
Qy	914	AGTCGCAATTAAGAGGATTAACAAGTGGAAATTTGAAGGCTTGAATCCTGCG	973	
Db	3333	AGTCGCAATTAAGAGGATTAACAAGTGGAAATTTGAAGGCTTGAATCCTGCG	3392	
Qy	974	TGACCTGTTTGAATCTTGAATCTGGGTCAACAGGCGCTTTTCCAAGAAAGTATCAA	1033	
Db	3393	TGACCTGTTTGAATCTTGAATCTGGGTCAACAGGCGCTTTTCCAAGAAAGTATCAA	3452	
Qy	1034	GACTTTGATTTTTCACACCGGGGCGCTGCGCTGCTGTTGCTTTTGAAGTTTAT	1093	
Db	3453	GACTTTGATTTTTCACACCGGGGCGCTGCGCTGCTGTTGCTTTTGAAGTTTAT	3512	
Qy	1094	AAAGGATTAATGAGCGGAAGAAACCATCTGAGCGGGGGGTACCTGCTGGAATTTCTGGC	1153	
Db	3513	AAAGGATTAATGAGCGGAAGAAACCATCTGAGCGGGGGGTACCTGCTGGAATTTCTGGC	3572	
Qy	1154	CATGATCTGTGAGAGCGGTGTGAGACACAAGATGCGCTGACTGTTGTCTTCCGT	1213	
Db	3573	CATGATCTGTGAGAGCGGTGTGAGACACAAGATGCGCTGACTGTTGTCTTCCGT	3632	
Qy	1214	CCGCCCGGCAATATACCGACGAGAGACAGACAGACAGACAGAGAAAGCCAGCGCG	1273	
Db	3633	CCGCCCGGCAATATACCGACGAGAGACAGACAGACAGACAGAGAAAGCCAGCGCG	3692	
Qy	1274	GGGCGAGGAGAGAGCCATGGAACCGAGAGCGGGCGCTGACCCTCGGGGAATGAATTT	1333	
Db	3693	GGGCGAGGAGAGAGCCATGGAACCGAGAGCGGGCGCTGACCCTCGGGGAATGAATTT	3752	
Qy	1334	GTAACAGTGTGTAATCTGTATCCAAAGCTGAGACGATTTTGAACAATTAAGAGATGG	1393	
Db	3753	GTAACAGTGTGTAATCTGTATCCAAAGCTGAGACGATTTTGAACAATTAAGAGATGG	3812	
Qy	1394	CAGGGGCTAAAGGGGGTAAAGAGGAGCGGGGGCTTGTAGGCTACAGAGAGGCTAAG	1453	
Db	3813	CAGGGGCTAAAGGGGGTAAAGAGGAGCGGGGGCTTGTAGGCTACAGAGAGGCTAAG	3872	

Qy	1454	AATCTAGCTTTAGCTTAATGACACAGACCGTCTGAGTGTATTACTTTTCAACAGATC	1513	
Db	3873	AATCTAGCTTTAGCTTAATGACACAGACCGTCTGAGTGTATTACTTTTCAACAGATC	3932	
Qy	1514	AAGGATTAATGCGCTTAATGACTTGATCTGTGGCGGAGAAATTCATAGACAGCTG	1573	
Db	3933	AAGGATTAATGCGCTTAATGACTTGATCTGTGGCGGAGAAATTCATAGACAGCTG	3992	
Qy	1574	ACCACTTAATGCGCTGACCGACGGGATGATTTTGAAGAGCTAATAGGTATTAAGCAAG	1633	
Db	3993	ACCACTTAATGCGCTGACCGACGGGATGATTTTGAAGAGCTAATAGGTATTAAGCAAG	4052	
Qy	1634	GTCGCACTTAAGGCCAGATTCAGATCAAGATCAGCAAACTTGTAATATCAGGAATGT	1693	
Db	4053	GTCGCACTTAAGGCCAGATTCAGATCAAGATCAGCAAACTTGTAATATCAGGAATGT	4112	
Qy	1694	TGCTAATTTCTGGGAACGGGGCGAGGTGAGATTAAGATACGAGAGATAGGGTGCCTTT	1753	
Db	4113	TGCTAATTTCTGGGAACGGGGCGAGGTGAGATTAAGATACGAGAGATAGGGTGCCTTT	4172	
Qy	1754	AGATGATGATGATTAATTAATGTGGCGGGGTGCTTGCAATGACGGGGTGTATTATG	1813	
Db	4173	AGATGATGATGATTAATTAATGTGGCGGGGTGCTTGCAATGACGGGGTGTATTATG	4232	
Qy	1814	AATGTAAGTTTACTGCGCCCAATTTTACGGTACGGTCTTCTGSCCAATACCAACCTT	1873	
Db	4233	AATGTAAGTTTACTGCGCCCAATTTTACGGTACGGTCTTCTGSCCAATACCAACCTT	4292	
Qy	1874	ATCTTAACCGGTGTAGCTTCTATAGGTTTAAACAATCTGTGTGAACCTGACCGAT	1933	
Db	4293	ATCTTAACCGGTGTAGCTTCTATAGGTTTAAACAATCTGTGTGAACCTGACCGAT	4352	
Qy	1934	GTAAGGTTTGGGGCTGTGCTTTTACTGCTGTGGAAGGGGGGTGTGTGCCCCAA	1993	
Db	4353	GTAAGGTTTGGGGCTGTGCTTTTACTGCTGTGGAAGGGGGGTGTGTGCCCCAA	4412	
Qy	1994	AGCAGGCTTCAATTAAGAAATGCTCTTGAAGAGTACCTTGGGTATCTGTCTGAG	2053	
Db	4413	AGCAGGCTTCAATTAAGAAATGCTCTTGAAGAGTACCTTGGGTATCTGTCTGAG	4472	
Qy	2054	GGTAACTCCAGGGTGGCCCAATATGSGCTCCGACTGTGGTCTTCACTAGTGA	2113	
Db	4473	GGTAACTCCAGGGTGGCCCAATATGSGCTCCGACTGTGGTCTTCACTAGTGA	4532	
Qy	2114	AGCTGTGCTGTGATTAAGCAATATGATATGTGSCAACTGCGAGGACAGGGCCTCAG	2173	
Db	4533	AGCTGTGCTGTGATTAAGCAATATGATATGTGSCAACTGCGAGGACAGGGCCTCAG	4592	
Qy	2174	ATGCTGACCTGCTGGAACGGCACTGTACCTGCTGAAGACATTCAGTACGACGAC	2233	
Db	4593	ATGCTGACCTGCTGGAACGGCACTGTACCTGCTGAAGACATTCAGTACGACGAC	4652	
Qy	2234	TCTGCAAGGCTGTGCCAGATGTTTGAACATTAACACTGACCCGCTGTTCTTGCAATTG	2293	
Db	4653	TCTGCAAGGCTGTGCCAGATGTTTGAACATTAACACTGACCCGCTGTTCTTGCAATTG	4712	
Qy	2294	GTTAAACAGAGGGGGGTCTCTACCTTAACCAATGCAATTTGAATCACTAAGAATTTG	2353	
Db	4713	GTTAAACAGAGGGGGGTCTCTACCTTAACCAATGCAATTTGAATCACTAAGAATTTG	4772	
Qy	2354	CTTGAGCCCGAGACATGTCCAAAGTGAACCTGAAACGGGGTGTGTGACATGACCATGAAG	2413	
Db	4773	CTTGAGCCCGAGACATGTCCAAAGTGAACCTGAAACGGGGTGTGTGACATGACCATGAAG	4832	
Qy	2414	ATCTGAAAGGTGCTGAGGTACATGAGAACCCGACACAGGTGCAACCTCTGCGAGTGTGGC	2473	
Db	4833	ATCTGAAAGGTGCTGAGGTACATGAGAACCCGACACAGGTGCAACCTCTGCGAGTGTGGC	4892	
Qy	2474	GTTAAACATTAATTAAGAACCGAGCTGTGATGTGTGAATGACCGAGAGCTAGGCGGAT	2533	
Db	4893	GTTAAACATTAATTAAGAACCGAGCTGTGATGTGTGAATGACCGAGAGCTAGGCGGAT	4952	

Db 4113 TGCACATTTCTGGGAACGGGGCCGAGGTGAGATAGATACGAGAGATAGAGGTGGCCTTT 4172
Qy 1754 AGATGTACATGATATATATGTGGCCGGGGGTGCTGGCATGACGGGGGTGTTATATG 1813
Db 4173 AGATGTACATGATATATATGTGGCCGGGGGTGCTGGCATGACGGGGGTGTTATATG 4232
Qy 1814 AATGTAGGTTTACCTGGCCCAATTTTAGCGGTTACCGTTTCCCTGGGCCAATACCACTT 1873
Db 4233 AATGTAGGTTTACCTGGCCCAATTTTAGCGGTTACCGTTTCCCTGGGCCAATACCACTT 4292
Qy 1874 ATCTCAACGAGTGTATAGCTTATAGGTTTAAACAATACCTGTGTGAAGCCTGACCGAT 1933
Db 4293 ATCTCAACGAGTGTATAGCTTATAGGTTTAAACAATACCTGTGTGAAGCCTGACCGAT 4352
Qy 1934 GTAAAGGTTCCGGGGCTGTGCTTTTACTGTCTGTGTGAAGGGGGGTGTGTGCCCCAA 1993
Db 4353 GTAAAGGTTCCGGGGCTGTGCTTTTACTGTCTGTGTGAAGGGGGGTGTGTGCCCCAA 4412
Qy 1994 AGCAGGGCTTCAATTAAGAAATGCTCTTTGAAAGGTACCTTGGGGTATCTGTCTGAG 2053
Db 4413 AGCAGGGCTTCAATTAAGAAATGCTCTTTGAAAGGTATCTTGGGTATCTGTCTGAG 4472
Qy 2054 GGTAACTCCAGGGTGCAGCAATGTGCTCTCCGACTGTGTTGCTTCATCTAGTGA 2113
Db 4473 GGTAACTCCAGGGTGCAGCAATGTGCTCTCCGACTGTGTTGCTTCATCTAGTGA 4532
Qy 2114 AGCGTGTGTGTATTAAGCATTAATGTATGTGGCACTGTGAGAGACAGGGCTCTGAG 2173
Db 4533 AGCGTGTGTGTATTAAGCATTAATGTATGTGGCACTGTGAGAGACAGGGCTCTGAG 4592
Qy 2174 ATGCTGACTGTGTGTGAG 2233
Db 4593 ATGCTGACTGTGTGTGAG 4652
Qy 2234 TCTGCAAGGCTGTGCAAGTGTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2293
Db 4653 TCTGCAAGGCTGTGCAAGTGTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4712
Qy 2294 GGTAAACGAG 2353
Db 4713 GGTAAACGAG 4772
Qy 2354 CTTGAGCCCGAGAGAGATGCCAAGGTGAACCTGAACGGGGGTGTTGACATGACATGAAG 2413
Db 4773 CTTGAGCCCGAGAGAGATGCCAAGGTGAACCTGAACGGGGGTGTTGACATGACATGAAG 4832
Qy 2414 ATCTGAAAGGTGTGAGGTAGATGAGACCCGACACAGGTGAGACCTGTGCAAGTGTGC 2473
Db 4833 ATCTGAAAGGTGTGAGGTAGATGAGACCCGACACAGGTGAGACCTGTGCAAGTGTGC 4892
Qy 2474 GGTAAACATTAATTAAGAACAGAGCTGTGTATGTGTGATGTGAACGAGAGAGAGAGAGAG 2533
Db 4893 GGTAAACATTAATTAAGAACAGAGCTGTGTATGTGTGATGTGAACGAGAGAGAGAGAGAG 4952
Qy 2534 CACTTGTGTGTGTGAGCTGTGACCCGAGCTGAGTTTGTGCTTAAGGATGAAGATACAGATTGA 2593
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Qy 2594 G 2594
Db 5013 G 5013

RESULT 15
US-09-244-752-4
; Sequence 4, Application US/09244752
; Patent No. 6063622
; GENERAL INFORMATION:
; APPLICANT: Chamberlain, Jeffrey S.
; APPLICANT: Amalitano, Andrea
; APPLICANT: Hauber, Michael A.
; APPLICANT: Kumar-Singh, Rajendra

APPLICANT: Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,752
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/735,609
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-02484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 34303 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-09-244-752-4
Query Match 83.3%; Score 2161; DB 3; Length 34303;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 434 CAATAGTAGTACGAGTAGTGTGACTCCGGTCTTCTTAACACACTCTCGATACACCCC 493
Db 2853 CAATAGTAGTACGAGTAGTGTGACTCCGGTCTTCTTAACACACTCTCTGATACACCCC 2912
Qy 494 GGTGTCCCGCTGTGCCCATTAACCAAGTTGCCGTAGAGTTGTGTGGCGTCCGACAGC 553
Db 2913 GGTGTCCCGCTGTGCCCATTAACCAAGTTGCCGTAGAGTTGTGTGGCGTCCGACAGC 2972
Qy 554 TGTGGAATGTATCGAGACTTGTCTTAACGAGCTGTGGCAACCTTTGACTGAGCTGTAA 613
Db 2973 TGTGGAATGTATCGAGACTTGTCTTAACGAGCTGTGGCAACCTTTGACTGAGCTGTAA 3032
Qy 614 ACGCCCAAGGCAATAGGTGAACCTGTGATTCGTGTGTGTGAACGCTTTGTGTGC 673
Db 3033 ACGCCCAAGGCAATAGGTGAACCTGTGATTCGTGTGTGTGAACGCTTTGTGTGC 3092
Qy 674 TGAATGAGTTGATGAATTAATTAAGGTGAGATATGTTTAACTTGACATGCGGTGT 733
Db 3093 TGAATGAGTTGATGAATTAATTAAGGTGAGATATGTTTAACTTGACATGCGGTGT 3152
Qy 734 AAATGGGGCGGGGCTTAAAGGTTATTAATGCGCGGTGAGTAATCTTGTTACATCTGA 793
Db 3153 AAATGGGGCGGGGCTTAAAGGTTATTAATGCGCGGTGAGTAATCTTGTTACATCTGA 3212
Qy 794 CCTCATGAGGCTTGGAGGTGTGTGAAGATTTTCTGCTGTGCGTAACCTTGAGAAC 853
Db 3213 CCTCATGAGGCTTGGAGGTGTGTGAAGATTTTCTGCTGTGCGTAACCTTGAGAAC 3272
Qy 854 GAGCTTAACAGTACCTTGTGTTTGTGAAGTTTCTGTGGGCTCATCCAGGCAAGTT 913

Db 3273 GAGCTTAACAGTACCTTGTGTTGGAGGTTCTGTGGGCTCATCCAGCAAGTT 3332
 Qy 914 AGCTGCAGAAATTAAGAGATTAACAAGTGGAAATTTGAAGCTTTTGAATCTGTGG 973
 Db 3333 AGTGTGAGAAATTAAGAGATTAACAAGTGGAAATTTGAAGCTTTTGAATCTGTGG 3392
 Qy 974 TGAGCTGTTTAAATCTTGAATCTGTGGGTCACAGGCGCTTTTCCAGAGAAAGTCATCA 1033
 Db 3393 TGAGCTGTTTAAATCTTGAATCTGTGGGTCACAGGCGCTTTTCCAGAGAAAGTCATCA 3452
 Qy 1034 GACTTTGATTTTTCACACCGGGGCGGCTGTGGCTGTGTCTTTTGAAGTTTAT 1093
 Db 3453 GACTTTGATTTTTCACACCGGGGCGGCTGTGGCTGTGTCTTTTGAAGTTTAT 3512
 Qy 1094 AAAGATTAATGAGACGAAGAAACCCTATCTGAGCGGGGGTAACTGTGGAATTTCTGGC 1153
 Db 3513 AAAGATTAATGAGACGAAGAAACCCTATCTGAGCGGGGGTAACTGTGGAATTTCTGGC 3572
 Qy 1154 CATGCACTGTGAGAGGGGTTGTGAGACAGAGAAATGGCCCTGCTACTGTGTCTTCCGT 1213
 Db 3573 CATGCACTGTGAGAGGGGTTGTGAGACAGAGAAATGGCCCTGCTACTGTGTCTTCCGT 3632
 Qy 1214 CCGGCGCGGCGATTAATACCGAGCGAGAGACAGACAGACAGAGAGAAAGCCAGGCGG 1273
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 Qy 1274 GCGGAG 1333
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 Qy 1334 GTACAGGAG 1393
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 Qy 1394 CAGGAG 1453
 Db 3813 CAGGAG 3872
 Qy 1454 AATCTAGCTTTTAACTTAATGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1513
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 Qy 1514 AAGGATTAATGAG 1573
 Db 3933 AAGGATTAATGAG 3992
 Qy 1574 ACCACTTAAGCTGAG 1633
 Db 3993 ACCACTTAAGCTGAG 4052
 Qy 1634 GTGGCACTTAAG 1693
 Db 4053 GTGGCACTTAAG 4112
 Qy 1694 TGCTACATTTTCTGGGAAAGGGGGCGAGGTGAGAGATTAAGAGAGAGAGAGAGAGAG 1753
 Db 4113 TGCTACATTTTCTGGGAAAGGGGGCGAGGTGAGAGATTAAGAGAGAGAGAGAGAGAG 4172
 Qy 1754 AGATGTAGCATGATTAATATATGAGCGGGGCTGTGAGATGAGAGAGAGAGAGAGAGAG 1813
 Db 4173 AGATGTAGCATGATTAATATATGAGCGGGGCTGTGAGATGAGAGAGAGAGAGAGAGAG 4232
 Qy 1814 AATGTAAAGTTTACTGGCCCAATTTTAAAGCGGTACGATTTTCTGGCCAATACCACTT 1873
 Db 4233 AATGTAAAGTTTACTGGCCCAATTTTAAAGCGGTACGATTTTCTGGCCAATACCACTT 4292
 Qy 1874 ATCTTACACGGGTATGATTAATATGAGCGGGGCTTAAACAATCTGTGAGAGAGAGAG 1933
 Db 4293 ATCTTACACGGGTATGATTAATATGAGCGGGGCTTAAACAATCTGTGAGAGAGAGAG 4352
 Qy 1934 GTAAAGGTTCCGGGCTGTGCTTTTACTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAG 1993
 Db 4353 GTAAAGGTTCCGGGCTGTGCTTTTACTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAG 4412

Qy 1994 AGCAGGCTTCAATTAAGAAATGCTCTTTGAAGAGTACCTTGGGTATCTGTGAG 2053
 Db 4413 AGCAGGCTTCAATTAAGAAATGCTCTTTGAAGAGTACCTTGGGTATCTGTGAG 4472
 Qy 2054 GGTAACTCAGAGGAGCGCAAAATGTGGCCCGACGTGGTGGTGGTGGTGGTGGTGGTGG 2113
 Db 4473 GGTAACTCAGAGGAGCGCAAAATGTGGCCCGACGTGGTGGTGGTGGTGGTGGTGGTGG 4532
 Qy 2114 AGCGTGTGTGATTAAGCATTAATGATGATGATGATGATGATGATGATGATGATGATG 2173
 Db 4533 AGCGTGTGTGATTAAGCATTAATGATGATGATGATGATGATGATGATGATGATGATG 4592
 Qy 2174 ATGCTGACTGCTGTGAG 2233
 Db 4593 ATGCTGACTGCTGTGAG 4652
 Qy 2234 TCTGCAAGGCTGGCCAGTGTGAGATTAACATGACCCGCTGTCTGTGATTTG 2293
 Db 4653 TCTGCAAGGCTGGCCAGTGTGAGATTAACATGACCCGCTGTCTGTGATTTG 4712
 Qy 2294 GGTAAAG 2353
 Db 4713 GGTAAAG 4772
 Qy 2354 CTTAG 2413
 Db 4773 CTTAG 4832
 Qy 2414 ATCTGAAAGGTGTGAGAGTACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2473
 Db 4833 ATCTGAAAGGTGTGAGAGTACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4892
 Qy 2474 GGTAAACATTAATTAAGAAACAGCTGTGATGATGATGATGATGATGATGATGATGATG 2533
 Db 4893 GGTAAACATTAATTAAGAAACAGCTGTGATGATGATGATGATGATGATGATGATGATG 4952
 Qy 2534 CACTTGTGTGCTGGCTGCAAG 2593
 Db 4953 CACTTGTGTGCTGGCTGCAAG 5012
 Qy 2594 G 2594
 Db 5013 G 5013

Search completed: October 31, 2005, 01:17:04
 Job time : 438 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 30, 2005, 19:25:15 ; Search time 2034 Seconds
(without alignments)
10532.852 Million cell updates/sec

Title: US-10-790-562-33_COPY_459_3052

Perfect score: 2594

Sequence: 1 atcagctctactctgcacga.....cgaatgaagatcacagatcgag 2594

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 9784742 seqs, 4129495052 residues

Total number of hits satisfying chosen parameters: 19569484

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2594	100.0	3052	US-11-070-890-33	Sequence 33, Appl
2	2594	100.0	7607	US-09-847-101B-34	Sequence 34, Appl
3	2594	100.0	7607	US-09-482-682-48	Sequence 48, Appl
4	2594	100.0	7607	US-10-403-337-41	Sequence 41, Appl
5	2594	100.0	7607	US-10-351-890-41	Sequence 41, Appl

6	2594	100.0	9905	24	US-10-731-961-3	Sequence 3, Appl
7	2594	100.0	11152	9	US-09-847-101B-12	Sequence 12, Appl
8	2594	100.0	11152	10	US-09-482-682-12	Sequence 12, Appl
9	2594	100.0	14455	9	US-09-847-101B-15	Sequence 15, Appl
10	2594	100.0	14455	10	US-09-482-682-15	Sequence 15, Appl
11	2594	100.0	32802	21	US-10-766-307A-3	Sequence 3, Appl
12	2594	100.0	35935	9	US-09-725-720-43	Sequence 43, Appl
13	2594	100.0	35935	9	US-09-782-378A-4	Sequence 4, Appl
14	2594	100.0	35935	9	US-09-782-378A-5	Sequence 5, Appl
15	2594	100.0	35935	10	US-09-739-007-43	Sequence 43, Appl
16	2594	100.0	35935	19	US-10-264-839-12	Sequence 12, Appl
17	2594	100.0	35935	19	US-10-432-989-1	Sequence 1, Appl
18	2594	100.0	35935	21	US-10-766-307A-4	Sequence 4, Appl
19	2594	100.0	35935	21	US-10-482-178-8	Sequence 8, Appl
20	2594	100.0	35935	21	US-10-482-178-9	Sequence 9, Appl
21	2594	100.0	35935	24	US-10-433-681-1	Sequence 1, Appl
22	2594	100.0	35935	24	US-10-612-285-1	Sequence 1, Appl
23	2594	100.0	35935	22	US-10-794-514A-732	Sequence 732, App
24	2594	100.0	35978	9	US-09-956-335-1	Sequence 1, Appl
25	2582	99.5	35871	9	US-09-956-335-2	Sequence 2, Appl
26	2579.8	99.5	35712	22	US-10-860-630-1	Sequence 1, Appl
27	2579.8	99.5	35909	22	US-10-860-630-2	Sequence 2, Appl
28	2498	96.3	35937	9	US-09-782-378A-3	Sequence 3, Appl
29	2498	96.3	35937	22	US-10-794-514A-731	Sequence 731, App
30	2497.4	96.3	35759	20	US-10-645-883A-9	Sequence 9, Appl
31	2297.4	88.6	4020	26	US-11-074-694-5	Sequence 5, Appl
32	2068.2	79.7	4304	26	US-11-074-694-7	Sequence 7, Appl
33	1829	70.5	2144	22	US-10-857-137-4	Sequence 4, Appl
34	1829	70.5	2144	22	US-10-613-106-4	Sequence 2, Appl
35	1585	61.1	31976	21	US-10-766-307A-2	Sequence 2, Appl
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39	1485.6	57.3	2751	26	US-11-074-694-6	Sequence 6, Appl
40	1289.8	49.7	3201	26	US-11-074-694-4	Sequence 4, Appl
41	1270	49.0	1270	16	US-10-124-608C-3	Sequence 3, Appl
42	865	33.3	2041	24	US-10-925-205-11	Sequence 11, Appl
43	864	33.3	1802	16	US-10-081-969-3	Sequence 3, Appl
44	862	33.2	2038	24	US-10-925-205-9	Sequence 9, Appl
45	841	32.4	2055	24	US-10-925-205-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-11-070-890-33

Sequence 33, Application US/11070890

Publication NO. US20050170463A1

GENERAL INFORMATION:

APPLICANT: Bouc, Abraham

TITLE OF INVENTION: RECOMBINANT PROTEIN PRODUCTION IN PERMANENT AMNIOCYTIC CELLS THAT

FILE REFERENCE: 2578-6828US

CURRENT APPLICATION NUMBER: US/11/070, 890

CURRENT FILING DATE: 2005-03-04

PRIOR APPLICATION NUMBER: 09/549,463

PRIOR FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/129,452

PRIOR FILING DATE: 1999-04-15

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn version 3.1

SEQ ID NO 33

LENGTH: 3052

TYPE: DNA

ORGANISM: Human Adenovirus Type 5

FEATURES:

OTHER INFORMATION: Nucleotides 459-3510 of Human Adenovirus Type 5

US-11-070-890-33

Query Match 100.0%; Score 2594; DB 26; Length 3052;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
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Db	459	ATGCATCTTACTGCGCACAGAGCTGGCTTTTCCACCCCACTGACGACGAGATGAAAGGGT	518	
Qy	61	GAGAGTTTGTGTAGATTATGTGGAGACCCCGGGACGGTTGCAAGGCTTGTCAATTAT	120	
Db	519	GAGAGTTTGTGTAGATTATGTGGAGACCCCGGGACGGTTGCAAGGCTTGTCAATTAT	578	
Qy	121	CACCGAGGAATACGGGGGACCCAGATATATGTGTGCTTTGCTATATAGAGACTGT	180	
Db	579	CACCGAGGAATACGGGGGACCCAGATATATGTGTGCTTTGCTATATAGAGACTGT	638	
Qy	181	GGCATGTTTGTCTACAGTAAGTGAATAATTATGGGAGAGGGTGTATAGTGTGGTTTG	240	
Db	639	GGCATGTTTGTCTACAGTAAGTGAATAATTATGGGAGAGGGTGTATAGTGTGGTTTG	698	
Qy	241	GTGTGTAATTTTTTTTTTAAATTTTACAGTTTGTGGTTTAAAGAAATTTGTATGTGA	300	
Db	699	GTGTGTAATTTTTTTTTTAAATTTTACAGTTTGTGGTTTAAAGAAATTTGTATGTGA	758	
Qy	301	TTTTTTTAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCGAGCCGAGACCGAGCCTG	360	
Db	759	TTTTTTTAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCGAGCCGAGACCGAGCCTG	818	
Qy	361	CAAGACCTACCCCGCCTCTTAAATGGGCGCTGTCTATCTTGAGAGCCCGACATCACTG	420	
Db	819	CAAGACCTACCCCGCCTCTTAAATGGGCGCTGTCTATCTTGAGAGCCCGACATCACTG	878	
Qy	421	TGTCTAGAGAAATGCAATAGTATGATGAGATAGCTGATGACTCCGCTCTTCTAACAACCTC	480	
Db	879	TGTCTAGAGAAATGCAATAGTATGATGAGATAGCTGATGACTCCGCTCTTCTAACAACCTC	938	
Qy	481	CTGAGATACACCCGGTGTCCCGCTGTGCCCCCATTTAAACAAGTCCGTGAGAGTTGTG	540	
Db	939	CTGAGATACACCCGGTGTCCCGCTGTGCCCCCATTTAAACAAGTCCGTGAGAGTTGTG	998	
Qy	541	GGCGTCGACAGGCTGTGAATGTATCGAGGACTTGCTTAAAGAGCTGGGGACCTTTGG	600	
Db	999	GGCGTCGACAGGCTGTGAATGTATCGAGGACTTGCTTAAAGAGCTGGGGACCTTTGG	1058	
Qy	601	ACTTGAGCTGTAAACGCCACAGGCCATTAAGGTGTAAACCTGTGATGCGTGTGTGTAA	660	
Db	1059	ACTTGAGCTGTAAACGCCACAGGCCATTAAGGTGTAAACCTGTGATGCGTGTGTGTAA	1118	
Qy	661	CGCCTTGTGTCTGAATGAGTTGATGTAAAGTTTAATAAAGGTGATGAATGTTTAACT	720	
Db	1119	CGCCTTGTGTCTGAATGAGTTGATGTAAAGTTTAATAAAGGTGATGAATGTTTAACT	1178	
Qy	721	TGCATGGGCTGTAAATGGGCGGGGCTTAAAGGCTATATATGCGCGTGGCTAATCT	780	
Db	1179	TGCATGGGCTGTAAATGGGCGGGGCTTAAAGGCTATATATGCGCGTGGCTAATCT	1238	
Qy	781	TGTGTACATCTGACCTCATGAGGCTTGGAGTGTGTTGGAAGATTTTCTGCTGTGCTGA	840	
Db	1239	TGTGTACATCTGACCTCATGAGGCTTGGAGTGTGTTGGAAGATTTTCTGCTGTGCTGA	1298	
Qy	841	ACTTGTGGAACAGAGCTCTAACAGTACCTCTGTGTTTGGAGTTTCTGTGGGGCTCAT	900	
Db	1299	ACTTGTGGAACAGAGCTCTAACAGTACCTCTGTGTTTGGAGTTTCTGTGGGGCTCAT	1358	
Qy	901	CCCGAGGCAAGTTAGTGTGAGAAATTAAGAGGATTAAGAAGGGAATTTGAAGGCTTT	960	
Db	1359	CCCGAGGCAAGTTAGTGTGAGAAATTAAGAGGATTAAGAAGGGAATTTGAAGGCTTT	1418	
Qy	961	TGAATCCTGTGTAGCTGTGTGTGATTTCTTGAATCTGGGTCAACAGGCGCTTTTCAAG	1020	
Db	1419	TGAATCCTGTGTGTAGCTGTGTGTGATTTCTTGAATCTGGGTCAACAGGCGCTTTTCAAG	1478	
Qy	1021	AGAAAGTCATCAAGACTTTGGATTTTTCACAACCGGGGCGCGCTGGCTGTGTGCTT	1080	
Db	1479	AGAAAGTCATCAAGACTTTGGATTTTTCACAACCGGGGCGCGCTGGCTGTGTGCTT	1538	

Qy	1081	TTTTGAGTTTATTAAGATTAATGAGCGAAGAAACCATCTGAGCGGGGGTACCTGC	1140	
Db	1539	TTTTGAGTTTATTAAGATTAATGAGCGAAGAAACCATCTGAGCGGGGGTACCTGC	1598	
Qy	1141	TGATTTTCTGGCCATCATCTGTGAGAGCGGTTGTGAGACACAGAAATGCGCTGTAC	1200	
Db	1599	TGATTTTCTGGCCATCATCTGTGAGAGCGGTTGTGAGACACAGAAATGCGCTGTAC	1658	
Qy	1201	TGTTGTCTTCCGTCCGCCCGCATATACCAGAGGAGACACACAGACAGAGAGG	1260	
Db	1659	TGTTGTCTTCCGTCCGCCCGCATATACCAGAGGAGACACACAGACAGAGAGG	1718	
Qy	1261	AAGCCAGCGCGCGCAGAGACAGGCCATGGAACCCGAGAGCGGCTGTGACCTC	1320	
Db	1719	AAGCCAGCGCGCGCAGAGACAGGCCATGGAACCCGAGAGCGGCTGTGACCTC	1778	
Qy	1321	GGGAATGAATGTTGTACAGGTGTGCTGTAATGTATCCAGAACTGAGAGCATTTTGACAT	1380	
Db	1779	GGGAATGAATGTTGTACAGGTGTGCTGTAATGTATCCAGAACTGAGAGCATTTTGACAT	1838	
Qy	1381	TACAGAGATGGGCGAGGGCTTAAAGGGGTAAAGAGGAGCGGGGGCTTGTGAGCTAC	1440	
Db	1839	TACAGAGATGGGCGAGGGCTTAAAGGGGTAAAGAGGAGCGGGGGCTTGTGAGCTAC	1898	
Qy	1441	AGAGAGGCTAGGAATCTAGCTTTTACCTTAATGACAGACACCGTCTGTGATTAATAC	1500	
Db	1899	AGAGAGGCTAGGAATCTAGCTTTTACCTTAATGACAGACACCGTCTGTGATTAATAC	1958	
Qy	1501	TTTTCAACAGTCAAGATTAATTCGCTAAATGAGCTTGTATCTGTGCGCAGAAATATC	1560	
Db	1959	TTTTCAACAGATCAAGATTAATTCGCTAAATGAGCTTGTATCTGTGCGCAGAAATATC	2018	
Qy	1561	CATAGACAGCTGACCACTTAATGTGCTGACGCCAGGGGATGATTTTGAAGAGCTAATTAG	1620	
Db	2019	CATAGACAGCTGACCACTTAATGTGCTGACGCCAGGGGATGATTTTGAAGAGCTAATTAG	2078	
Qy	1621	GGTATATGCAAAAGGTGACACTTAGAGCCAGATTGCAAGTACAAAGTACAGCAACTTGTAA	1680	
Db	2079	GGTATATGCAAAAGGTGACACTTAGAGCCAGATTGCAAGTACAAAGTACAGCAACTTGTAA	2138	
Qy	1681	TATCAGGAATTTTGTCTACATTTCTGGGAAACGGGGCCGAGGTGAGATGATACGAGGA	1740	
Db	2139	TATCAGGAATTTTGTCTACATTTCTGGGAAACGGGGCCGAGGTGAGATGATACGAGGA	2198	
Qy	1741	TAGGCTGCGCTTATGATGATGATGATTAATATGTGCGCGGGGTGCTTGGCAATGACGG	1800	
Db	2199	TAGGCTGCGCTTATGATGATGATGATTAATATGTGCGCGGGGTGCTTGGCAATGACGG	2258	
Qy	1801	GGTGTATTAATGAATGATGAAGTTTACCTGGCCCAATTTTATGCGGTACGGTTTCTGTC	1860	
Db	2259	GGTGTATTAATGAATGATGAAGTTTACCTGGCCCAATTTTATGCGGTACGGTTTCTGTC	2318	
Qy	1861	CAATATCAACCTTATCTTACACGGGTGTAAGCTTCTATGTGGTTTAAACATATCTGTGTGA	1920	
Db	2319	CAATATCAACCTTATCTTACACGGGTGTAAGCTTCTATGTGGTTTAAACATATCTGTGTGA	2378	
Qy	1921	AGCTTGAACCGATTAAGGTTGCGGGCTGTGCTTTTATCTGCTGTGGAAGGGGGTGT	1980	
Db	2379	AGCTTGAACCGATTAAGGTTGCGGGCTGTGCTTTTATCTGCTGTGGAAGGGGGTGT	2438	
Qy	1981	GTGTGCGCCCAAAAGCAGGGCTTCAATTAAGAAATGCTCTTTGAAAGGTATACCTTGGG	2040	
Db	2439	GTGTGCGCCCAAAAGCAGGGCTTCAATTAAGAAATGCTCTTTGAAAGGTATACCTTGGG	2498	
Qy	2041	TATCTGTCTGAGGGTAACTTCAGGGTGTGCGCAATATGTGCTCCGACTGTGTGTGCTT	2100	
Db	2499	TATCTGTCTGAGGGTAACTTCAGGGTGTGCGCAATATGTGCTCCGACTGTGTGTGCTT	2558	
Qy	2101	CATCTATGTAAGACCTGTGCTGTGATTAAGCAATTAATGTATGTGCAACTGCGAGGA	2160	
Db	2559	CATCTATGTAAGACCTGTGCTGTGATTAAGCAATTAATGTATGTGCAACTGCGAGGA	2618	

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DB 2619 CAGGCGCTCGAAGCTGACCTGCTCGGAGGCACTGCACTGCTGTAAGACATTCA 2678
| | | | |
QY 2221 CGTAGCCGACCACTCGGCAAGGCTGCGCAAGTGTGAGCATTAACATGACCCGCTG 2280
| | | | |
DB 2679 CGTAGCCGACCACTCGGCAAGGCTGCGCAAGTGTGAGCATTAACATGACCCGCTG 2738
| | | | |
QY 2281 TTCCTTGACATTTGGGTAAACAGAGAGGGGGGTGTTCTTCACTTACCAATGCAATTTGAGTCA 2340
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DB 2739 TTCCTTGACATTTGGGTAAACAGAGAGGGGGGTGTTCTTCACTTACCAATGCAATTTGAGTCA 2798
| | | | |
QY 2241 CACATGATATTTGCTGAGCCCGAGAGAGATGTCACAGGTGAACCTGGAACCGGGGTGTTGA 2400
| | | | |
DB 2799 CACATGATATTTGCTGAGCCCGAGAGAGATGTCACAGGTGAACCTGGAACCGGGGTGTTGA 2858
| | | | |
QY 2401 CATGACCATGAAAGATCTGGAAGTGTGAGGTACGATGAGACCCGACCAAGGTGAGACC 2460
| | | | |
DB 2859 CATGACCATGAAAGATCTGGAAGTGTGAGGTACGATGAGACCCGACCAAGGTGAGACC 2918
| | | | |
QY 2461 CTGCGAGTGTGGCGGTAAACATTTAGGAACCAAGCTGTGATGTGATGACCGAGA 2520
| | | | |
DB 2919 CTGCGAGTGTGGCGGTAAACATTTAGGAACCAAGCTGTGATGTGATGACCGAGA 2978
| | | | |
QY 2521 GCTGAGGCCGATCATCTTGCTGCTGCGCTGCAACCCGCGCTGAGTTGGCTTACGAGTGA 2580
| | | | |
DB 2979 GCTGAGGCCGATCATCTTGCTGCTGCGCTGCAACCCGCGCTGAGTTGGCTTACGAGTGA 3038
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QY 2581 AGATACAGATTGAG 2594
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DB 3039 AGATACAGATTGAG 3052
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RESULT 2

US-09-847-101B-34

Sequence 34, Application US/09847101B
Publication No. US20020193327A1

GENERAL INFORMATION:

APPLICANT: VON SEGERN, DANIEL

APPLICANT: NEMEROW, GLEN R.

APPLICANT: FRIEDLANDER, MARTIN

TITLE OF INVENTION: VECTORS FOR OCULAR TRANSDUCTION AND USE THEREFOR FOR GENETIC THER

FILE REFERENCE: 22908-1226B

CURRENT APPLICATION NUMBER: US/09/847,101B

CURRENT FILING DATE: 2001-05-01

PRIOR APPLICATION NUMBER: 09/562,934

PRIOR FILING DATE: 2000-05-01

NUMBER OF SEQ ID NOS: 50

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 34

LENGTH: 7607

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: plasmid GRES-E1-SV40-Hygro

US-09-847-101B-34

Query Match 100.0%; Score 2594; DB 9; Length 7607;
Basic Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GAGAGTTTGTGATTAGATTATGTGAGACACCCGCGGACGAGTTCAGAGTCTTGCATTAT 120
| | | | |
DB 1394 GAGAGTTTGTGATTAGATTATGTGAGACACCCGCGGACGAGTTCAGAGTCTTGCATTAT 1453
| | | | |
QY 121 CACCGAGGAATACGCGGAGACCAAGATATTATGTGCTGCTTTGCTATATGAGACCTGT 180
| | | | |
DB 1454 CACCGAGGAATACGCGGAGACCAAGATATTATGTGCTGCTTTGCTATATGAGACCTGT 1513
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QY 181 GGCATGTTTGTCTACAGTAAGTGAATAATATGCGCAGTGGGTGATAGAGTGTGGGTTG 240
| | | | |
DB 1514 GGCATGTTTGTCTACAGTAAGTGAATAATATGCGCAGTGGGTGATAGAGTGTGGGTTG 1573
| | | | |
QY 241 GTGAGTGAATTTTTTTTTTTTAAATTTTACAGTTTGTGCTTTAAAGAAATTTGTAATGGA 300
| | | | |
DB 1574 GTGAGTGAATTTTTTTTTTTTAAATTTTACAGTTTGTGCTTTAAAGAAATTTGTAATGGA 1633
| | | | |
QY 301 TTTTAAAAAGATCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGAGACCTG 360
| | | | |
DB 1634 TTTTAAAAAGATCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGAGACCTG 1693
| | | | |
QY 361 CAAGACTTACCCGCGCTCTTAATATGCGCCTGCTATCTGAGACGCGCCGACATCACTG 420
| | | | |
DB 1694 CAAGACTTACCCGCGCTCTTAATATGCGCCTGCTATCTGAGACGCGCCGACATCACTG 1753
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QY 421 TGTCTAGGAATGCAATAGTATGATGAGTGTGAGCTGCTGCTGCTCTTCTAACAACCTC 480
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QY 481 CTGAGATACACCCGCGTGTCCGCTGTGCCCCATTTAAACAGTTGCCGTGAGAGTTGGTG 540
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DB 1814 CTGAGATACACCCGCGTGTCCGCTGTGCCCCATTTAAACAGTTGCCGTGAGAGTTGGTG 1873
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DB 1874 GCGCTGCCGAGGCTGTGGAATGTATCGAGACTTGTCTTAACGACCTGGGCAACCTTGG 1933
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QY 601 ACTGAGCTGTAAACGCCGCCGAGCATTAAGGTGTAACCTGTGATGCTGTGTTAACT 660
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DB 1934 ACTGAGCTGTAAACGCCGCCGAGCATTAAGGTGTAACCTGTGATGCTGTGTTAACT 1993
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QY 661 CGCCTTGTGTTGCTGAATGAGTTGATGTAATTAATTAAGGAGTAATGTTTAACT 720
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DB 1994 CGCCTTGTGTTGCTGAATGAGTTGATGTAATTAATTAAGGAGTAATGTTTAACT 2053
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QY 721 TGCAATGCGGTGTAATGAGGCGGGGCTTAAAGGATATATATGCGCGGTGAGCTAATCT 780
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DB 2174 ACTGTGGAACAGAGCTCTAACAGTACTTGTGTTTGGAGGTTTCTGTGGGCTCAT 2233
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DB 2234 CCCAGGCAAGTTAGTGTGCAGAATTAAAGAGATTACAGTGGGAATTTGAAGAGCTTT 2293
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QY 961 TGAATCTGTGAGGAGCTGTTGATCTTGTGATCTGGGTCACAGGCGCTTTCCAG 1020
| | | | |
DB 2294 TGAATCTGTGAGGAGCTGTTGATCTTGTGATCTGGGTCACAGGCGCTTTCCAG 2353
| | | | |
QY 1021 AGAAGTCAATCAAGACTTGGATTTTTCACACCGGCGCGCTGCGGCTGTGTTGCTT 1080
| | | | |
DB 2354 AGAAGTCAATCAAGACTTGGATTTTTCACACCGGCGCGCTGCGGCTGTGTTGCTT 2413
| | | | |
QY 1081 TTTTGAATTTTAAAGATTAATGAGCGGAAGAAACCCATCTGAGCGGGGGGTAACTGCG 1140
| | | | |
DB 2414 TTTTGAATTTTAAAGATTAATGAGCGGAAGAAACCCATCTGAGCGGGGGGTAACTGCG 2473
| | | | |
QY 1141 TGGATTTTTCGCGCATCTGTGAGAGCGGTTGTGAGACACAAGATTCGCTGCTAC 1200
| | | | |
DB 2474 TGGATTTTTCGCGCATCTGTGAGAGCGGTTGTGAGACACAAGATTCGCTGCTAC 2533
| | | | |
QY 1201 TGTGTCTTCCGTCGCGCGCGGATTAATACGAGAGAGACGACGACGACGAGAGG 1260
| | | | |
DB 2534 TGTGTCTTCCGTCGCGCGCGGATTAATACGAGAGAGACGACGACGACGAGAGG 2593
| | | | |
QY 1261 AAGCCAGCGCGCGGAGAGAGAGCCCATGGAACCCGAGAGCGGCTGTGACCTTC 1320
| | | | |

Db	2594		2653
Qy	1321		1380
Db	2554		2713
Qy	1381		1440
Db	2714		2773
Qy	1441		1500
Db	2774		2833
Qy	1501		1560
Db	2834		2893
Qy	1561		1620
Db	2894		2953
Qy	1621		1680
Db	2954		3013
Qy	1681		1740
Db	3014		3073
Qy	1741		1800
Db	3074		3133
Qy	1801		1860
Db	3134		3193
Qy	1861		1920
Db	3194		3253
Qy	1921		1980
Db	3254		3313
Qy	1981		2040
Db	3314		3373
Qy	2041		2100
Db	3374		3433
Qy	2101		2160
Db	3434		3493
Qy	2161		2220
Db	3494		3553
Qy	2221		2280
Db	3554		3613
Qy	2281		2340
Db	3614		3673
Qy	2341		2400

Db	3674	CACTAAGATATTTGCTTGAGCCCGAGAGCATGTCCAAAGTGAACCTGAACGGGGTGTGGA	3723
Qy	2401	CATGACATGAAGATCTTGGAAGGTGCTGAGTAGATGAGAACCCGGCACAGGTGCAACC	2460
Db	3734	CATGACCATGAAGATCTTGGAAGGTGCTGAGTAGATGAGAACCCGGCACAGGTGCAACC	3793
Qy	2461	CTGCGAGTGGGGGTGAACATATTAGAACCGAGCTGTGATGTGATGACCGAGGA	2520
Db	3794	CTGCGAGTGGGGGTGAACATATTAGAACCGAGCTGTGATGTGATGACCGAGGA	3853
Qy	2521	GCTGAGCCCGATCACTTGTGTCTGCTGACCCCGGCTGAGTTTGCTTACGATGA	2580
Db	3854	GCTGAGCCCGATCACTTGTGTCTGCTGACCCCGGCTGAGTTTGCTTACGATGA	3913
Qy	2581	AGATACGATTTGAG	2594
Db	3914	AGATACGATTTGAG	3927
RESULT 3			
US-09-482-682-48			
Sequence 48, Application US/09482682			
Publication No. US20030157688A1			
GENERAL INFORMATION:			
APPLICANT: VON SEGGERN, DANIEL			
APPLICANT: NEMEROW, GLEN R.			
APPLICANT: HALLENBECK, PAUL			
APPLICANT: STEVENSON, SUSAN			
TITLE OF INVENTION: ADENOVIRUS VECTORS, PACKAGING CELL LINES, COMPOSITIONS,			
FILE REFERENCE: 1294.0010001			
CURRENT APPLICATION NUMBER: US/09/482,682			
NUMBER OF INVENTION: AND METHODS FOR PREPARATION AND USE			
CURRENT FILING DATE: 2000-01-14			
NUMBER OF SEQ ID NOS: 76			
SOFTWARE: PatentIn Ver. 2.1			
SEQ ID NO 48			
LENGTH: 7607			
TYPE: DNA			
ORGANISM: Artificial Sequence			
FEATURE:			
OTHER INFORMATION: Description of Artificial Sequence: plasmid			
US-09-482-682-48			
Query Match 100.0%; Score 2594; DB 10; Length 7607;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	ATCGATCTTACCTGCAAGAGGCTGCTTCCACCAGTGAAGAGATGAAGAGGT	60
Db	1334	ATCGATCTTACCTGCAAGAGGCTGCTTCCACCAGTGAAGAGATGAAGAGGT	1393
Qy	61	GAGGAGTTTGTGTTAATATATGTGACACCCCGGGACCGTTGCAGGTCTTGTCAATTAT	120
Db	1394	GAGGAGTTTGTGTTAATATATGTGACACCCCGGGACCGTTGCAGGTCTTGTCAATTAT	1453
Qy	121	CACCGAGGAATAGGGGGGACCCAGATATTATGTGCTCGCTTGTATATAGGACCTGT	180
Db	1454	CACCGAGGAATAGGGGGGACCCAGATATTATGTGCTCGCTTGTATATAGGACCTGT	1513
Qy	181	GGCATGTTTGTCTACATTAAGTGAATATAGGACAGTGGTGTATAGAGTGGGTTTG	240
Db	1514	GGCATGTTTGTCTACATTAAGTGAATATAGGACAGTGGTGTATAGAGTGGGTTTG	1573
Qy	241	GTGTGTAATTTTATTTTAAATTTTAAAGTTTGTGTTTAAAGATTTGTATTTGTA	300
Db	1574	GTGTGTAATTTTATTTTAAATTTTAAAGTTTGTGTTTAAAGATTTGTATTTGTA	1633
Qy	301	TTTTTTTAAAGGTCGTGTCTGAACCTGAGCCTGAGCCCGGACCGAAGACCGAGCCTG	360
Db	1634	TTTTTTTAAAGGTCGTGTCTGAACCTGAGCCTGAGCCCGGACCGAAGACCGAGCCTG	1693
Qy	361	CAGACCTACCCGCGTCTTAATATGCGCCTGTATCTTGAGACGCCGACATCACCTG	420

Db 1694 CAAAGCTACCCGCGCTCTTAATAATGCGCCCTGCTATCTGAGAGCCGACATCACTG 1753
Qy 421 TGTCTAGAGAAATGCAATAGTATGATGAGATAGCTGTGACTCCGGTCTTTCTAACACACCTC 480
Db 1754 TGTCTAGAGAAATGCAATAGTATGATGAGATAGCTGTGACTCCGGTCTTTCTAACACACCTC 1813
Qy 481 CTGAGATACACCCGGTGGTCCGCTGTGCCCCATTAAACCAAGTTGCCGTGAGAGTTGGTG 540
Db 1814 CTGAGATACACCCGGTGGTCCGCTGTGCCCCATTAAACCAAGTTGCCGTGAGAGTTGGTG 1873
Qy 541 GGCCTGCGCAGAGCTGTGGAATGTATCGAGACTTGCTTAACAGGCTGAGGCAACTTTGG 600
Db 1874 GGCCTGCGCAGAGCTGTGGAATGTATCGAGACTTGCTTAACAGGCTGAGGCAACTTTGG 1933
Qy 601 ACTTGAAGCTGTAAACGCCCAAGCCATAGGTTAAACCTGTGATTCGTGTGTGTAA 660
Db 1934 ACTTGAAGCTGTAAACGCCCAAGCCATAGGTTAAACCTGTGATTCGTGTGTGTAA 1993
Qy 661 GCGCTTGT 720
Db 1994 GCGCTTGT 2053
Qy 721 TGCATGCGCTGTAAATGAGGCGGGGCTTAAAGGGTATATATGCGCGGTGGAATCT 780
Db 2054 TGCATGCGCTGTAAATGAGGCGGGGCTTAAAGGGTATATATGCGCGGTGGAATCT 2113
Qy 781 TGTGTACATCTGACCTCATGAGAGCTTGGAGTGTGGAGATTTTCTGTGTGCTA 840
Db 2114 TGTGTACATCTGACCTCATGAGAGCTTGGAGTGTGGAGATTTTCTGTGTGCTA 2173
Qy 841 ACTTGTGTGGAACAGAGCTCTTAACAGTACTCTGTGTTTGTGAGGTTTCTGTGGGCTCAT 900
Db 2174 ACTTGTGTGGAACAGAGCTCTTAACAGTACTCTGTGTTTGTGAGGTTTCTGTGGGCTCAT 2233
Qy 901 CCCAGGCAAAAGTTAGTGTGAGAAATTAAGAGAAATTAAGAGAAATTAAGAGCTT 960
Db 2234 CCCAGGCAAAAGTTAGTGTGAGAAATTAAGAGAAATTAAGAGAAATTAAGAGCTT 2293
Qy 961 TGAATCTGTGTGAGAGCTGTGTTGATCTTTGAAATCTGGGTACACAGAGCTTTTCCAG 1020
Db 2294 TGAATCTGTGTGAGAGCTGTGTTGATCTTTGAAATCTGGGTACACAGAGCTTTTCCAG 2353
Qy 1021 AGAAGTCAATAGACTTTTGTGATTTTTCACACCGGGGCGGCTGCGGCTGTGCTT 1080
Db 2354 AGAAGTCAATAGACTTTTGTGATTTTTCACACCGGGGCGGCTGCGGCTGTGCTT 2413
Qy 1081 TTTTGAAGTTTATAAGGATTAATGAGCGAAGAAATCCATCTGAGCGGGGGTAACTGCG 1140
Db 2414 TTTTGAAGTTTATAAGGATTAATGAGCGAAGAAATCCATCTGAGCGGGGGTAACTGCG 2473
Qy 1141 TGAATTTTCTGGCCATGATCTGTGAGAGCGGTTGTGAGACAGAGAAATGCGCTGTAC 1200
Db 2474 TGAATTTTCTGGCCATGATCTGTGAGAGCGGTTGTGAGACAGAGAAATGCGCTGTAC 2533
Qy 1201 TGTGTCTTCCGTCGCGCGCGGCAATATACCGAGCGAGAGCAACAGACAGACAGAGAG 1260
Db 2534 TGTGTCTTCCGTCGCGCGCGGCAATATACCGAGCGAGAGCAACAGACAGACAGAGAG 2593
Qy 1261 AAGCGAGCGCGCGCGAGAGAGAGAGCCATGGAATCCGAGAGCGGCTGTGACCTTC 1320
Db 2594 AAGCGAGCGCGCGCGAGAGAGAGAGCCATGGAATCCGAGAGCGGCTGTGACCTTC 2653
Qy 1321 GGAATGATTTGTATACAGTGTGCTGAATCTGTATCCAGAACTGAGAGCAATTTTGACAT 1380
Db 2654 GGAATGATTTGTATACAGTGTGCTGAATCTGTATCCAGAACTGAGAGCAATTTTGACAT 2713
Qy 1381 TACAGAGATGAGGCAAGGAGCTTAAAGGGGCTTAAAGAGAGAGCGGGGCTGTGAGGCTAC 1440
Db 2714 TACAGAGATGAGGCAAGGAGCTTAAAGGGGCTTAAAGAGAGAGCGGGGCTGTGAGGCTAC 2773
Qy 1441 AGAGAGGCTAGGAATCTAGCTTTAGCTTAATGACAGACACGCTCTGAGTATTTAC 1500

Db 2774 AGAGAGGCTAGGAATCTAGCTTTAGCTTAATGACAGACACGCTCTGAGTATTTAC 2833
Qy 1501 TTTTCAACAGATCAAGATTAATGCGCTAATGAGCTTGTGTGCGGAGAGATATTC 1560
Db 2834 TTTTCAACAGATCAAGATTAATGCGCTAATGAGCTTGTGTGCGGAGAGATATTC 2893
Qy 1561 CATAGAGAGCTGACCACTTCTGCTGACAGCGGAGATGATTTTGAAGGCTATTAG 1620
Db 2894 CATAGAGAGCTGACCACTTCTGCTGACAGCGGAGATGATTTTGAAGGCTATTAG 2953
Qy 1621 GGTATATGCAAAAGGTGCACTTGAAGCCAGATTGCAAGTACAGCAACTTGTAA 1680
Db 2954 GGTATATGCAAAAGGTGCACTTGAAGCCAGATTGCAAGTACAGCAACTTGTAA 3013
Qy 1681 TATCAGGAATTTGTGCTACATTTCTGGGAACGGGGCCGAGGTGAGATAGTACGAGGA 1740
Db 3014 TATCAGGAATTTGTGCTACATTTCTGGGAACGGGGCCGAGGTGAGATAGTACGAGGA 3073
Qy 1741 TAGGTTGCTTTAGATGATGATGATTAATATGTGCGGGGCTGTGGCATGACGG 1800
Db 3074 TAGGTTGCTTTAGATGATGATGATTAATATGTGCGGGGCTGTGGCATGACGG 3133
Qy 1801 GGTGATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
Db 3134 GGTGATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3193
Qy 1861 CAATACCAACCTTATCTTACACGAGGTGATAGCTTCTATGAGTTTAAACAATACCTGTGGA 1920
Db 3194 CAATACCAACCTTATCTTACACGAGGTGATAGCTTCTATGAGTTTAAACAATACCTGTGGA 3253
Qy 1921 AGCTGGAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
Db 3254 AGCTGGAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3313
Qy 1981 GTGTGCGCCCAAAAGCAAGGCTTCAATTAAGAAATGCTCTTGAAGGTGTACTTGGG 2040
Db 3314 GTGTGCGCCCAAAAGCAAGGCTTCAATTAAGAAATGCTCTTGAAGGTGTACTTGGG 3373
Qy 2041 TATCTGTCTGAGGGTAACTTCAAGGTTGCGCCACAATGTGCGCTCCGACTGTGTTGCTT 2100
Db 3374 TATCTGTCTGAGGGTAACTTCAAGGTTGCGCCACAATGTGCGCTCCGACTGTGTTGCTT 3433
Qy 2101 CATCTAGTGAAGGCGTGTGATTAAGATTAACATGATGATGATGATGATGATGATGAT 2160
Db 3434 CATCTAGTGAAGGCGTGTGATTAAGATTAACATGATGATGATGATGATGATGATGAT 3493
Qy 2161 CAGGCGCTCTCAGATGCGACCTGCTCGGACGGCACTGTCACTGCGAAGACCATTC 2220
Db 3494 CAGGCGCTCTCAGATGCGACCTGCTCGGACGGCACTGTCACTGCGAAGACCATTC 3553
Qy 2221 CGTAGCCAGCACTCTGCAAGGCTGTGCGCAGTGTGAGCATTAACACTGACCCGCTG 2280
Db 3554 CGTAGCCAGCACTCTGCAAGGCTGTGCGCAGTGTGAGCATTAACACTGACCCGCTG 3613
Qy 2281 TTCCTTGCAATTTGGGTAAACAGAGGGGGGTCTTCTTACCTTAACATGCAATTTGAGTCA 2340
Db 3614 TTCCTTGCAATTTGGGTAAACAGAGGGGGGTCTTCTTACCTTAACATGCAATTTGAGTCA 3673
Qy 2341 CACTAAGATATTTGTTAGGCGCGAGACATGTCCAAAGTGAACCTGAACGGGGGTTTGA 2400
Db 3674 CACTAAGATATTTGTTAGGCGCGAGACATGTCCAAAGTGAACCTGAACGGGGGTTTGA 3733
Qy 2401 CATGACCATGAGATCTGGAAGGTGCTGAGGTAAGTGAAGACCCGACCAAGTGCAGACC 2460
Db 3734 CATGACCATGAGATCTGGAAGGTGCTGAGGTAAGTGAAGACCCGACCAAGTGCAGACC 3793
Qy 2461 CTGCGAGTGTGGCGGTAAACATATTAGAAACCAAGCTGTGATGCTGAATGTAACCGAGGA 2520
Db 3794 CTGCGAGTGTGGCGGTAAACATATTAGAAACCAAGCTGTGATGCTGAATGTAACCGAGGA 3853
Qy 2521 GCTGAGGCGCGATCACTTGTGCTGCGCTGACCCCGCTGAGTTTGGCTTACGAGTGA 2580
Db 3854 GCTGAGGCGCGATCACTTGTGCTGCGCTGACCCCGCTGAGTTTGGCTTACGAGTGA 3913

OY 2581 AGATACAGATTGAG 2594
Db 3914 AGATACAGATTGAG 3927

RESULT 4
US-10-403-337-41
Sequence 41, Application US/10403337
Publication No. US20030215948A1
GENERAL INFORMATION:
APPLICANT: Kaleko, Michael
APPLICANT: Nemerow, Glen R.
APPLICANT: Smith, Theodore
APPLICANT: Stevenson, Susan C.
TITLE OR INVENTION: Fiber Shaft Modifications for Efficient Targeting
FILE REFERENCE: 22908-1236B
CURRENT APPLICATION NUMBER: US/10/403,337
CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: 10/351,890
PRIOR FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: 60/350,388
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/391,967
PRIOR FILING DATE: 2002-06-26
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn version 3.0
SEQ ID NO 41
LENGTH: 7607
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Plasmid GRS-El-SV40-Hygro
US-10-403-337-41

Query Match 100.0%; Score 2594; DB 18; Length 7607;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGCATCTTACCTGCCACGAGAGCTGGCTTTCCACCCAGTACGACGAGATGAAGAGGT 60
Db 1334 ATGCATCTTACCTGCCACGAGAGCTGGCTTTCCACCCAGTACGACGAGATGAAGAGGT 1393
OY 61 GAGAGTTTGTGTAGATTAATGTGAGACACCCGGGACGTTGCGAGTCTTGCATTAT 120
Db 1394 GAGAGTTTGTGTAGATTAATGTGAGACACCCGGGACGTTGCGAGTCTTGCATTAT 1453
OY 121 CACCGAGGAATACGGGGGACCCAGATATTAATGTGCTTTGCTATATGAGAGCTGT 180
Db 1454 CACCGAGGAATACGGGGGACCCAGATATTAATGTGCTTTGCTATATGAGAGCTGT 1513
OY 181 GGCATGTTTGTCTACAGTAAGTAAATTAAGGACAGTGGGTATGAGTGGTGGTTG 240
Db 1514 GGCATGTTTGTCTACAGTAAGTAAATTAAGGACAGTGGGTATGAGTGGTGGTTG 1573
OY 241 GTGTGTAATTTTATTTTAAATTTTACAGTTTGTGTAAAGATTTGTAATTTGA 300
Db 1574 GTGTGTAATTTTATTTTAAATTTTACAGTTTGTGTAAAGATTTTGTATTTGGA 1633
OY 301 TTTTAAAAAGTCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGAGCCTG 360
Db 1634 TTTTAAAAAGTCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGAGCCTG 1693
OY 361 CAAGACCTACCCGCGCTCTAAATAGGGCGCTGCTATCTGAGACGCCGACATCACTG 420
Db 1694 CAAGACCTACCCGCGCTCTAAATAGGGCGCTGCTATCTGAGACGCCGACATCACTG 1753
OY 421 TGTCTAGAGATGCAATAGTATGAGTACGATGCTGCGTCTCTTAACACACTC 480
Db 1754 TGTCTAGAGATGCAATAGTATGAGTACGATGCTGCGTCTCTTAACACACTC 1813
OY 481 CTGAGATACACCCGGTGTCCCGCTGTGCCCATTAACCAAGTTGCCGTGAGAGTTGTTG 540
Db 1813 CTGAGATACACCCGGTGTCCCGCTGTGCCCATTAACCAAGTTGCCGTGAGAGTTGTTG 540

Db 1814 CTGAGATACACCCGGTGTCCCGCTGTGCCCATTAACCAAGTTGCCGTGAGAGTTGTTG 1873
OY 541 GCGTCCCGCAGGCTGTGGAATGTATCGAGAGCTTGTCTTAACGAGACCTGGGCAACTTTGG 600
Db 1874 GCGTCCCGCAGGCTGTGGAATGTATCGAGAGCTTGTCTTAACGAGACCTGGGCAACTTTGG 1933
OY 601 ACTGAGCTGTAAACGCCCGAGCCATAGGTGTAAACCTGTGATTCGTGTGTAA 660
Db 1934 ACTGAGCTGTAAACGCCCGAGCCATAGGTGTAAACCTGTGATTCGTGTGTAA 1993
OY 661 CGCCTTTGTTTGTCTGAATGAGTTGATGTAAAGTTAATPAAGGCTGAGATTAATGTTAACT 720
Db 1994 CGCCTTTGTTTGTCTGAATGAGTTGATGTAAAGTTAATPAAGGCTGAGATTAATGTTAACT 2053
OY 721 TGCATGGCGTGTAAATGGGCGGGGCTTAAAGGTTATATATGCGCGTGGGCTAACT 780
Db 2054 TGCATGGCGTGTAAATGGGCGGGGCTTAAAGGTTATATATGCGCGTGGGCTAACT 2113
OY 781 TGGTTACATCTGACCTGATGAGGCTTGGAGTGTGGAAGATTTTCTGCTGCGTA 840
Db 2114 TGGTTACATCTGACCTGATGAGGCTTGGAGTGTGGAAGATTTTCTGCTGCGTA 2173
OY 841 ACTTGTGGAACAGAGCTCTAACAGTACCTTCTGTTTGGAGGTTTCTGTGGGCTCAT 900
Db 2174 ACTTGTGGAACAGAGCTCTAACAGTACCTTCTGTTTGGAGGTTTCTGTGGGCTCAT 2233
OY 901 CCCAGGCAAGTTAGTGTGAGATTAAGAGATTAAGGAGTTCAAGTGGGAATTTGAAGCTTT 960
Db 2234 CCCAGGCAAGTTAGTGTGAGATTAAGAGATTAAGGAGTTCAAGTGGGAATTTGAAGCTTT 2293
OY 961 TGAATCCTGTGTGAGCTGTTTGAATCTTTGAATCTGGGTCAACGAGCGCTTTTCCAG 1020
Db 2294 TGAATCCTGTGTGAGCTGTTTGAATCTTTGAATCTGGGTCAACGAGCGCTTTTCCAG 2353
OY 1021 AGAAGTCAATCAGACTTTGATTTTCCACACCGGGCGGCTGCGCTGTGCTT 1080
Db 2354 AGAAGTCAATCAGACTTTGATTTTCCACACCGGGCGGCTGCGCTGTGCTT 2413
OY 1081 TTTTGAATTTAATGAAGTAAATGAGCGAAGAACCCATCTGAGCGGGGGTAACTGCG 1140
Db 2414 TTTTGAATTTAATGAAGTAAATGAGCGAAGAACCCATCTGAGCGGGGGTAACTGCG 2473
OY 1141 TGGATTTTCTGGCCATCATCTGTGAGAGCGGTTGTGAGACACAAGATCGCTGTAC 1200
Db 2474 TGGATTTTCTGGCCATCATCTGTGAGAGCGGTTGTGAGACACAAGATCGCTGTAC 2533
OY 1201 TGTGTCTTCCTGCGCCCGGCGATTAATCCGACGAGAGACAGACAGACAGAGAG 1260
Db 2534 TGTGTCTTCCTGCGCCCGGCGATTAATCCGACGAGAGACAGACAGACAGAGAG 2593
OY 1261 AAGCCAGCGCGCGGCGAGAGAGGCCCATGGAACCCGAGAGCGGCTGTGACCTC 1320
Db 2594 AAGCCAGCGCGCGGCGAGAGAGGCCCATGGAACCCGAGAGCGGCTGTGACCTC 2653
OY 1321 GGGATGAATGTTTGTACAGGTGCTGAACTGTATCCAGAACTGAGACGATTTTGAAT 1380
Db 2654 GGGATGAATGTTTGTACAGGTGCTGAACTGTATCCAGAACTGAGACGATTTTGAAT 2713
OY 1381 TACAGAGATGGGAGGCGGCTAAAGGGGCTAAAGGAGCGGGGGCTTGTGAGGCTAC 1440
Db 2714 TACAGAGATGGGAGGCGGCTAAAGGGGCTAAAGGAGCGGGGGCTTGTGAGGCTAC 2773
OY 1441 AGAGAGGCTAGGAATCAGCTTTAGCTTAATGACAGACAGCGTCTGAGTGAATAC 1500
Db 2774 AGAGAGGCTAGGAATCAGCTTTAGCTTTATATATACAGACAGCGTCTGAGTGAATAC 2833
OY 1501 TTTTCAACAGATCAAGATTAATGCGTAAATGAGCTTATGCTGTGGCGCAAGATATTC 1560
Db 2834 TTTTCAACAGATCAAGATTAATGCGTAAATGAGCTTATGCTGTGGCGCAAGATATTC 2893
OY 1561 CATAGAGAGCTGACCACTTAATGCTGTGACAGCCAGGGGATTAATTTTGAAGAGGCTATTAG 1620
Db 2894 CATAGAGAGCTGACCACTTAATGCTGTGACAGCCAGGGGATTAATTTTGAAGAGGCTATTAG 2953

QY	1621	GGTAAATACAAAGGCGCATTAAGCCAGATTGCGAAGTACAAATACACAAACTTGTAA	1680
Db	2954	GGTAAATACAAAGGCGCATTAAGCCAGATTGCGAAGTACAAATACACAAACTTGTAA	3013
QY	1681	TATCAGAAATGTTGCTCACTTTCTGGGAAACGGGGCCGAGGTGAGATAGATAACGAGGA	1740
Db	3014	TATCAGAAATGTTGCTCACTTTCTGGGAAACGGGGCCGAGGTGAGATAGATAACGAGGA	3073
QY	1741	TAGGTTGGCTTTAAGTGAATGAATATATGTGGCCGGGGGTGCTTGGCATAGACGG	1800
Db	3074	TAGGTTGGCTTTAAGTGAATGAATATATGTGGCCGGGGGTGCTTGGCATAGACGG	3133
QY	1801	GGTGGTTATTAAGAAATGAAGTTAACTAGCCGCCCAATTTAGCGGTACGGTTTCTGGC	1860
Db	3134	GGTGGTTATTAAGAAATGAAGTTAACTAGCCGCCCAATTTAGCGGTACGGTTTCTGGC	3193
QY	1861	CAATACCAACCTTATCTTACACGGTGAAGCTTATAGGGTTTAAACAATACCTGTGGA	1920
Db	3194	CAATACCAACCTTATCTTACACGGTGAAGCTTATAGGGTTTAAACAATACCTGTGGA	3255
QY	1921	AGCTTGAACCGATGTAAGGTTCCGGGCGTGGCTTTTATCTGTCTGGAAGGGGTGCT	1980
Db	3254	AGCTTGAACCGATGTAAGGTTCCGGGCGTGGCTTTTATCTGTCTGGAAGGGGTGCT	3313
QY	1981	GTGTGCCCCCAAAACAGGGGCTCAATTAAGAAATGCGCTTTGAAAGGTGAACCTTGG	2040
Db	3314	GTGTGCCCCCAAAACAGGGGCTCAATTAAGAAATGCGCTTTGAAAGGTGAACCTTGG	3373
QY	2041	TATCCTGTCTAGGGTAACTCCAGGGTCCGCCAATGTGGCTTCCGACTGTGGTCTT	2100
Db	3374	TATCCTGTCTAGGGTAACTCCAGGGTCCGCCAATGTGGCTTCCGACTGTGGTCTT	3433
QY	2101	CATGTTAGTGAAGAAGCGTGGCTGTATTAAGCATTAATGTATGTGCAACTGCGAGGA	2160
Db	3434	CATGTTAGTGAAGAAGCGTGGCTGTATTAAGCATTAATGTATGTGCAACTGCGAGGA	3493
QY	2161	CAGGGCCTCTCAAGTGTGACCTGTCTCGGACCGCAACTGTCACTGCTGAAGACCAATTA	2220
Db	3494	CAGGGCCTCTCAAGTGTGACCTGTCTCGGACCGCAACTGTCACTGCTGAAGACCAATTA	3553
QY	2221	CGTAGCCAGCACTCTGCGCAAGGCTGGCCAGTGTTTAGACATAATCTGACCCGCTG	2280
Db	3554	CGTAGCCAGCACTCTGCGCAAGGCTGGCCAGTGTTTAGACATAATCTGACCCGCTG	3613
QY	2281	TTCTTGTGATTTGGGTAAACAGAGGGGGGTGTCTAAGCTTAACCAATGCAATTTGAATCA	2340
Db	3614	TTCTTGTGATTTGGGTAAACAGAGGGGGGTGTCTAAGCTTAACCAATGCAATTTGAATCA	3673
QY	2341	CACCTAAGATATTGCTGTAGCCCGAGAGCATGTCCAAAGGTGAACCTGAACGGGGTGTGA	2400
Db	3674	CACCTAAGATATTGCTGTAGCCCGAGAGCATGTCCAAAGGTGAACCTGAACGGGGTGTGA	3733
QY	2401	CATGACCATGAAGATCTGAAGGTGCTGAGGTAACGATGACACCCGACACAGGTGCAGACC	2460
Db	3734	CATGACCATGAAGATCTGAAGGTGCTGAGGTAACGATGACACCCGACACAGGTGCAGACC	3793
QY	2461	CTGCGAAGTGTGGCGGTAAACAATTAAGGAACCAAGCTGTGATGTCTGATATGTAACGAGGA	2520
Db	3794	CTGCGAAGTGTGGCGGTAAACAATTAAGGAACCAAGCTGTGATGTCTGATATGTAACGAGGA	3853
QY	2521	GCTGAGGCCCATCACTTGTGTGCTGGCTGCAACCGCGCTGAGTGTGGCTCTAGACGATGA	2580
Db	3854	GCTGAGGCCCATCACTTGTGTGCTGGCTGCAACCGCGCTGAGTGTGGCTCTAGACGATGA	3913
QY	2581	AGATACAGATTTGAG 2594	
Db	3914	AGATACAGATTTGAG 3927	

Query Match	100.0%	Score 2594	DB 18	Length 7607	Beet Local Similarity 100.0%	Pred. No. 0	Matches 2594	Conservative 0	Mismatches 0	Indels 0	Gaps 0
GENERAL INFORMATION:	US20040002060A1										
APPLICANT:	Stevenson, Susan C.										
APPLICANT:	Kaleko, Michael										
APPLICANT:	Smith, Theodore										
APPLICANT:	Nemerow, Glen R.										
TITLE OF INVENTION:	Fiber Shaft Modifications for Efficient Targeting										
FILE REFERENCE:	22908-1236										
CURRENT APPLICATION NUMBER:	US/0/351,890										
PRIOR FILING DATE:	2003-01-28										
PRIOR APPLICATION NUMBER:	60/350,388										
PRIOR FILING DATE:	2002-01-24										
PRIOR APPLICATION NUMBER:	60/391,967										
PRIOR FILING DATE:	2002-06-26										
NUMBER OF SEQ ID NOS:	72										
SOFTWARE:	Patentin version 3.0										
SEQ ID NO 41											
LENGTH:	7607										
TYPE:	DNA										
ORGANISM:	Artificial Sequence										
FEATURES:											
OTHER INFORMATION:	Plasmid GRES-BL-SV40-Hygro										
US-10-351-890-41											
1	ATCGATCTTACCTCCACGAGGCTGCTTCCACCCAGTGACGACGAGATGAAGAGGGT	60									
1334	ATCGATCTTACCTCCACGAGGCTGCTTCCACCCAGTGACGACGAGATGAAGAGGGT	1395									
61	GAGAGTTTGTGTAGATTATGTGAGGACCCCGGCGACGGTTGCAAGTCTTGCATTAT	120									
1394	GAGAGTTTGTGTAGATTATGTGAGGACCCCGGCGACGGTTGCAAGTCTTGCATTAT	1453									
121	CACCGGAGGATTAAGGGGGGACCCGAGATTATATGTGTTGCTTGTCTAATATGAGACCTGT	180									
1454	CACCGGAGGATTAAGGGGGGACCCGAGATTATATGTGTTGCTTGTCTAATATGAGACCTGT	1513									
181	GGCATGTTTGTCTACAGTAAGTGAATAATTATGAGGACGTGGGTGATAGAGTGGGTTTG	240									
1514	GGCATGTTTGTCTACAGTAAGTGAATAATTATGAGGACGTGGGTGATAGAGTGGGTTTG	1573									
241	GTGTGTATATTTTTTTTAAATTTTAACTGTTTGTGTTTAAAGATTTGTATTTGTA	300									
1574	GTGTGTATATTTTTTTTAAATTTTAACTGTTTGTGTTTAAAGATTTGTATTTGTA	1633									
301	TTTTTTTAAAGTCTGTGTCTGAACCTGAGCCGAGCCGAGCCAGAACCGAGCCTG	360									
1634	TTTTTTTAAAGTCTGTGTCTGAACCTGAGCCGAGCCGAGCCAGAACCGAGCCTG	1693									
361	CAGAAGCTACCCGCGTCTTAAATATGCGGCTGATCTTGAGACGCCGACATCACCTG	420									
1694	CAGAAGCTACCCGCGTCTTAAATATGCGGCTGATCTTGAGACGCCGACATCACCTG	1755									
421	TGTCTAAGAAATGCAATATATATATAGTATAGTGTACTGCTCCGGTCTTCTTAACAACCTC	480									
1754	TGTCTAAGAAATGCAATATATATATAGTATAGTGTACTGCTCCGGTCTTCTTAACAACCTC	1813									
481	CTGAGATTAACCCCGTGTCCGCTGTGCCCATTTAAACAGATTGCCGTGAGAGTTGGT	540									
1814	CTGAGATTAACCCCGTGTCCGCTGTGCCCATTTAAACAGATTGCCGTGAGAGTTGGT	1873									
541	GGCGTCCGACGCTGTGTGAATATATCGAGACCTTGCTTAACGAGCTTGGCAACTTTGG	600									
1874	GGCGTCCGACGCTGTGTGAATATATCGAGACCTTGCTTAACGAGCTTGGCAACTTTGG	1933									
601	ACTTGAAGCTGAACGCCCGACGACATTAAGATGAATCTGTGATGCGTGTGTGTT										

Db 1594 CGCTTTGTTGCTGAGTGAATGATGATTTAATAAGGCTGAGTAATGTTAACT 2053
Qy 721 TGCATGCGCTTTAAATGCGCGCGGCTTAAAGGATATATATGCGCGCTAATCT 780
Db 2054 TGCATGCGCTTTAAATGCGCGCGGCTTAAAGGATATATATGCGCGCTAATCT 2113
Qy 781 TGCATGCTGACCTCAATGAGGCTTGGAGGCTTGGAGGATTTTCTGCTGAGGTA 840
Db 2114 TGCATGCTGACCTCAATGAGGCTTGGAGGCTTGGAGGATTTTCTGCTGAGGTA 2173
Qy 841 ACTGCTGGAACAGAGCTCTAACAAGTACCTCTGCTTTTGGAGGTTTCTGCGGCTCAT 900
Db 2174 ACTGCTGGAACAGAGCTCTAACAAGTACCTCTGCTTTTGGAGGTTTCTGCGGCTCAT 2233
Qy 901 CCCAGGCAAAAGTTAGTCTGCAAGATTTAAGAGATTTACAAGTGGAAATTTGAAGACTTT 960
Db 2234 CCCAGGCAAAAGTTAGTCTGCAAGATTTAAGAGATTTACAAGTGGAAATTTGAAGACTTT 2293
Qy 961 TGAATCCGTGAGGCTGTTGATCTTTGAATCTGGGTCAACAGGCGCTTTTCCAG 1020
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Qy 1021 AGAAGTCATCAAGACTTTGGATTTTTCACACCGGCGCGCTGCGGCTGCTGTGCTT 1080
Db 2354 AGAAGTCATCAAGACTTTGGATTTTTCACACCGGCGCGCTGCGGCTGCTGTGCTT 2413
Qy 1081 TTTTGAAGTTTAAAGATTAATGAGACGAAGAACCCATCTGAGCGGCGGCTTACCTGC 1140
Db 2414 TTTTGAAGTTTAAAGATTAATGAGACGAAGAACCCATCTGAGCGGCGGCTTACCTGC 2473
Qy 1141 TGAATTTTCTGCGCATCTGAGAGAGCGGTTGTGAGACACAAAGATGCGCTGCTAC 1200
Db 2474 TGAATTTTCTGCGCATCTGAGAGAGCGGTTGTGAGACACAAAGATGCGCTGCTAC 2533
Qy 1201 TGTGTCTTCCGTCGCGCCGCGCATTAATACGACGAGAGACAGACGACGAGAGAG 1260
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Qy 1261 AAGCAGCGCGCGCGCGAGAGACGAGCCATGGAACCCGAGACCGGCTTGCACCTTC 1320
Db 2594 AAGCAGCGCGCGCGCGAGAGACGAGCCATGGAACCCGAGACCGGCTTGCACCTTC 2653
Qy 1321 GGAATGATTTGTGATCAGTGTGCTGAATCTGATCAGAACCTGAGAGCGCATTTGACAT 1380
Db 2654 GGAATGATTTGTGATCAGTGTGCTGAATCTGATCAGAACCTGAGAGCGCATTTGACAT 2713
Qy 1381 TACAGAGATGGGCAAGGGCTTAAAGGGGTTAAAGGAGCGGCGGCTTGTGAGGCTAC 1440
Db 2714 TACAGAGATGGGCAAGGGCTTAAAGGGGTTAAAGGAGCGGCGGCTTGTGAGGCTAC 2773
Qy 1441 AGAGAGAGCTGAGATCTTACTTTAGCTTAAATGACCAAGACCGTCTGTAGTGTATAC 1500
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Qy 1501 TTTTCAACAGATCAAGATTAATGCGCTAATGAGCTTATGCGTGGCGAGAAATATTC 1560
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Qy 1561 CATAGAGAGCTGACCACTTACTGCTGACAGCCAGGGGATGATTTTGAAGGCTATTTAG 1620
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Qy 1621 GGTATATGCAAAAGGTGCACTTAAGCCGAGATTGCAAGTACAAAGTCAAGCAATTTGTAA 1680
Db 2954 GGTATATGCAAAAGGTGCACTTAAGCCGAGATTGCAAGTACAAAGTCAAGCAATTTGTAA 3013
Qy 1681 TATCAGAAATTTGTTCTCATTTTCTGGGAGCGGCGGCGAGGTTGAGATGATGAGAGGA 1740
Db 3014 TATCAGAAATTTGTTCTCATTTTCTGGGAGCGGCGGCGAGGTTGAGATGATGAGAGGA 3073
Qy 1741 TAGGCTGCGCTTTAGATGTAGCATGATTAATATGTGCGCGGCGGCTTGTGACGAGCGG 1800

Db 3074 TAGGCTGCGCTTTAGATGTAGCATGATTAATATGTGCGCGGCGGCTTGTGACGAGCG 3133
Qy 1801 GGTGTTATTAATGATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAG 1860
Db 3134 GGTGTTATTAATGATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAG 3193
Qy 1861 CAATACCAACCTTATCTTACACGAGTGAAGCTTATGAGGTTTAAACATACCTGTGTGA 1920
Db 3194 CAATACCAACCTTATCTTACACGAGTGAAGCTTATGAGGTTTAAACATACCTGTGTGA 3253
Qy 1921 AGCTGACCGATGATTAAGGTTGCGGCGCTGCTTTTACTGCTGCTGGAAGGCGGCTGT 1980
Db 3254 AGCTGACCGATGATTAAGGTTGCGGCGCTGCTTTTACTGCTGCTGGAAGGCGGCTGT 3313
Qy 1981 GTGTGCGCCCAAAAGCGAGGCTTCAATTAAGAAATGCTCTTTGAAGGTTACTTGGG 2040
Db 3314 GTGTGCGCCCAAAAGCGAGGCTTCAATTAAGAAATGCTCTTTGAAGGTTACTTGGG 3373
Qy 2041 TATCTGTGAGGCTTAATCTCAAGGCTGCGCACAAATGAGCTCCGACTGTGCTT 2100
Db 3374 TATCTGTGAGGCTTAATCTCAAGGCTGCGCACAAATGAGCTCCGACTGTGCTT 3433
Qy 2101 CATCTAGTGAAGGCTGCTGATTAAGCATTAACATGATATGTGCAACTGCGAGGA 2160
Db 3434 CATCTAGTGAAGGCTGCTGATTAAGCATTAACATGATATGTGCAACTGCGAGGA 3493
Qy 2161 CAGGCGCTCTCAGATGCTGACCTGCTGGAACGCAACTGTACCTGCAAGACATTCA 2220
Db 3494 CAGGCGCTCTCAGATGCTGACCTGCTGGAACGCAACTGTACCTGCAAGACATTCA 3553
Qy 2221 CGTAGCCAGCACTCTGCAAGGCTGCGCAAGTGTGAGCATTAACATCTGACCCGCTG 2280
Db 3554 CGTAGCCAGCACTCTGCAAGGCTGCGCAAGTGTGAGCATTAACATCTGACCCGCTG 3613
Qy 2281 TTCCTTGATTTGGGTAAACAGAGGCGGCTGCTTACTTACCAATGCAATTTGAGTCA 2340
Db 3614 TTCCTTGATTTGGGTAAACAGAGGCGGCTGCTTACTTACCAATGCAATTTGAGTCA 3673
Qy 2341 CACTAATATATGTTAGGCGGAGACATGTCGAAGTGAACCTGAACCGGCGGTTTGA 2400
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Qy 2401 CATGACCATGAAGTCTGGAAGGCTGAGGTAAGTGAACCCGACCAAGTGCAGACC 2460
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Qy 2461 CTGCGAGTGTGCGGTAAACATATTAGGAACCAAGCTGTGATGCTGATGTGACCGAGA 2520
Db 3794 CTGCGAGTGTGCGGTAAACATATTAGGAACCAAGCTGTGATGCTGATGTGACCGAGA 3853
Qy 2521 GCTGAGGCGGATCACTTGGTGTGCGCTGCAACCGGCTGAGTTTGGCTTAAGGATGA 2580
Db 3854 GCTGAGGCGGATCACTTGGTGTGCGCTGCAACCGGCTGAGTTTGGCTTAAGGATGA 3913
Qy 2581 AGATACAGATTGAG 2594
Db 3914 AGATACAGATTGAG 3927

RESULT 6
US-10-731-961-3
; Sequence 3, Application US/10731961
; Publication No. US20050130306A1
; GENERAL INFORMATION:
; APPLICANT: Voelklmy, Richard W.
; TITLE OF INVENTION: VIRAL VECTORS WHOSE REPLICATION AND, OPTIONALLY, PASSENGER GENE
; TITLE OF INVENTION: ARE CONTROLLED BY A GENE SWITCH ACTIVATED BY HEAT IN THE PRESENCE
; FILE REFERENCE: Replicating virus
; CURRENT APPLICATION NUMBER: US/10731,961
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 09/939,161
; PRIOR FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: 60/191,580
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patent version 3.3
SEQ ID NO 3
LENGTH: 9905
TYPE: DNA
ORGANISM: Artificial
FEATURES:
OTHER INFORMATION: pxc1 plasmid
US-10-731-961-3

Query Match 100.0%; Score 2594; DB 24; Length 9905;

Beet Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 916 ATGCATCTTACCTCCGACGAGGCTGCTTTCCACCAGCTGACGAGAGATGAGAGGCT 975
QY 61 GAGAGATTGTTGATTGATTATGAGAGACCCCGGGACCGGTTGACGGTCTTGTATTAT 120
DB 976 GAGAGATTGTTGATTGATTATGAGAGACCCCGGGACCGGTTGACGGTCTTGTATTAT 1035
QY 121 CACCGGAGGATTAAGGAGGACCCAGATATATATGTTGCTTGTATATGAGACCTGT 180
DB 1036 CACCGGAGGATTAAGGAGGACCCAGATATATATGTTGCTTGTATATGAGACCTGT 1095
QY 181 GGCATGTTTGTCTACAGTAAGTGAATAATTATGGGAGTGGGATGATGAGTGGGTTTG 240
DB 1096 GGCATGTTTGTCTACAGTAAGTGAATAATTATGGGAGTGGGATGATGAGTGGGTTTG 1155
QY 241 GTGGGTAAATTTTTTTTAAATTTTAAAGTTTGTGGTTTAAAGATTTTGTATTGTA 300
DB 1156 GTGGGTAAATTTTTTTTAAATTTTAAAGTTTGTGGTTTAAAGATTTTGTATTGTA 1215
QY 301 TTTTTTAAAGGTCCTGTCTGTAACCTGAGCCTGAGCCGAGCCAGAACCGGAGCTTG 360
DB 1216 TTTTTTAAAGGTCCTGTCTGTAACCTGAGCCTGAGCCGAGCCAGAACCGGAGCTTG 1275
QY 361 CAAGACCTACCCGCGCTCTAAATATGAGGCTGCTATCTTGAAGCCGACATCACTTG 420
DB 1276 CAAGACCTACCCGCGCTCTAAATATGAGGCTGCTATCTTGAAGCCGACATCACTTG 1335
QY 421 TGTCTAAGAAATGCAATATGATAGTACGATAGCTGATCTCGGTTCTTAAACAACCTC 480
DB 1336 TGTCTAAGAAATGCAATATGATAGTACGATAGCTGATCTCGGTTCTTAAACAACCTC 1395
QY 481 CTGAGATTAACCCGCTGCTGCTGAGCCCATTTAAACCACTTGCCTGAGAGTTGTTG 540
DB 1396 CTGAGATTAACCCGCTGCTGCTGAGCCCATTTAAACCACTTGCCTGAGAGTTGTTG 1455
QY 541 GGCCTGCGCAGGCTGATGATATGATGAGAGCTTGCTTAACGAGCTGGGCAACTTTTG 600
DB 1456 GGCCTGCGCAGGCTGATGATATGATGAGAGCTTGCTTAACGAGCTGGGCAACTTTTG 1515
QY 601 ACTTGAGCTGTAAACGCCCCAGGCAATTAAGGTGTAAACCTGTGATTTGCTGTGTAA 660
DB 1516 ACTTGAGCTGTAAACGCCCCAGGCAATTAAGGTGTAAACCTGTGATTTGCTGTGTAA 1575
QY 661 CGCCTTGTGTTGCTGATGATGATGATTAATTAAGGAGGATTAATGTTTAACT 720
DB 1576 CGCCTTGTGTTGCTGATGATGATGATTAATTAAGGAGGATTAATGTTTAACT 1635
QY 721 TGATGAGCTGTAAATGGGCGGGGCTTAAAGGATATATATGCGCGGTGCTAACT 780
DB 1636 TGATGAGCTGTAAATGGGCGGGGCTTAAAGGATATATATGCGCGGTGCTAACT 1695
QY 781 TGATTAATCTGACCTCAATGAGGCTTGGAGGTGTTTGAAGATTTTCTGCTGTGCTGA 840
DB 1696 TGATTAATCTGACCTCAATGAGGCTTGGAGGTGTTTGAAGATTTTCTGCTGTGCTGA 1755
QY 841 ACTTGTCTGGAACAGAGCTTAACAGTACTTGTGTTTGAAGGTTTCTGTGGGCTCAT 900
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DB 1756 ACTTGTCTGGAACAGAGCTTAACAGTACTTGTGTTTGAAGGTTTCTGTGGGCTCAT 1815
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QY 961 TGAATCTGTGTGAGCTGTTTGAATCTTGTGAATCTGGGTACACAGGCGCTTTTCAAG 1020
DB 1876 TGAATCTGTGTGAGCTGTTTGAATCTTGTGAATCTGGGTACACAGGCGCTTTTCAAG 1935
QY 1021 AGAAGTCAATCAACCTTTGATTTTCCACACCGGGCGGCTGCGCTGCTGTGCTT 1080
DB 1936 AGAAGTCAATCAACCTTTGATTTTCCACACCGGGCGGCTGCGCTGCTGTGCTT 1995
QY 1081 TTTTGAATTTTAAAGATTAATGAGCGGAAGAACCCATCTGAGCGGAGGATCACTGC 1140
DB 1996 TTTTGAATTTTAAAGATTAATGAGCGGAAGAACCCATCTGAGCGGAGGATCACTGC 2055
QY 1141 TGATTTTCTGCGCATGATCTGTGAGAGCGGTTGTGAGACACAAGATCGCTGTAC 1200
DB 2056 TGATTTTCTGCGCATGATCTGTGAGAGCGGTTGTGAGACACAAGATCGCTGTAC 2115
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DB 2116 TGTGTCTTCCGTCGCGCCGCGCAATATACGAGAGGAGCAGACAGACAGAGAGAG 2175
QY 1261 AAGCAGGCGCGCGCGCAGAGCAGAGCCCATGGAACCCGAGAGCGGCTTGACCTTC 1320
DB 2176 AAGCAGGCGCGCGCGCAGAGCAGAGCCCATGGAACCCGAGAGCGGCTTGACCTTC 2235
QY 1321 GGAATGATATGTTGATACAGTGTGCTGAACTGTATTCAGAACTGAGACGATTTTGAAT 1380
DB 2236 GGAATGATATGTTGATACAGTGTGCTGAACTGTATTCAGAACTGAGACGATTTTGAAT 2295
QY 1381 TACAGAGATGAGGAGGCGCTAAAGGGGGTAAAGAGGAGGGGGCTTGTGAGGCTAC 1440
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DB 2416 TTTTCAACAGATCAAGATTAATGCGCTAATGAGCTTGTGCTGCGCAGAAATATTC 2475
QY 1561 CATAGACAGCTGACCACTTAATGCTGCAAGCCGAGGAGATTTTGAAGAGGCTATTAAG 1620
DB 2476 CATAGACAGCTGACCACTTAATGCTGCAAGCCGAGGAGATTTTGAAGAGGCTATTAAG 2535
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DB 2536 GGTATATGCAAAAGGTGAGCACTTAAGGCGCAGATTGCAATGACAGCAAACTTGTAA 2595
QY 2536 GGTATATGCAAAAGGTGAGCACTTAAGGCGCAGATTGCAATGACAGCAAACTTGTAA 2655
DB 2596 TATCAGAAATTTGTTGCTACATTTCTGGAAACGGGGCGGAGGTGAGATAGGAGGA 2655
QY 1741 TAGGTTGCGCTTGAAGTGAATGATTAATATGATGAGGCGGCTGTTGGCAGAGAGCG 1800
DB 2656 TAGGTTGCGCTTGAAGTGAATGATTAATATGATGAGGCGGCTGTTGGCAGAGAGCG 2715
QY 1801 GGTGTTATTAATGATTAAGGTTTACCTGAGCCCAATTTTACGCGTACGTTTCTGCGC 1860
DB 2716 GGTGTTATTAATGATTAAGGTTTACCTGAGCCCAATTTTACGCGTACGTTTCTGCGC 2775
QY 1861 CAATACCAACCTTAATCTTAACCGGTGAAGCTTCTATGCGTTTAAACAATCTGTGTGA 1920
DB 2776 CAATACCAACCTTAATCTTAACCGGTGAAGCTTCTATGCGTTTAAACAATCTGTGTGA 2835
QY 1921 AGCCTGAGCCGAGTGAAGGTTGCGGCTGCTTTTACGTGCTGAGAGGGGCTGCT 1980
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Db 2836 AGCTGAGCCGATGTAAGGGTTCGGGGCTGTGCTTTTACTGTGTGTAAGAGGGGTGT 2895
Qy 1981 GTGTGCCCCCAAAAGCAGGGGTTTCAATTAAAGAAATGCTCTTTTAAAGTTACTTGGG 2040
Db 2896 GTGTGCCCCCAAAAGCAGGGGTTTCAATTAAAGAAATGCTCTTTTAAAGTTACTTGGG 2955
Qy 2041 TATCTGTCTGAGGGTAACTCCAGGGTGGCCACAAATGTGGCTCCGACTGTGGTGTCTT 2100
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Qy 2101 CATCTGATGTAAGAGCGTGGCTGTGATTAGCATTAACATGATGTGGCAACTCGAGAGA 2160
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Qy 2161 CAGGGCCCTCAGATGCTGACCTGTGCGAAGGCACTGTCACTGTGCTGAAAGACATTCA 2220
Db 3076 CAGGGCCCTCAGATGCTGACCTGTGCGAAGGCACTGTCACTGTGCTGAAAGACATTCA 3135
Qy 2221 CGTAGCCAGCACTCTGCAAGGCTGGCCAGTGTGTAAGCATTAACATCACTGACCCGCTG 2280
Db 3136 CGTAGCCAGCACTCTGCAAGGCTGGCCAGTGTGTAAGCATTAACATCACTGACCCGCTG 3195
Qy 2281 TTCTTGATTTGGGTAAACAGAGAGGGGGTGTCTTACCTTACCAATGCAATTGAGTCA 2340
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Qy 2401 CATGACCATGAAGATCTGGAAGTGTGAGGTAGCATAGAGACCCGACAGGTGAGACC 2460
Db 3316 CATGACCATGAAGATCTGGAAGTGTGAGGTAGCATAGAGACCCGACAGGTGAGACC 3375
Qy 2461 CTGGAAGTGTGGCGGTAAACAATTAAGAACACAGCTGTGATGCTGATGTGACCGAGA 2520
Db 3376 CTGGAAGTGTGGCGGTAAACAATTAAGAACACAGCTGTGATGCTGATGTGACCGAGA 3435
Qy 2521 GCTAGAGCCGATCATCTGTGTGCTGGCCTGACACCGGCGTAGTTGGCTCTAGCGATGA 2580
Db 3436 GCTAGAGCCGATCATCTGTGTGCTGGCCTGACACCGGCGTAGTTGGCTCTAGCGATGA 3495
Qy 2581 AGATACAGATTGAG 2594
Db 3496 AGATACAGATTGAG 3509

RESULT 7
US-09-847-101B-12
; Sequence 12, Application US/09847101B
; Publication No. US20020193327A1
; GENERAL INFORMATION:
; APPLICANT: VON SEGERN, DANIEL
; APPLICANT: NEMEROW, GLEN R.
; APPLICANT: FRIEDLANDER, MARTIN
; TITLE OF INVENTION: VECTORS FOR OCULAR TRANSDUCTION AND USE THEREFOR FOR GENETIC THER
; FILE REFERENCE: 22908-1226B
; CURRENT APPLICATION NUMBER: US/09/847,101B
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/562,934
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 11152
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-847-101B-12

Query Match 100.0%; Score 2594; DB 9; Length 11152;
; Best Local Similarity 100.0%; Pred. No. 0;

Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGCATCTTACCTGCCACGAGGCTGTTCACCCAGGTACGACGAGATGAAGAGGCT 60
Db 1825 ATGCATCTTACCTGCCACGAGGCTGTTCACCCAGGTACGACGAGATGAAGAGGCT 1884
Qy 61 GAGGAGTTTGTGTTAGATTATGTGAGACACCCGGGACAGGTTGACAGTCTTGTCAATTAT 120
Db 1885 GAGGAGTTTGTGTTAGATTATGTGAGACACCCGGGACAGGTTGACAGTCTTGTCAATTAT 1944
Qy 121 CACCGAGAAATACGGGGGACCCAGATATTATGTTCCTTGTCTATATGAGACCTGT 180
Db 1945 CACCGAGAAATACGGGGGACCCAGATATTATGTTCCTTGTCTATATGAGACCTGT 2004
Qy 181 GGCAATTTTGTCTACATTAAGTGAATAATTATGGAACATGGGTGTATAGTGTGGTTTG 240
Db 2005 GGCAATTTTGTCTACATTAAGTGAATAATTATGGAACATGGGTGTATAGTGTGGTTTG 2064
Qy 241 GTGTGTAATTTTATTTTATTTTACAGTTTGTGTGTTTAAAGAAATTTTGTATTGTGA 300
Db 2065 GTGTGTAATTTTATTTTATTTTACAGTTTGTGTGTTTAAAGAAATTTTGTATTGTGA 2124
Qy 301 TTTTAAAAAGTCTGTGTCTGAACTGAGCCTGAGCCCGACCAAGCCGAGCCTG 360
Db 2125 TTTTAAAAAGTCTGTGTCTGAACTGAGCCTGAGCCCGACCAAGCCGAGCCTG 2184
Qy 361 CAAGACCTACCCGCGCTTAAATAGGGGCTGTACTCTGAGAGGGCCGACATCACTG 420
Db 2185 CAAGACCTACCCGCGCTTAAATAGGGGCTGTACTCTGAGAGGGCCGACATCACTG 2244
Qy 421 TGTCTAGAGATGCAATAGTATAGTACGAGTATGCTGACTCGGTCTCTTAAACACACTC 480
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Qy 481 CTGAGATACACCCGGTGTCTCCGTGCCCCATTAAACCAAGTTGCGGTGAGTGTG 540
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Db 2365 GGGCGCCAGGCGTGTGAATGTATGAGGACTTGTAAAGAGCCTGAGGCAACTTTGG 2424
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Qy 781 TGGTTACATCTGACCTCATGAGGCTTGGAGTGTGTTGGAAGATTTTCTGCTGTGCTA 840
Db 2605 TGGTTACATCTGACCTCATGAGGCTTGGAGTGTGTTGGAAGATTTTCTGCTGTGCTA 2664
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Db 2845 AGAAGTCAATCAAGACTTTGATTTTTCACACCGGGGCGGCTGCGGCTGTGTGCTT 2904

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1141 TGGATTTTCTGGCCATGTCATCTGTGAGAGCGGTTGTGAGACACAAGATGCGCTGCTAC 1200
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3025 TGTGTCTTCGCTCCGCCCGGATTAATACCGAGAGAGAGAGAGAGAGAGAGAGAGAG 3084
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3145 GGGAAATGAATGTTGTACAGAGTGGCTGAACCTGTATACAGAACTGAGACGATTTTGACAT 3204
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1441 AGAGAGAGCTAGGAATCTAGCTTTTACCTTAATGACAGACAGCGTCTGAGTGTATAC 1500
3265 AGAGAGAGCTAGGAATCTAGCTTTTACCTTAATGACAGACAGCGTCTGAGTGTATAC 3324
1501 TTTTCAACAGATCAAGATTAATGAGCTTAATGAGCTTAATGAGCTTAATGAGCTTAATTC 1560
3325 TTTTCAACAGATCAAGATTAATGAGCTTAATGAGCTTAATGAGCTTAATGAGCTTAATTC 3384
1561 CATNAGAGAGCTGACCACTTACTGCGCTGACAGCGAGATGATTTTGAAGAGCTATTAG 1620
3385 CATNAGAGAGCTGACCACTTACTGCGCTGACAGCGAGATGATTTTGAAGAGCTATTAG 3444
1621 GGTATATGCAAAAGGTGCACTTAAGCCAGATTTGCAATGACAGATCAAGATCAAGATCA 1680
3445 GGTATATGCAAAAGGTGCACTTAAGCCAGATTTGCAATGACAGATCAAGATCAAGATCA 3504
1681 TATCAGAAATGTTGCTACATTTCTGAGGAGCGGGCGAGGTTGAGATGATGAGGAGAG 1740
3505 TATCAGAAATGTTGCTACATTTCTGAGGAGCGGGCGAGGTTGAGATGATGAGGAGAG 3564
1741 TAGGAGCTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1800
3565 TAGGAGCTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3624
1801 GGTGCTTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1860
3625 GGTGCTTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3684
1861 CAATACCAACCTTATCTACACGGGTAAAGCTTATGAGGTTTAAATATCTGCTGCTGCTG 1920
3685 CAATACCAACCTTATCTACACGGGTAAAGCTTATGAGGTTTAAATATCTGCTGCTGCTG 3744
1921 AGCTGAGACCGATGATGAGGTTGCGGGCTGCTCTTACTGCTGCTGAGAGAGGAGTGT 1980
3745 AGCTGAGACCGATGATGAGGTTGCGGGCTGCTCTTACTGCTGCTGAGAGAGGAGTGT 3804
1981 GTGTGCGCCCAAAAGCAGAGGCTTCAATTAAGAAATGCTCTTTGAAAGGTGATCTTGGG 2040
3805 GTGTGCGCCCAAAAGCAGAGGCTTCAATTAAGAAATGCTCTTTGAAAGGTGATCTTGGG 3864
2041 TATCTGCTGAGGAGTAACTCAAGGAGTGCACAAATGAGCTTCCGATGCTGCTGCTT 2100
3865 TATCTGCTGAGGAGTAACTCAAGGAGTGCACAAATGAGCTTCCGATGCTGCTGCTT 3924
2101 CATCTAGTAAAGCGTGGCTGTGATTAAGCATTAACATGATGATGAGCACTGCGAGAG 2160
3925 CATCTAGTAAAGCGTGGCTGTGATTAAGCATTAACATGATGATGAGCACTGCGAGAG 3984

QY 2161 CAGGAGCTCTGAGATGCTGACCTGCTCGGAGCGCACTGTCACTGCTGTAAGACATTTCA 2220
DB 3985 CAGGAGCTCTGAGATGCTGACCTGCTCGGAGCGCACTGTCACTGCTGTAAGACATTTCA 4044
QY 2221 CGTAGCCAGACCTCTCGCAGAGGCTGCGCAGTGTGTTGAGCATTAATATGAGACCGGCTG 2280
DB 4045 CGTAGCCAGACCTCTCGCAGAGGCTGCGCAGTGTGTTGAGCATTAATATGAGACCGGCTG 4104
QY 2281 TTCCTTGATTTGGGTAAACAGAGAGGAGGAGTGTCTTCACTTAACCAATGCAATTTGATCA 2340
DB 4105 TTCCTTGATTTGGGTAAACAGAGAGGAGGAGTGTCTTCACTTAACCAATGCAATTTGATCA 4164
QY 2341 CACTAAGATTTTGTGTTGAGCCCGAGAGCATGTCCAAAGTGAACCTGAACCGGGGTGTTGA 2400
DB 4165 CACTAAGATTTTGTGTTGAGCCCGAGAGCATGTCCAAAGTGAACCTGAACCGGGGTGTTGA 4224
QY 2401 CATGACATGAAGATCTGGAAGGTGCTGAGGATGATGAGACCCGACACAGGTGAGAGC 2460
DB 4225 CATGACATGAAGATCTGGAAGGTGCTGAGGATGATGAGACCCGACACAGGTGAGAGC 4284
QY 2461 CTGCGAGTGTGCGGTTAAACATATTAGAACCAAGCTGTGATGCTGATGATGATGATG 2520
DB 4285 CTGCGAGTGTGCGGTTAAACATATTAGAACCAAGCTGTGATGCTGATGATGATGATG 4344
QY 2521 GCTGAGGCGCCATCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2580
DB 4345 GCTGAGGCGCCATCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4404
QY 2581 AGATPACAGATTGAG 2594
DB 4405 AGATPACAGATTGAG 4418

RESULT 8
US-09-482-682-12
; Sequence 12, Application US/09482682
; Publication No. US20030157688b1
; GENERAL INFORMATION:
; APPLICANT: VON SEGGERN, DANIEL
; APPLICANT: NEMEROW, GLEN R.
; APPLICANT: HALENEBECK, PAUL
; APPLICANT: STEVENSON, SUSAN
; APPLICANT: SKRIPCHENKO, YELENA
; TITLE OF INVENTION: ADENOVIRUS VECTORS, PACKAGING CELL LINES, COMPOSITIONS,
; TITLE OF INVENTION: AND METHODS FOR PREPARATION AND USE
; FILE REFERENCE: 1294.001001
; CURRENT APPLICATION NUMBER: US/09/482.682
; CURRENT FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 11152
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-482-682-12

Query Match 100.0%; Score 2594; DB 10; Length 11152;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATCGATCTTACCTTCCAGAGAGGCTGCTTTTCCACCCAGTGAAGAGATGAAGAGGCT 60
DB 1825 ATCGATCTTACCTTCCAGAGAGGCTGCTTTTCCACCCAGTGAAGAGATGAAGAGGCT 1884
QY 61 GAGAGATTTGTGTTAATGATATGATGAGACACCCCGGAGACGTTTCAGAGTCTTGTCAATTAT 120
DB 1885 GAGAGATTTGTGTTAATGATATGATGAGACACCCCGGAGACGTTTCAGAGTCTTGTCAATTAT 1944
QY 121 CACCGAGAGAAATGAGGAGGAGACCGAGATATTATGTTGCTTGTCTATATGAGAGCTGT 180
DB 1945 CACCGAGAGAAATGAGGAGGAGACCGAGATATTATGTTGCTTGTCTATATGAGAGCTGT 2004

QY 181 GGCAATTTTGTCTACAGTAAGTGAATAATATGGGCAATGGGTGATAGAGTGGGTGG 240
Db 2005 GGCAATTTTGTCTACAGTAAGTGAATAATATGGGCAATGGGTGATAGAGTGGGTGG 2064
QY 241 GTGTGTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 300
Db 2065 GTGTGTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 2124
QY 301 TTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 360
Db 2125 TTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 2184
QY 361 CAAGACCTAACCCGCGCTCTAAATTTGAGGCGCTGATCTGAGAGCGCCGCAATCACCTG 420
Db 2185 CAAGACCTAACCCGCGCTCTAAATTTGAGGCGCTGATCTGAGAGCGCCGCAATCACCTG 2244
QY 421 TGTCTAGAGAAATGCAATAGTATAGTACGATAGCTGATCTCGGTCTCTTAAACAACCTC 480
Db 2245 TGTCTAGAGAAATGCAATAGTATAGTACGATAGCTGATCTCGGTCTCTTAAACAACCTC 2304
QY 481 CTGAGATACACCCGCGTGTCCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Db 2305 CTGAGATACACCCGCGTGTCCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2364
QY 541 GCGGTGCGCAGGCTGTGATGTATCGAGGACTTGCTTAAAGAGCTGGGCAACCTTTGG 600
Db 2365 GCGGTGCGCAGGCTGTGATGTATCGAGGACTTGCTTAAAGAGCTGGGCAACCTTTGG 2424
QY 601 ACTTGAAGCTGTAAACGCCCCAGGCCATTAAGGTGTAAACCTGTGATGCTGTGTGTAA 660
Db 2425 ACTTGAAGCTGTAAACGCCCCAGGCCATTAAGGTGTAAACCTGTGATGCTGTGTGTAA 2484
QY 661 CGCCTTTGTGTGCTGAATGATGTATGATTTAATAAGGTGTAAATGTTTAACT 720
Db 2485 CGCCTTTGTGTGCTGAATGATGTATGATTTAATAAGGTGTAAATGTTTAACT 2544
QY 721 TGCATGCGGTGTAAATGAGGCGGGGCTTAAAGGATATATATGCGGTGGCTAACT 780
Db 2545 TGCATGCGGTGTAAATGAGGCGGGGCTTAAAGGATATATATGCGGTGGCTAACT 2604
QY 781 TGGTTACATCTGACCTCATGAGGCTTGGAGGTGTTTGAAGATTTTCTGCTGTGCTA 840
Db 2605 TGGTTACATCTGACCTCATGAGGCTTGGAGGTGTTTGAAGATTTTCTGCTGTGCTA 2664
QY 841 ACTTGTCTGGAACAGAGCTCTTAACAGTACTCTTGTGTTTGAAGTTTCTGTGGGCTAT 900
Db 2665 ACTTGTCTGGAACAGAGCTCTTAACAGTACTCTTGTGTTTGAAGTTTCTGTGGGCTAT 2724
QY 901 CCCAGGCAAAAGTTAGTCTGAGAAATTAAGAGATTAACAAGGGAATTTGAAGAGCTTT 960
Db 2725 CCCAGGCAAAAGTTAGTCTGAGAAATTAAGAGATTAACAAGGGAATTTGAAGAGCTTT 2784
QY 961 TGAATCTGTGTGAGGCTGTTTAAATCTTTGAATCTGGGTCAACAGCGGCTTTTCCAG 1020
Db 2785 TGAATCTGTGTGAGGCTGTTTAAATCTTTGAATCTGGGTCAACAGCGGCTTTTCCAG 2844
QY 1021 AGAAGTATCAAGACTTTGATTTTCCACACCGGGGCGGCTGCGGCTGTGTTGCTT 1080
Db 2845 AGAAGTATCAAGACTTTGATTTTCCACACCGGGGCGGCTGCGGCTGTGTTGCTT 2904
QY 1081 TTTTGAAGTTTATTAAGATTAATGAGAGCAAAACCATCTGAGCGGGGGGTAACTTGC 1140
Db 2905 TTTTGAAGTTTATTAAGATTAATGAGAGCAAAACCATCTGAGCGGGGGGTAACTTGC 2964
QY 1141 TGAATTTTCTGGCCATGATCTGTGAGAGCGGTGTGAGACACAAGATCGCTGTAC 1200
Db 2965 TGAATTTTCTGGCCATGATCTGTGAGAGCGGTGTGAGACACAAGATCGCTGTAC 3024
QY 1201 TGTGTCTTCCGCTCGGCGCGATTAATACGACGAGAGACAGACAGACAGAGAGG 1260
Db 3025 TGTGTCTTCCGCTCGGCGCGATTAATACGACGAGAGACAGACAGAGAGAGG 3084

QY 1261 AAGCCAGCGCGCGCGCAGAGCAGAGCCCATGGAACCCGAGCGCGCTGACCTTC 1320
Db 3085 AAGCCAGCGCGCGCGCAGAGCAGAGCCCATGGAACCCGAGCGCGCTGACCTTC 3144
QY 1321 GGAATGAATGTTGTACAGGTGCTGAATCTGTATCCAGAACTGAGACGATTTTGACAT 1380
Db 3145 GGAATGAATGTTGTACAGGTGCTGAATCTGTATCCAGAACTGAGACGATTTTGACAT 3204
QY 1381 TACAGAGATGCGAGCGGCTTAAAGGGGGTAAAGAGGAGCGGGGGCTGTGAGGCTAC 1440
Db 3305 TACAGAGATGCGAGCGGCTTAAAGGGGGTAAAGAGGAGCGGGGGCTGTGAGGCTAC 3264
QY 1441 AGAGAGGCTAGGAATCTAGCTTTTAACTTAATGACAGACACCGCTCTGATGATTAAC 1500
Db 3365 AGAGAGGCTAGGAATCTAGCTTTTAACTTAATGACAGACACCGCTCTGATGATTAAC 3324
QY 1501 TTTTCAACAGATCAAGATTAATGCGGTAAATGACCTTGTATCTGTGCGCAGAAATTC 1560
Db 3325 TTTTCAACAGATCAAGATTAATGCGGTAAATGACCTTGTATCTGTGCGCAGAAATTC 3384
QY 1561 CATAGACAGCTGACCACTTAATGCTGCGACCGCAGGGGATGATTTTGAAGAGCTATTAG 1620
Db 3385 CATAGACAGCTGACCACTTAATGCTGCGACCGCAGGGGATGATTTTGAAGAGCTATTAG 3444
QY 1621 GGTATATGCAAAAGGTGACACTTAGGCGCAGATTGCAAGTACAGATCAACTTGTAA 1680
Db 3445 GGTATATGCAAAAGGTGACCACTTAGGCGCAGATTGCAAGTACAGATCAACTTGTAA 3504
QY 1681 TATCAGAAATTTGTTGTAATTTCTGAGAAACGGGGCGAGGTGAGATGATACGAGGA 1740
Db 3505 TATCAGAAATTTGTTGTAATTTCTGAGAAACGGGGCGAGGTGAGATGATGATACGAGGA 3564
QY 1741 TAGGTTGCGCTTTAAGTATGATGATTAATATGATGCGCGGGGGTGTGCTGCAATGSCG 1800
Db 3565 TAGGTTGCGCTTTAAGTATGATGATTAATATGATGCGCGGGGTGTGCTGCAATGSCG 3624
QY 1801 GATGTTATTAATGATGATTAAGTTTACTGCGCCCAATTTTAAAGCGGTTCCTGTCG 1860
Db 3625 GATGTTATTAATGATGATTAAGTTTACTGCGCCCAATTTTAAAGCGGTTCCTGTCG 3684
QY 1861 CAATACCAACCTTATCTTACACGCTGTAACTTATGAGTTTAAATATCTGTGTGGA 1920
Db 3685 CAATACCAACCTTATCTTACACGCTGTAACTTATGAGTTTAAATATCTGTGTGGA 3744
QY 1921 AGCTGTGACCGATGATGAGGTTGCGGGCTGTGCTTTTAACTGCTGTGAGAGGGGGTGT 1980
Db 3745 AGCTGTGACCGATGATGAGGTTGCGGGCTGTGCTTTTAACTGCTGTGAGAGGGGGTGT 3804
QY 1981 GTGTGCGCCCAAAAGCAGGCGCTTCAATTAAGAAATGCTCTTTGAAGGTGTACTTGG 2040
Db 3805 GTGTGCGCCCAAAAGCAGGCGCTTCAATTAAGAAATGCTCTTTGAAGGTGTACTTGG 3864
QY 2041 TATCTGTCTGAGGGTAACTTCAAGGCTGCGCACATGTGGCTTCCGACTGTGTTGCTT 2100
Db 3865 TATCTGTCTGAGGGTAACTTCAAGGCTGCGCACATGTGGCTTCCGACTGTGTTGCTT 3924
QY 2101 CATGCTAGTGAAGAGCGGTGTGATTAAGCATTAACATGATAGTGGCACTCGAGAGA 2160
Db 3925 CATGCTAGTGAAGAGCGGTGTGATTAAGCATTAACATGATAGTGGCACTCGAGAGA 3984
QY 2161 CAGGCGCTCTCAGATGCTGACCTGCTCGAGCGGCACTGTCACTGCTGAAGACATTC 2220
Db 3985 CAGGCGCTCTCAGATGCTGACCTGCTCGAGCGGCACTGTCACTGCTGAAGACATTC 4044
QY 2221 CGTAGCAGCCACTCTGCAAGGCTTGGCCAGTGTGAGCATTAACATGACCCGCTG 2280
Db 4045 CGTAGCAGCCACTCTGCAAGGCTTGGCCAGTGTGAGCATTAACATGACCCGCTG 4104
QY 2281 TTCTTTCATTTGGGTAAACAGAGAGGGGGTCTTCTTCACTTAACAAATGCAATTTGAGTCA 2340
Db 4105 TTCTTTCATTTGGGTAAACAGAGAGGGGGTCTTCTTCACTTAACAAATGCAATTTGAGTCA 4164
QY 2341 CACTAAGATATTTGCTTGAAGCCGAGACATGTCCAAGTGAACCTGAAACGGGGTGTGGA 2400

Db 3265 AGAGAGGCTAGAACTAGCTTTAGCTTAATGACAGACACCGTCCGTGATGTATTAC 3324
Qy 1501 TTTTCAACAGATCAAGATAATTGGCTTAATGAGCTTGAATCGTGGCGGCAAGTATTC 1560
Db 3325 TTTTCAACAGATCAAGATAATTGGCTTAATGAGCTTGAATCGTGGCGGCAAGTATTC 3384
Qy 1561 CATAGAGAGCTGACCACTTACTGCTGACAGCCAGGGAGATTTTGTAGAGAGCTATTAG 1620
Db 3385 CATAGAGAGCTGACCACTTACTGCTGACAGGGAGATGATTTGTAGAGAGCTATTAG 3444
Qy 1621 GGTATATGCAAAAGGTGCACTTAAAGCCAGATTGCAAGATCAAGATCAAGCAACTTTGAAA 1680
Db 3445 GGTATATGCAAAAGGTGCACTTAAAGCCAGATTGCAAGATCAAGATCAAGCAACTTTGAAA 3504
Qy 1681 TATCAGAAATTGTTGCTACATTTCTGGGGAACGGGGCCGAGGTGAGATAGATAGTAAAGGAGA 1740
Db 3505 TATCAGAAATTGTTGCTACATTTCTGGGGAACGGGGCCGAGGTGAGATAGTAAAGGAGA 3564
Qy 1741 TAGGGTGGCTTTAGATGTAGCATGATTAATATGTGCGGGGGTGTCTTGGCATGACGG 1800
Db 3565 TAGGGTGGCTTTAGATGTAGCATGATTAATATGTGCGGGGGTGTCTTGGCATGACGG 3624
Qy 1801 GGTGTTATTAATGATGATGAAGTTTACTGCCCCCAATTTTACGGTACGTTTCTCGGC 1860
Db 3625 GGTGTTATTAATGATGATGAAGTTTACTGCCCCCAATTTTACGGTACGTTTCTCGGC 3684
Qy 1861 CAATACCAACCTTATCCACACGGGTAAAGCTTATGAGGTTTAAACATATCTGTGAGA 1920
Db 3685 CAATACCAACCTTATCCACACGGGTAAAGCTTATGAGGTTTAAACATATCTGTGAGA 3744
Qy 1921 AGCCTGACCCGATGTAAAGGTTTCGGGGCTGTGCTTTTACTGTCTGTGAGAGGGGGTGT 1980
Db 3745 AGCCTGACCCGATGTAAAGGTTTCGGGGCTGTGCTTTTACTGTCTGTGAGAGGGGGTGT 3804
Qy 1981 GTGTGCCCCCAAAAGCAGAGGCTTCAATTAAGAAATGCTCTTTGAAAGGTGTAACCTTGGG 2040
Db 3805 GTGTGCCCCCAAAAGCAGAGGCTTCAATTAAGAAATGCTCTTTGAAAGGTGTAACCTTGGG 3864
Qy 2041 TATCTGTCTAGAGGTTAATCAAGGATGCGCACAAATGAGCTTCCGACTGAGTGTGTT 2100
Db 3865 TATCTGTCTAGAGGTTAATCAAGGATGCGCACAAATGAGCTTCCGACTGAGTGTGTT 3924
Qy 2101 CATGCTAGTGAAGGCGTGTGCTGATTTAGCATTAACATGATGATGCAACTGCGAGGA 2160
Db 3925 CATGCTAGTGAAGGCGTGTGCTGATTTAGCATTAACATGATGATGCAACTGCGAGGA 3984
Qy 2161 CAGGGCTCTAGATGCTGACCTGCTCGGACGGCACTGTCACTGCTGAAAGCACTTCA 2220
Db 3985 CAGGGCTCTAGATGCTGACCTGCTCGGACGGCACTGTCACTGCTGAAAGCACTTCA 4044
Qy 2221 CGTAGCCAGCACTCTGCGAAGGCTGCGCAAGTGTGAGCATTAACATGACCCGCTG 2280
Db 4045 CGTAGCCAGCACTCTGCGAAGGCTGCGCAAGTGTGAGCATTAACATGACCCGCTG 4104
Qy 2281 TTCTTGTGATTTGGGTAAACAGAGAGGGGGTGTCTTCACTTAACCAATGCAATTTGAGTCA 2340
Db 4105 TTCTTGTGATTTGGGTAAACAGAGAGGGGGTGTCTTCACTTAACCAATTTGAGTCA 4164
Qy 2341 CACTAAGATATTGCTTGAAGCCGAGAGCATGTCCAAGGTGAACCTGAAACGGGGTGTGGA 2400
Db 4165 CACTAAGATATTGCTTGAAGCCGAGAGCATGTCCAAGGTGAACCTGAAACGGGGTGTGGA 4224
Qy 2401 CATGACCATGAAGATCTGAAAGGTGCTGAGGTGAGATGAGACCCGACACAGGTGAGACC 2460
Db 4225 CATGACCATGAAGATCTGAAAGGTGCTGAGGTGAGATGAGACCCGACACAGGTGAGACC 4284
Qy 2461 CTGCGAGTGTGGCGGTAAACAATTATGAGAACAGCTGTGATGCTGAGTGTGACCGAGGA 2520
Db 4285 CTGCGAGTGTGGCGGTAAACAATTATGAGAACAGCTGTGATGCTGAGTGTGACCGAGGA 4344
Qy 2521 GCTGAGAGCCCGATCATCTTGGTGTGCTGCGACCCGCGCTGAGTGTGGCTCTAGGAGATGA 2580
Db 4345 GCTGAGAGCCCGATCATCTTGGTGTGCTGCGACCCGCGCTGAGTGTGGCTCTAGGAGATGA 4404

Qy 2581 AGATACAGATTGAG 2594
Db 4405 AGATACAGATTGAG 4418

RESULT 10
US-09-482-682-15
; Sequence 15. Application us/09482682
; Publication No. US20030157688A1
; GENERAL INFORMATION:
; APPLICANT: VON SEGGERN, DANIEL
; APPLICANT: NEMEROW, GLEN R.
; APPLICANT: HALLENBECK, PAUL
; APPLICANT: STEVENSON, SUSAN
; APPLICANT: SKRIPCENKO, YELENA
; TITLE OF INVENTION: ADENOVIRUS VECTORS, PACKAGING CELL LINES, COMPOSITIONS,
; FILE REFERENCE: 1294.0010001
; CURRENT APPLICATION NUMBER: us/09/482,682
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 15
; LENGTH: 14455
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-482-682-15

Query Match 100.0%; Score 2594; DB 10; Length 14455;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATCTTAACTTCGACAGAGGCTGCTTTCACACCAAGTACGACGAGATGAAGAGGCT 60
Db 1825 ATGATCTTAACTTCGACAGAGGCTGCTTTCACACCAAGTACGACGAGATGAAGAGGCT 1884
Qy 61 GAGAGTTTGTGTTAAGTTATGTGAGACACCCCGGGGACGGTTGCAGTCTTGCATTAT 120
Db 1885 GAGAGTTTGTGTTAAGTTATGTGAGACACCCCGGGGACGGTTGCAGTCTTGCATTAT 1944
Qy 121 CACCGAGAAATACGGGGGACCCAGATATTATGTTCGCTTGTCTATAGAGACCTGT 180
Db 1945 CACCGAGAAATACGGGGGACCCAGATATTATGTTCGCTTGTCTATAGAGACCTGT 2004
Qy 181 GGCATGTTTGTCTACAGTAAAGTAAATTAATGGCAAGTGGTATGAGTGTGGGTTTG 240
Db 2005 GGCATGTTTGTCTACAGTAAAGTAAATTAATGGCAAGTGGTATGAGTGTGGGTTTG 2064
Qy 241 GTGAGTAAATTTTATTTTAAATTTTAAAGTTTGTGTTTAAAGATTTGTATTTGA 300
Db 2065 GTGAGTAAATTTTATTTTAAATTTTAAAGTTTGTGTTTAAAGATTTGTATTTGA 2124
Qy 301 TTTTAAAGATCTGTGCTGAACCTGAGCTGAGCCCGAGACCGAGAGCTTG 360
Db 2125 TTTTAAAGATCTGTGCTGAACCTGAGCTGAGCCCGAGACCGAGAGCTTG 2184
Qy 361 CAAGACCTAACCCGCGTCTTAAATGCGGCTGCTATCTGAGACGCCGACATCACTG 420
Db 2185 CAAGACCTAACCCGCGTCTTAAATGCGGCTGCTATCTGAGACGCCGACATCACTG 2244
Qy 421 TGTCTAAGAAATGAATAGTATGCGATAGCTGTGATCCGCGCTTCTAACAACACTC 480
Db 2245 TGTCTAAGAAATGAATAGTATGCGATAGCTGTGATCCGCGCTTCTAACAACACTC 2304
Qy 481 CTGAGATACACCCGAGTGTCCGCTGTGCCCCATTAACAGATTGCGGTGAGAGTTGTTG 540
Db 2305 CTGAGATACACCCGAGTGTCCGCTGTGCCCCATTAACAGATTGCGGTGAGAGTTGTTG 2364
Qy 541 GCGGTGCGCAGGCTGTGGAATGTATCGAGGACTTGAACGAGCTGGGCAACTTTGG 600

FILE REFERENCE: 121300.00003
CURRENT APPLICATION NUMBER: US/10/766.307A
CURRENT FILING DATE: 2004-01-28
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 3
LENGTH: 32802
TYPE: DNA
ORGANISM: Adenovirus
US-10-766-307A-3

Query Match 100.0%; Score 2594; DB 21; Length 32802;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATCCATCTTACTGCGACAGAGCTGGCTTTCCACCACATGACGACGAGATGAAAGGCT 60
917 ATCCATCTTACTGCGACAGAGCTGGCTTTCCACCACATGACGACGAGATGAAAGGCT 976
61 GAGAGTTTGTGTAGATTATGTGAGACACCCGGGCAAGTTGCAAGTCTTGTCAATTAT 120
977 GAGAGTTTGTGTAGATTATGTGAGACACCCGGGCAAGTTGCAAGTCTTGTCAATTAT 1036
121 CACCGAGAAATACCGGGGACCCAGATATATGTGTGCTTGTCTATATAGACCTGT 180
1037 CACCGAGAAATACCGGGGACCCAGATATATGTGTGCTTGTCTATATAGACCTGT 1096
181 GGCATGTTGTCTACAGTAAGTGAATAATTTAGGAGAGTGGGATAGATGGTGGTTTG 240
1097 GGCATGTTGTCTACAGTAAGTGAATAATTTAGGAGAGTGGGATAGATGGTGGTTTG 1156
241 GGTGTGTAATTTTTTTTAAATTTTACAGTTTGTGTGTTTAAAGATTTTGTATTGTA 300
1157 GGTGTGTAATTTTTTTTAAATTTTACAGTTTGTGTGTTTAAAGATTTTGTATTGTA 1216
301 TTTTTTAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCGAGACCGAGCCTG 360
1217 TTTTTTAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCGAGACCGAGCCTG 1276
361 CAAGACTTACCCCGCTCTTAAATAGGGCGCTGCTATCTTGAGAGCCCGACATACCTG 420
1277 CAAGACTTACCCCGCTCTTAAATAGGGCGCTGCTATCTTGAGAGCCCGACATACCTG 1336
421 TGTCTAGAGAAATGCAATAGTATGATGAGATGCTGATCCGGTCTTCTAACAACCTC 480
1337 TGTCTAGAGAAATGCAATAGTATGATGAGATGCTGATCCGGTCTTCTAACAACCTC 1396
481 CTGAGATACACCCGGTGTCCGCTGTGCCCATTTAAACAAGTTGCGTGAAGTTGTG 540
1397 CTGAGATACACCCGGTGTCCGCTGTGCCCATTTAAACAAGTTGCGTGAAGTTGTG 1456
541 GCGCTGCGCAGGCTGTGAATGTATCGAGACTTCTTAAAGAGCTGGGCAACTTTGG 600
1457 GCGCTGCGCAGGCTGTGAATGTATCGAGACTTCTTAAAGAGCTGGGCAACTTTGG 1516
601 ACTTGAAGCTGTAAAGCCGCCAGCCATTAAGGTATAACCTGTGATTTGGGTGTGTTAA 660
1517 ACTTGAAGCTGTAAAGCCGCCAGCCATTAAGGTATAACCTGTGATTTGGGTGTGTTAA 1576
661 GCGCTTGTGTGCTGAATGAGTTGATGTAACTTTAATAAAGGTGAGATAATGTTTAACT 720
1577 GCGCTTGTGTGCTGAATGAGTTGATGTAACTTTAATAAAGGTGAGATAATGTTTAACT 1636
721 TGCATGGGCTGTAAATAGGGGCGGGCTTAAAGGATATATATGCGCGCTGGGCTAATCT 780
1637 TGCATGGGCTGTAAATAGGGGCGGGCTTAAAGGATATATATGCGCGCTGGGCTAATCT 1696
781 TGTGTACATCTGACCTTCAATGAGGCTTGGAGTGTGTTGAGAGATTTTCTGCTGTGCTTA 840
1697 TGTGTACATCTGACCTTCAATGAGGCTTGGAGTGTGTTGAGAGATTTTCTGCTGTGCTTA 1756
841 ACTTGTGGAACAGAGCTTCAACATGACTTGTGTTTGTGAGGTTTCTGTGGGCTCAT 900

1757 ACTTGTGGAACAGAGCTTCAACATGACTTGTGTTTGTGAGGTTTCTGTGGGCTCAT 1816
901 CCCAGGAAAGTTAGTCTGCAAGATTAAAGAGATTCAAGTGGGAATTTGAAGGCTTT 960
1817 CCCAGGAAAGTTAGTCTGCAAGATTAAAGAGATTCAAGTGGGAATTTGAAGGCTTT 1876
961 TGAATCTGTGTAGCTGTTTGAATCTTGTGAATCTGTGTACACAGGCGCTTTTCCAG 1020
1877 TGAATCTGTGTAGCTGTTTGAATCTTGTGAATCTGTGTACACAGGCGCTTTTCCAG 1936
1021 AGAAGTCAATCAGACTTTGATTTTTCACACCGGGCGCGCTGCGCTCTGTGCTT 1080
1937 AGAAGTCAATCAGACTTTGATTTTTCACACCGGGCGCGCTGCGCTCTGTGCTT 1996
1081 TTTTGAAGTTTATTAAGGATTAATGAGCGAAGAACCCATCTGAGCGGGGGTAACTGCG 1240
1997 TTTTGAAGTTTATTAAGGATTAATGAGCGAAGAACCCATCTGAGCGGGGGTAACTGCG 2056
1141 TGAATTTTCTGGCAGTCACTGTGAGAGCGGTTGTGAGACAGAGATTCGCTGTAC 1200
2057 TGAATTTTCTGGCAGTCACTGTGAGAGCGGTTGTGAGACAGAGATTCGCTGTAC 2116
1201 TGTGTCTTCCGTCGCCCGGCGATAATACCGAGAGAGACAGACAGACAGAGAGG 1260
2117 TGTGTCTTCCGTCGCCCGGCGATAATACCGAGAGAGACAGACAGACAGAGAGG 2176
1261 AAGCAGGCGCGCGCGAGAGAGAGCCCATGAAACCGAGAGCGGCGCTGAGCCTC 1320
2177 AAGCAGGCGCGCGCGAGAGAGAGCCCATGAAACCGAGAGCGGCGCTGAGCCTC 2236
1321 GGAATGATTTGTGTACAGTGTGCTGAATCTGTATCCAGAACTGAGAGCATTTTGACAT 1380
2237 GGAATGATTTGTGTACAGTGTGCTGAATCTGTATCCAGAACTGAGAGCATTTTGACAT 2296
1381 TACAGAGATGAGGCAAGGCGCTAAAGGCGGTAAAGAGGAGCGGCGGCTGTGAGGCTAC 1440
2297 TACAGAGATGAGGCAAGGCGCTAAAGGCGGTAAAGAGGAGCGGCGGCTGTGAGGCTAC 2356
1441 AGAGAGGCTTGAAGATCTAGCTTTTACCTTAATGACAGACACGCTCTGAGTATTAC 1500
2357 AGAGAGGCTTGAAGATCTAGCTTTTACCTTAATGACAGACACGCTCTGAGTATTAC 2416
1501 TTTTCAACAGATCAAGATTAATTCGCTAATGAGCTGATCTGTGCGCAGAAATATTC 1560
2417 TTTTCAACAGATCAAGATTAATTCGCTAATGAGCTGATCTGTGCGCAGAAATATTC 2476
1561 CATAGAGAGCTGACCACTTACTGCTGACAGCCAGGGGATGATTTTGAAGGCTATTAG 1620
2477 CATAGAGAGCTGACCACTTACTGCTGACAGCCAGGGGATGATTTTGAAGGCTATTAG 2536
1621 GGTATATGCAAAAGGTGGCACTTAGCCAGANTTGAAGTACAAAGATCAGCAACTTGTAA 1680
2537 GGTATATGCAAAAGGTGGCACTTAGCCAGANTTGAAGTACAAAGATCAGCAACTTGTAA 2596
1681 TATCAGGAATTTGTTCTACATTTCTGGGAAACGCGGCGAGGTGAGATGATACGAGAGA 1740
2597 TATCAGGAATTTGTTCTACATTTCTGGGAAACGCGGCGAGGTGAGATGATACGAGAGA 2656
1741 TAGGGTGCCTTTAGATGATGATGATTAATATGTGCGCGGGGCTGTTGGCATGACGG 1800
2657 TAGGGTGCCTTTAGATGATGATGATTAATATGTGCGCGGGGCTGTTGGCATGACGG 2716
1801 GGTGTATTAATGATGATGATGATTAATGATGATTAATGATGATGATGATGATGATGAT 1860
2717 GGTGTATTAATGATGATGATGATTAATGATGATTAATGATGATGATGATGATGATGAT 2776
1861 CAATACCAACTTATCTTACACGAGTGAAGCTTATGATGATTTTAAATATACCTGTGTA 1920
2777 CAATACCAACTTATCTTACACGAGTGAAGCTTATGATGATTTTAAATATACCTGTGTA 2836
1921 AGCCTGACCGAGTAAAGGTTGCGGGCTGTGCTTTTACTGTGCTGAGAGGGGCTGT 1980
2837 AGCCTGACCGAGTAAAGGTTGCGGGCTGTGCTTTTACTGTGCTGAGAGGGGCTGT 2896

QY 1981 GTGTGCCCCCAAGAGAGGCTTCAATTAAAGATGCTTTGAAAGGTGTAACCTTGCG 2040
DB 2897 GTGTGCCCCCAAGAGAGGCTTCAATTAAAGATGCTTTGAAAGGTGTAACCTTGCG 2956
QY 2041 TATCTGTCTAGAGGTTAACTCCAGAGGTGCGGCAATGAGGCTTCCGACTGTGTTGCTT 2100
DB 2957 TATCTGTCTAGAGGTTAACTCCAGAGGTGCGGCAATGAGGCTTCCGACTGTGTTGCTT 3016
QY 2101 CATGCTAGTGAAGAACGCTGCTGTGATTAAGCATTAACATGATGAGCAATGCGAGGA 2160
DB 3017 CATGCTAGTGAAGAACGCTGCTGTGATTAAGCATTAACATGATGAGCAATGCGAGGA 3076
QY 2161 CAGGCGCTCTAGAGGCTGACCTGCTCGGACGGAACCTGACCTGCTGGAAGCAATTCA 2220
DB 3077 CAGGCGCTCTAGAGGCTGACCTGCTCGGACGGAACCTGACCTGCTGGAAGCAATTCA 3136
QY 2221 CGTAGCCAGCCACTCTGCGCAAGGCTGCGCAAGTGTGAGCATTAACATGTAACCCGCTG 2280
DB 3137 CGTAGCCAGCCACTCTGCGCAAGGCTGCGCAAGTGTGAGCATTAACATGTAACCCGCTG 3196
QY 2281 TTCTTGCAATTTGGGTAAACAGAGAGGAGGTGTTCTTACCTTAACCAATGTAAGTCA 2340
DB 3197 TTCTTGCAATTTGGGTAAACAGAGAGGAGGTGTTCTTACCTTAACCAATGTAAGTCA 3256
QY 2341 CACTAAGATTTGCTGTAAGCCCGAGAGCATGTCGAAGTGAACCTGAAACGGGCTTTTGA 2400
DB 3257 CACTAAGATTTGCTGTAAGCCCGAGAGCATGTCGAAGTGAACCTGAAACGGGCTTTTGA 3316
QY 2401 CATGACCATGAAGATCTGGAAGGTGCTGAGGATGAGAACCCGACACAGGTGAGACC 2460
DB 3317 CATGACCATGAAGATCTGGAAGGTGCTGAGGATGAGAACCCGACACAGGTGAGACC 3376
QY 2461 CTGCGAGTGTGCGGTAAACATATTAGAACACGCTGTGATGCTGATGTGACCGAGGA 2520
DB 3377 CTGCGAGTGTGCGGTAAACATATTAGAACACGCTGTGATGCTGATGTGACCGAGGA 3436
QY 2521 GCTGAGGCCCCCATCACTTGTGTGCTGAGCTGACACCCGCTGAGTTGGCTGACGAGTGA 2580
DB 3437 GCTGAGGCCCCCATCACTTGTGTGCTGAGCTGACACCCGCTGAGTTGGCTGACGAGTGA 3496
QY 2581 AGATACAGATTGAG 2594
DB 3497 AGATACAGATTGAG 3510

RESULT 12
US-09-725-720-43
Sequence 43, Application US/09725720
Patent No. US20010049136A1
GENERAL INFORMATION:
APPLICANT: IMLER, Jean-Luc
APPLICANT: MEHTALI, Majid
APPLICANT: PAVIRANI, Andrea
TITLE OF INVENTION: DEFECTIVE ADENOVIRUSES AND CORRESPONDING
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: 1737 King Street, Suite 500
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22314-2756
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/725,720
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/379,452
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93 06482
FILING DATE: 28-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Dadio, Susan M.
REGISTRATION NUMBER: 40,373
REFERENCE/DOCKET NUMBER: 029395-002
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 35935 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-725-720-43

Query Match 100.0%; Score 2594; DB 9; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCATCTTACCTGCAACGAGGCTGCTTCCACCCAGTGAACGAGATGAAGAGCGT 60
DB 917 ATGCATCTTACCTGCAACGAGGCTGCTTCCACCCAGTGAACGAGATGAAGAGCGT 976
QY 61 GAGGAGTTTGTTAGATTATGAGAGACCCCGGACAGGTTGCAAGTCTTGTCTATTAT 120
DB 977 GAGGAGTTTGTTAGATTATGAGAGACCCCGGACAGGTTGCAAGTCTTGTCTATTAT 1036
QY 121 CACCGAGAAATACGGGAGACCCAGATATTATGTTGCTTGTCTATATAGACCTGT 180
DB 1037 CACCGAGAAATACGGGAGACCCAGATATTATGTTGCTTGTCTATATAGACCTGT 1096
QY 181 GGCATGTTTGCTCAGTAAGTGAATAATTATGGGACAGGAGTGAAGAGTGGGCTTG 240
DB 1097 GGCATGTTTGCTCAGTAAGTGAATAATTATGGGACAGGAGTGAAGAGTGGGCTTG 1156
QY 241 GTGTGTAATTTTATTTTAAATTTTACAGTTTGTGTTTAAAGATTTGTATTGTGA 300
DB 1157 GTGTGTAATTTTATTTTAAATTTTACAGTTTGTGTTTAAAGATTTGTATTGTGA 1216
QY 301 TTTTAAAGTCTGTGTCTGAACCTGAGCTGAGCCCGAGCCAGACCGAGCTG 360
DB 1217 TTTTAAAGTCTGTGTCTGAACCTGAGCTGAGCCCGAGCCAGACCGAGCTG 1276
QY 361 CAAGACCTACCCGCGCTTAAATGCGGCTGCTATCTGAGACGCGGACATCACCTG 420
DB 1277 CAAGACCTACCCGCGCTTAAATGCGGCTGCTATCTGAGACGCGGACATCACCTG 1336
QY 421 TGCTAGAGATGCAATAGTATGATGAGTATGATGATGATGATGATGATGATGATGATG 480
DB 1337 TGCTAGAGATGCAATAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 1396
QY 481 CTGAGATACACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
DB 1397 CTGAGATACACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1456
QY 541 GGGCTGCGAGGCTGTGGAATGATGAGAGCTGCTTAAAGAGACCTGAGGACCTTTGG 600
DB 1457 GGGCTGCGAGGCTGTGGAATGATGAGAGCTGCTTAAAGAGACCTGAGGACCTTTGG 1516
QY 601 ACTGAGCTGTAAACGCGCCAGGACCATAGGTGTAAACCTGTGATGCTGTGTGTTAA 660
DB 1517 ACTGAGCTGTAAACGCGCCAGGACCATAGGTGTAAACCTGTGATGCTGTGTGTTAA 1576
QY 661 CGCCTTGTGTTGCTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
DB 1577 CGCCTTGTGTTGCTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1636
QY 721 TGATGAGGCTGTAAAGGGGCGGGCTTAAAGGCTATATATGCGGCTGAGCTATCT 780

TYPE: DNA
ORGANISM: Human adenovirus type 5
US-09-782-378A-4

Query Match 100.0%; Score 2594; DB 9; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGCATCTTACCTGCGACGAGGCTGCTTTCCACCAGTACGACGAGAGTAAAGAGGT 60
|||||
1917 ATTCATCTTACCTGCGACGAGGCTGCTTTCCACCAGTACGACGAGAGTAAAGAGGT 976
61 GAGAGGTTGATGATTAATGATGAGAGACCCCGGGACAGGTGAGAGTCTTGCATTAAT 120
|||||
977 GAGAGGTTGATGATTAATGATGAGAGACCCCGGGACAGGTGAGAGTCTTGCATTAAT 1036
121 CACCGAGAGAAATACGGGGGACCCAGATTAATATGTTGCTTTGCTATATAGAGACTGT 180
1097 CACCGAGAGAAATACGGGGGACCCAGATTAATATGTTGCTTTGCTATATAGAGACTGT 1096
181 GGCATGTTTGTCTACAGTAAGTAAATTAATGAGCACTGGGTGATGAGTGGGTTTG 240
1097 GGCATGTTTGTCTACAGTAAGTAAATTAATGAGCACTGGGTGATGAGTGGGTTTG 1156
241 GGTGGTAAATTTTTTTTAAATTTTACAGTTTGTGGTTTAAAGATTTTGATTTGTA 300
1157 GGTGGTAAATTTTTTTTAAATTTTACAGTTTGTGGTTTAAAGATTTTGATTTGTA 1216
301 TTTTAAAAAGTCTGCTGTCTGAACCTGAGCCGAGCCGAGCAGAAACCGAGACTTG 360
1217 TTTTAAAAAGTCTGCTGTCTGAACCTGAGCCGAGCCGAGCAGAAACCGAGACTTG 1276
361 CAAGACTTACCGCGCGCTCTTAAATGCGCGCTGCTATCTTGAAGCGCCGACATCACTG 420
1277 CAAGACTTACCGCGCGCTCTTAAATGCGCGCTGCTATCTTGAAGCGCCGACATCACTG 1336
421 TGTCTAGAGATGCAATAGTATGTAACGGAATACCTGAGATTCGGCTCTTCAACACCTTC 480
1337 TGTCTAGAGATGCAATAGTATGTAACGGAATACCTGAGATTCGGCTCTTCAACACCTTC 1396
481 CTGAGATACACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
1397 CTGAGATACACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1456
541 GCGCTGCGCAGGCTGTGGAATGATTCAGAGACTTGTCTTACGAGCTGGGCAACTTTGG 600
1457 GCGCTGCGCAGGCTGTGGAATGATTCAGAGACTTGTCTTACGAGCTGGGCAACTTTGG 1516
601 ACTGAGCTGTAAACGCCCCAGGCCATTAAGGTGTAAACCTGTGATTTGGTGTGTAA 660
1517 ACTGAGCTGTAAACGCCCCAGGCCATTAAGGTGTAAACCTGTGATTTGGTGTGTAA 1576
661 CGCCTTTGTTGCTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
1577 CGCCTTTGTTGCTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1636
721 TGCATGCGTGTAAATGCGGCGGCTTAAAGGATATTAATGCGGCTGTAACT 780
1637 TGCATGCGTGTAAATGCGGCGGCTTAAAGGATATTAATGCGGCTGTAACT 1696
781 TGTGTAATCTGACCTCATGAGAGCTTGGAGCTTTGGAGATTTTCTGCTGTGCTA 840
1697 TGTGTAATCTGACCTCATGAGAGCTTGGAGCTTTGGAGATTTTCTGCTGTGCTA 1756
841 ACTGCTGGAACAGAGCTCTAACAGTACCTCTGCTTTTGAAGTTTCTGTGGGCTCAT 900
1757 ACTGCTGGAACAGAGCTCTAACAGTACCTCTGCTTTTGAAGTTTCTGTGGGCTCAT 1816
901 CCGCAGGCAAGTGAAGTCTGCAAGATTAAGAGATTAACAATGGGAAATTTGAAGACTTT 960
1817 CCGCAGGCAAGTGAAGTCTGCAAGATTAAGAGATTAACAATGGGAAATTTGAAGACTTT 1876
961 TGAATCTGTGTGAGCTGTTGATTTCTTGAATCTGGTCAACAAGCGCTTTCCAG 1020

DB 1877 TGAATCTGTGTGAGCTGTTGATTTCTTGAATCTGGTCAACAAGCGCTTTCCAG 1936
1021 AGAAGCTCATCAGACTTTGATTTTTCACACCGGGCGGCTGCGCTGCTGTGCTT 1080
1937 AGAAGCTCATCAGACTTTGATTTTTCACACCGGGCGGCTGCGCTGCTGTGCTT 1996
1081 TTTTGAAGTTTAAAGATTAATGAGAGCAAGAAACCATCTGAGCGGGGATTAACCTGC 1140
1997 TTTTGAAGTTTAAAGATTAATGAGAGCAAGAAACCATCTGAGCGGGGATTAACCTGC 2056
1141 TGGATTTTCTGGCCATGATCTGTGAGAGCGGTTGTGAGCAAGAAATGCGCTGCTAC 1200
2057 TGGATTTTCTGGCCATGATCTGTGAGAGCGGTTGTGAGCAAGAAATGCGCTGCTAC 2116
1201 TGTGTCTTCCGTCGCGCCCGGATTAATACCGAGAGAGACAGACAGACAGAGAG 1260
2117 TGTGTCTTCCGTCGCGCCCGGATTAATACCGAGAGAGACAGACAGACAGAGAG 2176
1281 AAGCCAGCGCGCGCGGAGAGAGAGCCCATGGAACCCGAGAGCCGCGCTGACCTTC 1320
2177 AAGCCAGCGCGCGCGGAGAGAGAGCCCATGGAACCCGAGAGCCGCGCTGACCTTC 2236
1321 GGGATGGAATGTTGTAACAGTGGCTGAACTGTATCCAGAACTGAGAGCGATTTTGAACAT 1380
2237 GGGATGGAATGTTGTAACAGTGGCTGAACTGTATCCAGAACTGAGAGCGATTTTGAACAT 2296
1381 TACAGAGATGAGGAGGAGGCTTAAAGGGGATTAAGAGGAGCGGGGCTTGTGAGGCTAC 1440
2297 TACAGAGATGAGGAGGAGGCTTAAAGGGGATTAAGAGGAGCGGGGCTTGTGAGGCTAC 2356
1441 AGAGAGGCTTNGAATCTAGCTTTTGAATTAATGACAGACACCGTCTGAGTATTAAC 1500
2357 AGAGAGGCTTNGAATCTAGCTTTTGAATTAATGACAGACACCGTCTGAGTATTAAC 2416
1501 TTTTCAACAGATCAAGGATTAATGAGCTTAATGAGCTGATCTGAGGCGAGAGTATTC 1560
2417 TTTTCAACAGATCAAGGATTAATGAGCTTAATGAGCTGATCTGAGGCGAGAGTATTC 2476
1561 CATAGAGAGCTGACCACTTAAGCTGCGAGCAGGAGGATTTTGAAGGCTATTAAG 1620
2477 CATAGAGAGCTGACCACTTAAGCTGCGAGCAGGAGGATTTTGAAGGCTATTAAG 2536
1621 GGTATATGCAAAAGGTGCACTTAAGCCAGATTCAGAGTCAAGATCAAGAACTTTGAAA 1680
2537 GGTATATGCAAAAGGTGCACTTAAGCCAGATTCAGAGTCAAGATCAAGAACTTTGAAA 2596
1681 TATCAGAAATTTGTTGCTAATTTCTGGGAAACGGGGCCGAGGTGAGATTAAGTACGAGAGA 1740
2597 TATCAGAAATTTGTTGCTAATTTCTGGGAAACGGGGCCGAGGTGAGATTAAGTACGAGAGA 2656
1741 TAGGGTGGCTTTTGAAGTATGATGATTAATATGAGCCGGGGGTGCTTGGCATGAGACGG 1800
2657 TAGGGTGGCTTTTGAAGTATGATGATTAATATGAGCCGGGGGTGCTTGGCATGAGACGG 2716
1801 GGTGTTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1860
2717 GGTGTTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2776
1861 CAATACCAACCTTAATCTTACACCGGTAAAGCTTAAAGGTTTAAACAATACCTGTGAGGA 1920
2777 CAATACCAACCTTAATCTTACACCGGTAAAGCTTAAAGGTTTAAACAATACCTGTGAGGA 2836
1921 AGCTGAGACGATGTAAGGTTTGGGGCTGTGCTTTTATCTGCTGTAAGGGGGTGTGT 1980
2837 AGCTGAGACGATGTAAGGTTTGGGGCTGTGCTTTTATCTGCTGTAAGGGGGTGTGT 2896
1981 GTGTGCGCCCAAAAGCAGGCTTCAATTAAGAAATGCTCTTTGAAAGGTGATCTTTGGG 2040
2897 GTGTGCGCCCAAAAGCAGGCTTCAATTAAGAAATGCTCTTTGAAAGGTGATCTTTGGG 2096
2041 TATCTGTCTGAGAGGTAATCTCAGGGTGGCACAAGTGGCCCTCGACCTGTGCTGCTT 2100

Db 2957 TATCCTGCTGTAGGGTAACTCCAGAGGTGCGCAACAATGTGGCTCCGACTGTGGTTCCT 3016
Qy 2101 CATCTAGTGAAGGCGTGTGTGATTAACATTAACATGTAATGTGGCACTCGGAGGA 2160
Db 3017 CATCTAGTGAAGGCGTGTGTGATTAACATTAACATGTAATGTGGCACTCGGAGGA 3076
Qy 2161 CAGGAGCTCTCAGATGTGACCTGCTCGGACGCAACTGTCACTGCTGGAAGACATTTCA 2220
Db 3077 CAGGAGCTCTCAGATGTGACCTGCTCGGACGCAACTGTCACTGCTGGAAGACATTTCA 3136
Qy 2221 CGTAGCCAGCCACTCTGCGAAGCCCTGCGCAAGTGTGGAGATTAACATTAAGTACCCGCTG 2280
Db 3137 CGTAGCCAGCCACTCTGCGAAGCCCTGCGCAAGTGTGGAGATTAACATTAAGTACCCGCTG 3196
Qy 2281 TTCTGTGATTTTGGGTAAACAGAGAGGGGGTGTTCCTTAACCTTAACAAATGCAATTTGAGTCA 2340
Db 3197 TTCTGTGATTTTGGGTAAACAGAGAGGGGGTGTTCCTTAACCTTAACAAATGCAATTTGAGTCA 3256
Qy 2341 CACTAAGATATTTGCTTGAGCCCGAGAGAGCATGTCCAAAGGTGAACCTGAACCGGGTGTTTGA 2400
Db 3257 CACTAAGATATTTGCTTGAGCCCGAGAGAGCATGTCCAAAGGTGAACCTGAACCGGGTGTTTGA 3316
Qy 2401 CATGACCAATGAAGATCTTGAAAGTGTCTGAGGTACGATGAGACCCGACACAGGTGCAAGCC 2460
Db 3317 CATGACCAATGAAGATCTTGAAAGTGTCTGAGGTACGATGAGACCCGACACAGGTGCAAGCC 3376
Qy 2461 CTGGAAGTGTGCGGTAAACATTTAAGAACACAGCCTGTGATGTGCTGATGTGACCGAGGA 2520
Db 3377 CTGGAAGTGTGCGGTAAACATTTAAGAACACAGCCTGTGATGTGCTGATGTGACCGAGGA 3436
Qy 2521 GCTGAGGCCCGATCACTTGTTGCTGACCTGACACCGCCTGAGTTTGCTCTAGCGATGA 2580
Db 3437 GCTGAGGCCCGATCACTTGTTGCTGACCTGACACCGCCTGAGTTTGCTCTAGCGATGA 3496
Qy 2581 AGATACAGATTGAG 2594
Db 3497 AGATACAGATTGAG 3510

RESULT 14
US-09-782-378A-5
; Sequence 5, Application US/09782378A
; Patent No. US20020102731A1
; GENERAL INFORMATION:
; APPLICANT: Hearing, Patrick
; APPLICANT: Bahou, Wadie
; APPLICANT: Sandelon, Ziv
; APPLICANT: Gnatenko, Dmitri
; TITLE OF INVENTION: Adenoviral Vectors
; FILE REFERENCE: STONYB-04970
; CURRENT APPLICATION NUMBER: US/09/782,378A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/237,747
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 35935
; TYPE: DNA
; ORGANISM: Human adenovirus type 5
; US-09-782-378A-5

Query Match 100.0%; Score 2594; DB 9; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATCGATCTTACCTGCGACGAGGCTGGCTTTCACCAAGCTGACGAGAGATGAAGAGGCT 60
Db 917 ATCGATCTTACCTGCGACGAGGCTGGCTTTCACCAAGCTGACGAGAGATGAAGAGGCT 976
Qy 61 GAGAGATTGTGTTAGATTATGTGAGACACCCCGGGACCGTTGCGAGGCTCTTGTCAATAT 120
Db 977 GAGAGATTGTGTTAGATTATGTGAGACACCCCGGGACCGTTGCGAGGCTCTTGTCAATAT 1036

Qy 121 CACCGAGGAATACGGGGGAGCCGAGATTAATGNGTTGACTTTTGCTATAAGGACCTGT 180
Db 1037 CACCGAGGAATACGGGGGAGCCGAGATTAATGNGTTGACTTTTGCTATAAGGACCTGT 1096
Qy 181 GGCATGTTTGTCTACAGTAAGTGAATTAATGCGCAGTGGGTGATAGAGTGGGTTTG 240
Db 1097 GGCATGTTTGTCTACAGTAAGTGAATTAATGCGCAGTGGGTGATAGAGTGGGTTTG 1156
Qy 241 GTGTGTAAATTTTTTTTTTAATTTTACAGTTTGTGTGTTTAAAGAAATTTGTATTGGA 300
Db 1157 GTGTGTAAATTTTTTTTTTAATTTTACAGTTTGTGTGTTTAAAGAAATTTGTATTGGA 1216
Qy 301 TTTTTTAAAGGCTGTGTCTGAACCTGAGCCTGAGCCCGAGACGAGAACCGGAGCCTG 360
Db 1217 TTTTTTAAAGGCTGTGTCTGAACCTGAGCCTGAGCCCGAGACGAGAACCGGAGCCTG 1276
Qy 361 CAAGACCTACCCGCGTCTTAAATGCGCGCTGTCTATCTTGAGACGCGCGACATCACTG 420
Db 1277 CAAGACCTACCCGCGTCTTAAATGCGCGCTGTCTATCTTGAGACGCGCGACATCACTG 1336
Qy 421 TGTCTAAGAAATGCAATGTAATGTAACGATAGCTGTGACTCGGTCCTTTCTAACAACCTC 480
Db 1337 TGTCTAAGAAATGCAATGTAATGTAACGATAGCTGTGACTCGGTCCTTTCTAACAACCTC 1396
Qy 481 CTGAGATTAACCCGCGTGTGCGCGCTGCGCCATTAACAGCTTGGCGTGAAGTGGTG 540
Db 1397 CTGAGATTAACCCGCGTGTGCGCGCTGCGCCATTAACAGCTTGGCGTGAAGTGGTG 1456
Qy 541 GGCCTGCGCAGGCTGTGGAATGTATCGAGGACTTGTAAAGAGCCTGGGCAACTTTTG 600
Db 1457 GGCCTGCGCAGGCTGTGGAATGTATCGAGGACTTGTAAAGAGCCTGGGCAACTTTTG 1516
Qy 601 ACTTGAAGCTGTAAACGCGCCAGGCGCATAGGTGTAAACCTGTGATGTGTGTGTGTTAA 660
Db 1517 ACTTGAAGCTGTAAACGCGCCAGGCGCATAGGTGTAAACCTGTGATGTGTGTGTGTTAA 1576
Qy 661 CGCCTTGTGTTGCTGAATGAGTTGATGTAAGTTAATTAAGGGTGAAGATAATGTTAACT 720
Db 1577 CGCCTTGTGTTGCTGAATGAGTTGATGTAAGTTAATTAAGGGTGAAGATAATGTTAACT 1636
Qy 721 TGCATGCGGTGTAAATGGGCGGGGCTTAAAGGGTATATATATGCGCGGTGCTAATCT 780
Db 1537 TGCATGCGGTGTAAATGGGCGGGGCTTAAAGGGTATATATATGCGCGGTGCTAATCT 1696
Qy 781 TGGTTAATCTGACCTCATAGAGGCTTGGAGTGTGTGAAAGATTTTTCGTGTGCTGA 840
Db 1697 TGGTTAATCTGACCTCATAGAGGCTTGGAGTGTGTGAAAGATTTTTCGTGTGCTGA 1756
Qy 841 ACTTGTGGAACAGAGCTCTTAACAGTACTCTTGTGTTGAGGTTTCTGTGGGCTCAT 900
Db 1757 ACTTGTGGAACAGAGCTCTTAACAGTACTCTTGTGTTGAGGTTTCTGTGGGCTCAT 1816
Qy 901 CCCAGGCAAGTTAGTGTGCAATTAAGAGATTAACAAGTGGAAATTTGAAGAGCTTT 960
Db 1817 CCCAGGCAAGTTAGTGTGCAATTAAGAGATTAACAAGTGGAAATTTGAAGAGCTTT 1876
Qy 961 TGAATCTGTGTGAGCTGTTTGAATCTTGTGAATCTGGGTCAACAGGCGCTTTTCCAG 1020
Db 1877 TGAATCTGTGTGAGCTGTTTGAATCTTGTGAATCTGGGTCAACAGGCGCTTTTCCAG 1936
Qy 1021 AGAAGTCATCAAGACTTTGATTTTTCACACCGGGGCGGCTGCGGCTGTGTGCTT 1080
Db 1937 AGAAGTCATCAAGACTTTGATTTTTCACACCGGGGCGGCTGCGGCTGTGTGCTT 1996
Qy 1081 TTTTGAATTTTAAAGATTAATGAGCGAAGAAACCATCTGAGCGGGGGTATCTGC 1140
Db 1997 TTTTGAATTTTAAAGATTAATGAGCGAAGAAACCATCTGAGCGGGGGTATCTGC 2056
Qy 1141 TGAATTTTTCGCAATGATCTGTGAGAGAGGCTTGTGAGACACAAGAAATGCGCTGTAC 1200
Db 2057 TGAATTTTTCGCAATGATCTGTGAGAGAGGCTTGTGAGACACAAGAAATGCGCTGTAC 2116

QY	1201	IGTGTCTTCGGTCCGCCCGGAGTAATACCGAGCGAGACGACGACGACGAGG	1260
Db	2117	TGTGTCTTCGGTCCGCCCGGAGTAATACCGAGCGAGACGACGACGAGG	2176
QY	1261	AAGCAGCGCGCGCGGACGAGACGACGCCATGMAACCCGAGCGCGGCTGACCTC	1320
Db	2177	AAGCAGCGCGCGCGGACGAGACGACGCCATGMAACCCGAGCGCGGCTGACCTC	2236
QY	1331	GGGAATGAATGTTGTACAGGTGGCTGAACTGTATCCAGACTGAGCGCATTTTGACAT	1380
Db	2237	GGGAATGAATGTTGTACAGGTGGCTGAACTGTATCCAGACTGAGCGCATTTTGACAT	2296
QY	1381	TACAGAGATGGGCGAGGGGCTTAAAGGGGGTAAAGGGAGCGGGGGCTTTGAGGCTAC	1440
Db	2287	TACAGAGATGGGCGAGGGGCTTAAAGGGGGTAAAGGGAGCGGGGGCTTTGAGGCTAC	2356
QY	1441	AGAGAGGCTAGSAATCTAGCTTTTAGCTTAATGACACGACACCGCTCTGAGTGAATTAC	1500
Db	2357	AGAGAGGCTAGSAATCTAGCTTTTAGCTTAATGACACGACACCGCTCTGAGTGAATTAC	2416
QY	1501	TTTTCAACAGATCAAGATTAATTCGCTTAATGAGCTTGATCTGCGGACGAAGTATTC	1560
Db	2417	TTTTCAACAGATCAAGATTAATTCGCTTAATGAGCTTGATCTGCGGACGAAGTATTC	2476
QY	1561	CATGAGAGCGTACCACTTACTGCTGCTGACACCGAGGGATGATTTTGAGAGGCTTAAG	1620
Db	2477	CATGAGAGCGTACCACTTACTGCTGCTGACACCGAGGGATGATTTTGAGAGGCTTAAG	2536
QY	1621	GGTATATCAAGAAGTGGCACTTAAGCCAGATTGCAAGTACAAAGATCAGCAAACTGTGAAA	1680
Db	2537	GGTATATCAAGAAGTGGCACTTAAGCCAGATTGCAAGTACAAAGATCAGCAAACTGTGAAA	2596
QY	1681	TATCAGGAATTTGTGCTACATTTCTGGGAACGGGGCCGAGGTGAGATAGTATACGAGGA	1740
Db	2597	TATCAGGAATTTGTGCTACATTTCTGGGAACGGGGCCGAGGTGAGATAGTATACGAGGA	2656
QY	1741	TAGGTTGGCTTTAGATGTACAGATGAATATATGTGGCCGGGGGTGCTTGGCATGAGACG	1800
Db	2657	TAGGTTGGCTTTAGATGTACAGATGAATATATGTGGCCGGGGGTGCTTGGCATGAGACG	2716
QY	1801	GGTGGTATATATGATGTAGAGTATTAACAGGCCCAATTTTAGCGGTACGGTTTCCTGGC	1860
Db	2717	GGTGGTATATATGATGTAGAGTATTAACAGGCCCAATTTTAGCGGTACGGTTTCCTGGC	2776
QY	1861	CAATACCAACCTTATCTTACACGCGTGAAGCTTCTATGGGTTTAAACAATCCTGTGCGA	1920
Db	2777	CAATACCAACCTTATCTTACACGCGTGAAGCTTCTATGGGTTTAAACAATCCTGTGCGA	2836
QY	1921	AGCCTGGAACCATGTAGAGGTTCCGGGCTGTGCTTTTACTGCTGCTGGAAGGGGGTGT	1980
Db	2837	AGCCTGGAACCATGTAGAGGTTCCGGGCTGTGCTTTTACTGCTGCTGGAAGGGGGTGT	2896
QY	1981	GTTGCGCCCCAAAAGCGGGGCTTAAATAAATGCTCTTTGAAAGGTACTCTGGG	2040
Db	2897	GTTGCGCCCCAAAAGCGGGGCTTAAATAAATGCTCTTTGAAAGGTACTCTGGG	2956
QY	2041	TATCTCGTCTGAGGGTAACTCCAGGGTGGCCACAAATGTGGCTCCGACTGTGTGCTT	2100
Db	2957	TATCTCGTCTGAGGGTAACTCCAGGGTGGCCACAAATGTGGCTCCGACTGTGTGCTT	3016
QY	2101	CATGCTAGTGAATAAGCGTGGCTGTGATTAAGCATTAACATGTATGTGGCAATCTGCGAGA	2160
Db	3017	CATGCTAGTGAATAAGCGTGGCTGTGATTAAGCATTAACATGTATGTGGCAATCTGCGAGA	3076
QY	2161	CAGGGGCTCTGAGATGCTGACCTGTCTGGAGCGCAATGTCACTGTCTGAAGACATTTCA	2220
Db	3077	CAGGGGCTCTGAGATGCTGACCTGTCTGGAGCGCAATGTCACTGTCTGAAGACATTTCA	3136
QY	2221	CGTAGCCAGCACTCTCGCAAGGCTGGCCAGTGTTTGAGCATTAACATCTGACCCGCTG	2280
Db	3137	CGTAGCCAGCACTCTCGCAAGGCTGGCCAGTGTTTGAGCATTAACATCTGACCCGCTG	3196
QY	2281	TTCTCTTGCAATTTGGGTAAACGAGAGGGGGGTGTCTTCACTTACCAATGCAATTTGAGTCA	2340

Query	Match	Similarity	Score	DB	Length	Matches
Best Local Similarity	100.0%	Score 2594	DB 10	Length 35935		
Matches 2594	Conservative	0	Mismatches	0	Indels	0
					Gaps	0

OY 1 ATGCATCTTACCTGCGACGAGGCTGGCTTTCCACCAGTGAAGAGAGAGAGAGGCT 60
Db 917 ATGCATCTTACCTGCGACGAGGCTGGCTTTCCACCAGTGAAGAGAGAGAGGCT 976
OY 61 GAGGAGTTTGTGTAGATTATGTGAGAGACCCCGGGACGGTTGCGAGCTTGTCAATAT 120
Db 977 GAGGAGTTTGTGTAGATTATGTGAGAGACCCCGGGACGGTTGCGAGCTTGTCAATAT 1036
OY 121 CACCGAGGAAATACGGGGGACCCAGATATATGTGTGCTTGTCTATATGAGACCTGT 180
Db 1037 CACCGAGGAAATACGGGGGACCCAGATATATGTGTGCTTGTCTATATGAGACCTGT 1096
OY 181 GGCATGTTTGTCTACATGATGAGAAATTTATGGGAGAGGGGATGAGTGTTGGGTTTG 240
Db 1097 GGCATGTTTGTCTACATGATGAGAAATTTATGGGAGAGGGGATGAGTGTTGGGTTTG 1156
OY 241 GTGTGTAAATTTTTTTTTTAAATTTTACAGTTTGTGTGTTTAAAGAAATTTGTATTGTA 300
Db 1157 GTGTGTAAATTTTTTTTTTAAATTTTACAGTTTGTGTGTTTAAAGAAATTTGTATTGTA 1216
OY 301 TTTTAAAAAGTCTGTGTCTGAACCTGAGCTGAGCCGAGCCGAGACCGGAGCTTG 360
Db 1217 TTTTAAAAAGTCTGTGTCTGAACCTGAGCTGAGCCGAGCCGAGACCGGAGCTTG 1276
OY 361 CAAGACCTAACCCGCGCTCTAAATGSGGCGCTGCTATCTGAGAGCCGCAATCACTG 420
Db 1277 CAAGACCTAACCCGCGCTCTAAATGSGGCGCTGCTATCTGAGAGCCGCAATCACTG 1336
OY 421 TGTCTAGAGAAATGCAATAGTATGATAGATAGCTGATGATCTCGGTCTCTTAACAACCTC 480
Db 1337 TGTCTAGAGAAATGCAATAGTATGATAGATAGCTGATGATCTCGGTCTCTTAACAACCTC 1396
OY 481 CTGAGATACACCCGGTGGTCCCCGTGTGCCCCATTTAAACCAAGTTCCGTGAGAGTTGGT 540
Db 1397 CTGAGATACACCCGGTGGTCCCCGTGTGCCCCATTTAAACCAAGTTCCGTGAGAGTTGGT 1456
OY 541 GGGCGTGCAGGCGTGTGAATGTATCGAGGACTTGCTTAAGAGCTTGGGACCTTTGG 600
Db 1457 GGGCGTGCAGGCGTGTGAATGTATCGAGGACTTGCTTAAGAGCTTGGGACCTTTGG 1516
OY 601 ACTTGAGCTGTAAACGCCACGAGCCATTAAGGTGTAAACCTGTGATTTGGTGTGTGTTAA 660
Db 1517 ACTTGAGCTGTAAACGCCACGAGCCATTAAGGTGTAAACCTGTGATTTGGTGTGTGTTAA 1576
OY 661 CGCTTTGTTGCTGAATGAGTTGATGTAAATTATTAAGGGTGAATATGTTTAACT 720
Db 1577 CGCTTTGTTGCTGAATGAGTTGATGTAAATTATTAAGGGTGAATATGTTTAACT 1636
OY 721 TGCATGGGCGTGTAAATGGGGCGGGGCTTAAAGGATATATAATGGCGGTGGGCTAACT 780
Db 1637 TGCATGGGCGTGTAAATGGGGCGGGGCTTAAAGGATATATAATGGCGGTGGGCTAACT 1696
OY 781 TGTATACATCTGACCTCATGAGAGCTTGGAGTGTGTTGGAAGATTTTCTGCTGTGCGTA 840
Db 1697 TGTATACATCTGACCTCATGAGAGCTTGGAGTGTGTTGGAAGATTTTCTGCTGTGCGTA 1756
OY 841 ACTTGCTGAACAGAGCTCTAAACATTAACCTTGTGTTTGAAGTTTCTGTGGGCTCAT 900
Db 1757 ACTTGCTGAACAGAGCTCTAAACATTAACCTTGTGTTTGAAGTTTCTGTGGGCTCAT 1816
OY 901 CCCAGGCAAGTGTACTGCAAGATTAAGGAGGATTAACAAGTGGGAATTTGAAGGCTTT 960
Db 1817 CCCAGGCAAGTGTACTGCAAGATTAAGGAGGATTAACAAGTGGGAATTTGAAGGCTTT 1876
OY 961 TGAATCTGTGTGAGCTGTTGATCTTTGAATCTGGGTCAACGAGCGCTTTTCCAG 1020
Db 1877 TGAATCTGTGTGAGCTGTTGATCTTTGAATCTGGGTCAACGAGCGCTTTTCCAG 1936
OY 1021 AGAAGCTATCAAGACTTTTGAATTTTTCACACCGGGGCGGCTGCGCTGTGTTGCTT 1080
Db 1937 AGAAGCTATCAAGACTTTTGAATTTTTCACACCGGGGCGGCTGCGCTGTGTTGCTT 1996

OY 1081 TTTTGAATTTTATTAAGATTAATGAGCGAAGAAACCAATCTGAGCGGGGCTACTGC 1140
Db 1997 TTTTGAATTTTATTAAGATTAATGAGCGAAGAAACCAATCTGAGCGGGGCTACTGC 2056
OY 1141 TGAATTTTCTGGCCATCATCTGTGAGAGCGGTTGTGAACACAAAGATGCTGCTTAC 1200
Db 2057 TGAATTTTCTGGCCATCATCTGTGAGAGCGGTTGTGAACACAAAGATGCTGCTTAC 2116
OY 1201 TGTGTCTTCCTCCCTCCGCGCCGATTAATACGAGGAGGAGACACAGAGAGAGAGG 1260
Db 2117 TGTGTCTTCCTCCCTCCGCGCCGATTAATACGAGGAGGAGACACAGAGAGAGAGG 2176
OY 1261 AAGCCAGCGCGCGCGCAGAGAGAGCCATGAACCCGAGAGCGGCTGTGACCTTC 1320
Db 2177 AAGCCAGCGCGCGCGCAGAGAGAGCCATGAACCCGAGAGCGGCTGTGACCTTC 2236
OY 1321 GGAATGAATGTTGTACAGGTGGCTGAACCTGTATCCAGAACTGAGACGCAATTTTGACAT 1380
Db 2237 GGAATGAATGTTGTACAGGTGGCTGAACCTGTATCCAGAACTGAGACGCAATTTTGACAT 2296
OY 1381 TACAGAGATGGGAGGCGCTAAAGGGGCTAAAGAGGAGGGGGGCTGTGAGGCTAC 1440
Db 2297 TACAGAGATGGGAGGCGCTAAAGGGGCTAAAGAGGAGGGGGCTGTGAGGCTAC 2356
OY 1441 AGAGAGGCTAGAAATAGCTTTTACCTTAATGACCAACACCGTCTGAGTATTAAC 1500
Db 2357 AGAGAGGCTAGAAATAGCTTTTACCTTAATGACCAACACCGTCTGAGTATTAAC 2416
OY 1501 TTTTCAACAGATCAAGATTAATGCGCTAATGAGCTTGTGCTGCGCAAGATATTC 1560
Db 2417 TTTTCAACAGATCAAGATTAATGCGCTAATGAGCTTGTGCTGCGCAAGATATTC 2476
OY 1561 CATAGACAGCTGACCACTTAATGCGCTGACGCGGAGGAGATTTTGAAGGCGCTATTAG 1620
Db 2477 CATAGACAGCTGACCACTTAATGCGCTGACGCGGAGGAGATTTTGAAGGCGCTATTAG 2536
OY 1621 GGTATATGCAAGGTGACACTTAAGCCAGATTTGCAATGACATCAAGATCAACAACTTGTAA 1680
Db 2537 GGTATATGCAAGGTGACACTTAAGCCAGATTTGCAATGACATCAAGATCAACAACTTGTAA 2596
OY 1681 TATCAGGAATTTGTTCTACATTTCTGAGAAACGGGGCGAGGTGAGATGATACGAGGA 1740
Db 2597 TATCAGGAATTTGTTCTACATTTCTGAGAAACGGGGCGAGGTGAGATGATACGAGGA 2656
OY 1741 TAGGCTGCGCTTTAGATGTAGCATGATTAATATGTGCGGGGGTGCCTGGCATGGAAG 1800
Db 2657 TAGGCTGCGCTTTAGATGTAGCATGATTAATATGTGCGGGGGTGCCTGGCATGGAAG 2716
OY 1801 GGTGTTATTTATGAATGATGAAGTTTACTGGCCCCAATTTTACGGGTACGTTTTCTGCGC 1860
Db 2717 GGTGTTATTTATGAATGATGAAGTTTACTGGCCCCAATTTTACGGGTACGTTTTCTGCGC 2776
OY 1861 CAATACCAACCTTATCTTACAGGTGTAGGCTTCTATGGGTTTAACAATACCTGTGGA 1920
Db 2777 CAATACCAACCTTATCTTACAGGTGTAGGCTTCTATGGGTTTAACAATACCTGTGGA 2836
OY 1921 AGCTTGACCGATGTAAAGGTTGCGGGCTGCTTTTACATGCTGCTGGAAGGGGGTGT 1980
Db 2837 AGCTTGACCGATGTAAAGGTTGCGGGCTGCTTTTACATGCTGCTGGAAGGGGGTGT 2896
OY 1981 GTGTGCGCCCAAAAGCAGGGCTTCAATTAAGAAATGCTCTTTGAAAGGTATACCTTGG 2040
Db 2897 GTGTGCGCCCAAAAGCAGGGCTTCAATTAAGAAATGCTCTTTGAAAGGTATACCTTGG 2956
OY 2041 TATCTGTCTGAGGGTAACTTCAGGGTGGCGCAATGTGCGCTTCCGACTGTGTTGCTT 2100
Db 2957 TATCTGTCTGAGGGTAACTTCAGGGTGGCGCAATGTGCGCTTCCGACTGTGTTGCTT 3016
OY 2101 CATGCTAGTGAAGACGTGCTGTGATTAAGCAATTAATGTGTAGTGGCACTGCGAGGA 2160
Db 3017 CATGCTAGTGAAGACGTGCTGTGATTAAGCAATTAATGTGTAGTGGCACTGCGAGGA 3076
OY 2161 CAGGCGCTCTCAGATGTGACTGTGCGAGCGCACTGTCACTGCTGAAGACCATTTCA 2220

Db	3077	CAGGCGCTCTGAGTGTGACCTGCTCGGACGGCACTGTCACTGCTGGAAGCATTCA	3136
OY	2221	CGTACCCAGCCACTCTGCGAAGGCTGCGCACTGTTTGAGCATTAACATCTGACCCGCTG	2280
Db	3137	CGTAGCCAGCCACTCTCGCAAGGCTGCGCACTGTTTGAGCATTAACATCTGACCCGCTG	3196
OY	2281	TTCCCTTGATTTGGGTACAGAGGGGGGTGTTCTTACCTTACCAATGCAATTTGAGTCA	2340
Db	3197	TTCCCTTGATTTGGGTACAGAGGGGGGTGTTCTTACCTTACCAATGCAATTTGAGTCA	3256
OY	2341	CACCTAAGATATTGCTTGAGCCCGAGAGCATGTCCAAGGTGAACCTGAACGGGGTGTGTA	2400
Db	3257	CACCTAAGATATTGCTTGAGCCCGAGAGCATGTCCAAGGTGAACCTGAACGGGGTGTGTA	3316
OY	2401	CATGACATGAAAGATCTGGAAGGTGCTGAGGTACGATGAGACCCGACCAAGGTGCAGACC	2460
Db	3317	CATGACATGAAAGATCTGGAAGGTGCTGAGGTACGATGAGACCCGACCAAGGTGCAGACC	3376
OY	2461	CTGCGAGTGTGGCGGTAAACATATTAGAACCAAGCTGTGATGCTGATGTGACCGAGGA	2520
Db	3377	CTGCGAGTGTGGCGGTAAACATATTAGAACCAAGCTGTGATGCTGATGTGACCGAGGA	3436
OY	2521	GCTGAGGCCCGATCACTTGTGCTGCTGCAACCGCGCTGAGTTTGCTCTAGCGATGA	2580
Db	3437	GCTGAGGCCCGATCACTTGTGCTGCTGCAACCGCGCTGAGTTTGCTCTAGCGATGA	3496
OY	2581	AGATACAGATTGAG	2594
Db	3497	AGATACAGATTGAG	3510

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